

EGFR BINDING COMPLEX AND METHOD OF MAKING AND USING THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of the filing date of U.S. Provisional Application Ser. No. 63/081,315 filed September 21, 2020, and U.S. Provisional Application Ser. No. 63/109,877 filed November 5, 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 cancer therapy using antibodies, and more particularly relates to making and using multi-specific antibodies.

BACKGROUND

Cetuximab is a chimeric (mouse/human) monoclonal antibody targeting the human epidermal growth factor receptor (EGFR). It was approved in the US and EU in 2004 for treatment of colorectal cancer and is also used to treat head and neck cancer.¹⁻³ In addition to the mAb, cetuximab has also been used in T-cell redirecting bispecific antibodies,⁴ antibody-peptide fusions, and antibody-drug conjugates.⁵

Cetuximab can bind to domain III of the extracellular domain of EGFR that is often overexpressed on tumor cells. The binding of cetuximab on tumor cells competitively inhibits binding of EGF and other ligands, prevents EGFR from dimerization, and prohibits receptor tyrosine autophosphorylation. As a result of inhibition and reduced EGFR-mediated signaling, the binding of cetuximab effectively downregulates tumor cell proliferation, angiogenesis, and metastasis while inducing apoptosis. In addition to targeting EGFR, the Fc domain of cetuximab can bind to CD16a and other Fc receptors and recruit and activate immune mechanisms, such as antibody-dependent cellular cytotoxicity.⁴ These anti-tumor properties of cetuximab are highly desirable for developing combinational therapies, either as a single agent or a component of regimen. However, there is a point of concern that cetuximab's variable regions (VH/Vk) remain on a mouse framework since its isolation from mouse hybridoma. It has been shown that the use of mouse sequences, such as mouse VH/Vk, can increase incidence of immunogenicity when proteins are administered to human patients. Thus, a protein therapeutics with humanized VH/Vk regions may decrease the risk of cetuximab-derived immunogenicity in humans.

SUMMARY

The following summary is illustrative only and is not intended to be in any way limiting. In addition to the illustrative aspects, embodiments, and features described above, further aspects, embodiments, and features will become apparent by reference to the drawings and the following detailed description.

The application provides, among others, binding domains and peptides having binding specificity to human epithelium growth factor receptor (EGFR), antibody-like proteins incorporating the anti-EGFR binding domains and peptides as disclosed herein, immunoconjugates and pharmaceutical compositions incorporating the anti-EGFR binding

domains and peptides as disclosed herein, methods of making and using such anti-EGFR binding domains, peptides and antibody-like proteins. In one embodiment, the anti-EGFR antibody-like proteins including antibodies, monoclonal antibodies, humanized antibodies, or chimeric antibodies. In one embodiment, the anti-EGFR antibody may be monospecific or multi-specific. In one embodiment, the multi-specific anti-EGFR antibody may be bispecific, tri-specific, tetra-specific, penta-specific, or hexa-specific. In one embodiment, the anti-EGFR antibody may be symmetric or asymmetric.

In one aspect, the application provides human EGFR binding peptide having a binding specificity to human EGFR. The peptide may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 57, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, a combination thereof.

In one embodiment, the EGFR binding peptide includes a variable heavy (VH) chain and a variable light (VL) chain. In one embodiment, the VH chains comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41. In one embodiment, the VL chain comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 3, 7, 11, 15, 19, 23, 27, 31, 35, 39, 43.

In one embodiment, the EGFR binding peptide includes a scFv domain and the scFv domain comprises the VH chain and VL chain as disclosed herein.

In one embodiment, the application provides an anti-EGFR scFv domain or peptides forming such scFv domain. In one embodiment, the scFv domain comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 57, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83. In one embodiment, the scFv domain comprises the VH chain and the VL chain as disclosed herein.

In one embodiment, the EGFR binding peptide may include a histidine residue linked to at least one end of the scFv domain (for example, ScFV-HIS). In one embodiment, the EGFR binding peptide may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to 57.

In one embodiment, the EGFR binding peptide may include a Fab domain, and the Fab domain comprises the VH chain and the VL chain as disclosed herein. In one embodiment, the EGFR binding peptide may further include a Fc domain linked to the Fab domain to provide a Fab-monoFc fusion protein. In one embodiment, the Fc domain comprises a sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NO. 45 and 47.

In another aspect, the application provides an antibody-like protein having a binding specificity to human EGFR. The antibody-like protein may include an EGFR binding domain having a variable heavy (VH) chain and a variable light (VL) chain. In one embodiment, the VH chains

comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, or 41. In one embodiment, the VL chain may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 3, 7, 11, 15, 19, 23, 27, 31, 35, 39, or 43.

In one embodiment, the antibody-like protein may include a scFv domain having an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, or 83.

In one embodiment, the antibody-like protein may be a monospecific antibody. In one embodiment, the antibody may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 137, 139, 141, 143; 141, 149, 151, 139, 145, 147 or a combination thereof. In one embodiment, the monospecific antibody may include pairs of light chains and heavy chains, or fragments thereof selected from the sequence combinations of SEQ ID NO. 137 and 139; 141 and 143; 141 and 149; 151 and 139; 145 and 147.

In one embodiment, the antibody-like protein may have a binding specificity to at least 2 different antigens selected from a tumor antigen, an immune signaling antigen, or a combination thereof.

In one embodiment, the antibody-like protein may be a bispecific antibody. In one embodiment, the bispecific antibody may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 137, 145, 139, 147, 141, 145, 143, 147, 141, 145, 149, 147, 151, 145, 139, 147 or a combination thereof. In one embodiment, the bispecific antibody may include the combinations of light chains and heavy chains (or fragments thereof) selected from the sequence combinations of SEQ ID NO. 137 and 145 and 139 and 147; 141 and 145 and 143 and 147; 141 and 145 and 149 and 147; 151 and 145 and 139 and 147.

In one embodiment, the antibody-like protein may have a binding specificity to at least 3 different antigens selected from a tumor antigen, an immune signaling antigen, or a combination thereof.

In one embodiment, the antibody-like protein may have a binding specificity to at least 4 different antigens selected from a tumor antigen, an immune signaling antigen, or a combination thereof.

In one embodiment, the antibody-like protein may have a binding specificity to at least 5 different antigens selected from a tumor antigen, an immune signaling antigen, or a combination thereof. In one embodiment, the antibody-like protein may be a penta-specific antibody.

In one embodiment, the penta-specific antibody may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 or a combination thereof. In one embodiment, the penta-specific antibody may include pairs of light chains and heavy chains or

fragments thereof selected from the sequence combinations of SEQ ID NO. 85 and 87; 89 and 91; 93 and 95; 97 and 99; 101 and 103; 105 and 107.

In one embodiment, the antibody-like protein may have a binding specificity to at least 6 different antigens selected from a tumor antigen, an immune signaling antigen, or a combination thereof. In one embodiment, the antibody-like protein may be a hexa-specific antibody.

In one embodiment, the hexa-specific antibody may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 109, 111, 113, 115, 117, 119 or a combination thereof. In one embodiment, the hexa-specific antibody may include a combination of light chains and heavy chain or fragments thereof selected from the combination of SEQ ID NO. 109 and 111; 113 and 115; 117 and 119.

In one embodiment, the antibody-like protein may include a heavy chain (HC) and a light chain (LC). In one embodiment, the HC comprises an amino acid sequence having at least 98%, 95%, or 92% of sequence identity to SEQ ID NO. 85, 89, 93, 97, 101, 105, 109, 113, 117, 137, 141, 145, 151; and the LC comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% of sequence identity to SEQ ID NO. 87, 91, 95, 99, 103, 107, 111, 115, 119, 139, 143, 147, 149.

In one embodiment, the antibody-like protein may include a heavy chain monomer and a light chain monomer, wherein the heavy chain monomer having a N-terminus and a C-terminus, comprising in tandem from the N-terminal to the C-terminal, an optional first binding domain (D1) at the N-terminal, a Fab region as a second binding domain (D2) comprising a light chain, a Fc domain, an optional third binding domain (D3), and an optional fourth binding domain (D4) at the C-terminal. The light chain may comprise an optional fifth binding domain (D5) covalently attached to the C-terminus, an optional sixth binding domain (D6) covalently attached to the N-terminus, or a combination thereof. At least one of D1, D2, D3, D4, D5 and D6 comprises the EGFR binding domain as disclosed herein.

In one embodiment, the D1 comprises the EGFR binding domain. In one embodiment, the D2 comprises the EGFR binding domain. In one embodiment, each of the D3, D4, D5 and D6 comprises the EGFR binding domain. In one embodiment, the D1, D2, D3, D4, D5 and D6 each has a binding specificity to a different antigen, wherein the antigen is a tumor antigen, an immune signaling antigen, or a combination thereof.

In one embodiment, the antibody-like protein may be a bispecific antibody. In one embodiment, the bispecific antibody is asymmetric with the D2 comprising the EGFR binding domain and the D3 has a binding specificity to CD3.

In one embodiment, bispecific antibody may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 137, 145, 139, 147, 141, 145, 143, 147, 141, 145, 149, 147, 151, 145, 139, 147 or a combination thereof. In one embodiment, the bispecific antibody may include the combinations of light

chains and heavy chains, or fragments thereof selected from the sequence combinations of 147; 141 and 145 and 149 and 147; 151 and 145 and 139 and 147.

In one embodiment, the antibody-like protein may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 137, 139, 141, 143, 141, 149, 151, 139, 145, 147 or a combination thereof. In one embodiment, the bispecific antibody may include the combinations of light chains and heavy chains, or fragments thereof selected from the sequence combinations of SEQ ID NO. 137 and 139, 141 and 143, 141 and 149, 151 and 139, 145 and 147.

In one aspect, the application provides the antibody-like protein having a Fab-Fc structure with one or more binding domains attached to the Fab-Fc structure. In one embodiment, the antibody-like protein has a N-terminus and a C-terminus and include a first monomer and a second monomer. The first monomer includes, from the N-terminus to the C-terminus, a first binding domain (mD1), a variable heavy (VH) chain, a CH1 domain, a first hinge, a first CH2 domain, a first CH3 domain, and a fourth binding domain (mD4). The second monomer includes from the N-terminus to the C-terminus, a second binding domain (mD2), a variable light (VL) chain, a CL domain, a second hinge, a second CH2 domain, and a second CH3 domain, and a fifth binding domain (mD5). The CH chain and CL chain forms a third binding domain (mD3). The first monomer and the second monomer may be covalently paired through at least one disulfide bond between the CH1 domain and the CL domain and at least one disulfide bond between the first hinge and the second hinge, and the antibody-like protein is at least bi-specific.

In one embodiment, at least one of the mD1, mD2, mD3, mD5, and mD5 in the antibody-like protein may include the EGFR binding domain as disclosed herein. In one embodiment, the mD3 domain comprises the EGFR binding domain. In one embodiment, the mD2 domain comprises the EGFR binding domain. In one embodiment, the mD2, mD4, mD5 each comprises the EGFR binding domain.

In one embodiment, the antibody-like protein may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO 121, 123, 125, 127, 129, 131, 133, 135 or a combination thereof. In one embodiment, the antibody-like protein may include the combinations of peptides or fragments thereof selected from the sequence combinations of 121 and 123; 125 and 127; 129 and 131; 133 and 135.

In one aspect, the application provides heavy chains. In one embodiment, the heavy chain may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 121, 125, 129, 133.

In one aspect, the application provides light chain. In one embodiment, the light chain may include an amino acid sequence having at least 70%, 80%, 85%, 90%, 92%, 95%, 98%, 99%, or 100% sequence identity to SEQ ID NO. 123, 127, 131, 135.

In one aspect, the application provides isolated nucleic acid sequence encoding the antibody-like protein, light chains, heavy chains, and peptide sequences as disclosed herein.

In one aspect, the application provides expression vector comprising the isolated nucleic acid sequences as disclosed herein.

In one aspect, the application provides host cell for producing the antibody-like protein, light chains, heavy chains, or combinations thereof. In one embodiment, the host cell includes the isolated nucleic acid sequence as disclosed herein. In one embodiment, the host cells may be prokaryotic or eukaryotic.

In one aspect, the application may include an immunoconjugate. In one embodiment, the immunoconjugate may include the antibody-like protein, the antibodies, anti-EGFR binding domains or peptides as disclosed herein, and a cytotoxic agent. In one embodiment, the cytotoxic agent may include a chemotherapeutic agent, a growth inhibitory agent, a toxin, or a radioactive isotope.

In one aspect, the application provides pharmaceutical composition for treating diseases or health conditions. In one embodiment, the pharmaceutical composition may include the antibody-like protein, antibodies, immunoconjugates, anti-EGFR binding domains or peptides as disclosed herein, and a pharmaceutically acceptable carrier.

In one embodiment, the pharmaceutical composition may further comprise a therapeutic agent. In one embodiment, the therapeutic agent may be a chemotherapeutic agent, a growth inhibitory agent, a toxin, a radioactive isotope, or a combination thereof. In one embodiment, the therapeutic agent may be, for example, capecitabine, cisplatin, trastuzumab, fulvestrant, tamoxifen, letrozole, exemestane, anastrozole, aminoglutethimide, testolactone, vorozole, formestane, fadrozole, letrozole, erlotinib, lapatinib, dasatinib, gefitinib, imatinib, pazopanib, lapatinib, sunitinib, nilotinib, sorafenib, nab-palitaxel, a derivative or a combination thereof.

In one aspect, the application provides methods for treating or preventing a cancer, an autoimmune disease, or an infectious disease in a subject. In one embodiment, the method may include the step of administering to the subject a pharmaceutical composition comprising a purified antibody-like protein, the antibody, the immunoconjugates, the anti-EGFR domains, or peptides as disclosed herein. In one embodiment, the subject is a mammal. In one embodiment, the subject is a human.

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

In one embodiment, the cancer may include cells expressing HER3 or EGFR. In one embodiment, the cancer may be, for example, breast cancer, colorectal cancer, pancreatic cancer, head and neck cancer, melanoma, ovarian cancer, prostate cancer, non-small lung cell cancer, small cell lung cancer, glioma, esophageal cancer, nasopharyngeal cancer, kidney cancer, gastric cancer, liver cancer, bladder cancer, cervical cancer, brain cancer, lymphoma, leukaemia, myeloma

In one aspect, the application provides method for producing the antibody-like protein,

antibody, the anti-EGFR domains, or peptides as disclosed herein. In one embodiment, the method may include the steps of culturing a host cell such that the DNA sequence encoding the antibody-like protein, the anti-EGFR domains or peptides as disclosed herein, is expressed, and purifying said multi-specific antibody-like protein, the anti-EGFR domains or peptides as disclosed herein.

In one aspect, the application provides a solution comprising an effective concentration of the antibody-like protein, the antibody, the immunoconjugates, the anti-EGFR domains or peptides as disclosed herein. In one embodiment, the solution is blood plasma in a subject. In one embodiment, the subject is a human.

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 depicts the alignment of cetuximab-derived VH (A) and VL (B) sequences in Kabat numbering, where N85E is aglycosylated cetuximab and H1 through H11 are humanized variants, the consensus sequences of VH and VL are generated by Geneious software (geneious.com), in which the consensus sequence is displayed above the alignment or assembly, and shows which residues are conserved (are always the same), and which residues are variable. A consensus is constructed from the most frequent residues at each site (alignment column), so that the total fraction of rows represented by the selected residues in that column reaches at least a specified threshold;

FIGURE 2 displays T20 humanness scores for cetuximab-derived VH (A) and Vk (B) domains, and (C) the predicted number of MHCII-binding peptides in cetuximab-derived variable regions, based on the MixMHC2pred algorithm;

FIGURE 3 shows the SEC profile of His-tagged anti-EGFR scFv domains indicating humanizing SI-79R1 (cetuximab) to SI-79R2 (H1) resulted in lower aggregation;

FIGURE 4 shows the Octet binding analysis of His-tagged anti-EGFR scFv domains, demonstrating that humanized cetuximab, H1, has similar binding to human EGFR as mouse scFv;

FIGURE 5 shows the result of thermal stability analysis of His-tagged anti-EGFR scFv domains, indicating that humanized cetuximab, SI-79R2, is significantly more stable than SI-79R1 as measured by DLS (unfolding at higher temperature);

FIGURE 6 shows the results of chemical denaturation stability analysis of His-tagged anti-EGFR scFv domains, indicating that humanized Cetuximab, SI-79R2, is significantly more stable than SI-79R1 as measured by guanidine and urea denaturation (higher concentration of guanidine/urea required to unfold);

FIGURE 7 shows analytical size-exclusion chromatograms for scFv-monoFc (A) and mAb proteins (B) immediately after first step protein A purification, and non-reducing SDS-PAGE of purified scFv-monoFc proteins (C), where data are representative of two independent expressions and purifications, N85E is aglycosylated cetuximab, and H1 through H11 are humanized variants;

FIGURE 8 shows the binding kinetics of cetuximab-derived scFv-monoFc proteins (A) and mAbs (B) as determined by biolayer interferometry using anti-human Fc (AHC) sensors and soluble recombinant extracellular domain of human EGFR, where data are representative of two independent experiments, K_D values are shown in **Tables 6-8**, N85E is aglycosylated cetuximab, and H1 through H11 are humanized variants;

FIGURE 9 shows thermal stability of cetuximab-derived scFv-monoFc proteins (A) and mAbs (B) as determined by dynamic light scattering, where data are representative of two independent experiments, unfolding temperatures (the point at which the radius surpassed 10 nm) are shown in **Tables 7-8**, N85E is aglycosylated cetuximab, and H1 through H11 are humanized variants;

FIGURE 10 shows cation exchange chromatography of α CD3 $\times$ α EGFR bispecific antibodies and their parental α CD3 and α EGFR antibodies showing their characteristic retention times;

FIGURE 11 shows T cell-dependent cellular cytotoxicity (TDCC) of α CD3 $\times$ α EGFR bispecific antibodies, using luciferized EGFR-bearing BxPC-3 cell line as target cells incubated with activated T cells and the α EGFR arm, including wild-type cetuximab, aglycosylated cetuximab (N85E), and humanized version H7, and luminescence signals as the endpoint of viable BxPC-3 cells after 72 hours (EC50 values are shown in **Table 8**);

FIGURE 12 demonstrates GNC antibodies in a schematic diagram showing the configuration: 1) the variable regions of Fab in black (D2), both the constant regions of Fab and the Fc region in white; 2) additional scFv antigen binding domains in shaded boxes (each replaceable by a receptor-ligand binding); 3) a heavy chain monomer linking D1 to its N-terminus and/or D3 and/or D4 tandemly to its C-terminus through D4; and 4) a light chain monomer linking D5 and/or D6 to its N- and C-terminus, resulting in hexa-GNC and penta-GNC antibodies, respectively;

FIGURE 13 shows the analytical SEC profile of anti-huEGFR penta-GNC antibodies, comprising either a humanizing anti-EGFR scFv (SI-55P3, H1 scFv; SI-55P4, H1 scFv; SI-79P2, H4 scFv; SI-79P3, H4 scFv; and SI-55P9, H7 scFv) or a Fab region (SI-77P1, H7 Fab), have low aggregation after protein A purification.

FIGURE 14 shows the Octet binding analysis of anti-huEGFR penta-GNC antibodies, indicating that the penta-GNC antibodies having either a humanizing anti-EGFR scFv (SI-55P3, H1 scFv; SI-79P2, H4 scFv; and SI-79P3, H4 scFv) or a Fab region (SI-77P1, H7 Fab) retain tight binding;

FIGURE 15 demonstrates that the penta-GNC antibodies having humanized anti-EGFR scFv (SI-55P9, H7 scFv) or Fab (SI-77P1, H7 Fab) elicit potent TDCC to EGFR-expressing tumor cells;

FIGURE 16 shows analytical SEC profiles of anti-huEGFR hexa-GNC antibodies, indicating that the hexa-GNC antibodies having either a humanized anti-EGFR scFv (SI-55H11, H7 scFv) or a Fab

region (SI-77H4, H7 Fab) have lower aggregation than the hexa-GNC having anti-EGFR domain derived from Cetuximab;

FIGURE 17 shows the Octet binding analysis of anti-huEGFR hexa-GNC antibodies indicates that the hexa-GNC antibodies having either a humanizing anti-EGFR scFv (SI-55H11, H7 scFv) or a Fab region (SI-77H4, H7 Fab) retain binding to EGFR comparable to the Cetuximab-derived hexa-GNC antibody, SI-77H4;

FIGURE 18 shows that the hexa-GNC antibodies having humanized anti-EGFR scFv (SI-55H11, H7 scFv) elicit potent TDCC to EGFR-expressing tumor cells;

FIGURE 19 depicts (A) a schematic diagram of asymmetric bispecific antibodies, of which the α EGFR Fab is derived from one of three cetuximab Fabs (wild-type with or without N85E, or with humanized VH/VL; the second Fab is α CD3 Fab; and the CH3 domain contains the K409R mutation; and (B) miniGNC antibody-like proteins in a schematic diagram showing the heterodimeric configuration: 1) the variable regions of a single Fab in black (mD3), both the constant regions of Fab and the Fc region in white; 2) additional scFv antigen binding domains in shaded boxes (each replaceable by a receptor-ligand binding); 3) Chain A monomer linking mD1 to its N-terminus and mD4 to its C-terminus; and 4) Chain B monomer linking mD2 to its N-terminus and mD5 to its C-terminus;

FIGURE 20 shows the analytical SEC profiles of anti-huEGFR penta-miniGNC antibodies, indicating that the penta-miniGNC antibodies having either a humanizing anti-EGFR scFv (SI-68P7, H1 scFv; SI-79P1, H4 scFv; and SI-68P13, H7 scFv) or a Fab domain (SI-68P17, H7 Fab) have low aggregation.;

FIGURE 21 shows the Octet binding analysis of anti-huEGFR penta-miniGNC antibodies, indicating that the penta-miniGNC antibodies having either a humanized anti-EGFR scFv (SI-709P1, H4 scFv; SI-68P13, H7 scFv) or a Fab region (SI-68P17, H7 Fab) retain binding to EGFR; and

FIGURE 22 shows that the penta-miniGNC antibodies having a humanized anti-EGFR scFv (SI-68P13, H7 scFv) or a Fab region (SI-68P17, H7 Fab) elicit potent TDCC to EGFR-expressing tumor cells.

DETAILED DESCRIPTION

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

The 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 EGFR (**Table 1, Figure 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 and 3; 5 and 7; 9 and 11; 13 and 15; 17 and 19; 21 and 23; 25 and 27; 29 and 31; 33 and 35; 37 and 39; 41 and 43; 55; 57; 59; 61; 63; 65; 67; 69; 71; 73; 75; 77; 79; 81; 83; 85 and 87; 89 and 91; 93 and 95; 97 and 99; 101 and 103; 105 and 107; 109 and 111; 113 and 115; 117 and 119; 121 and 123; 125 and 127; 129 and 131; 133 and 135; 137 and 139; 141 and 143; 141 and 149; 151 and 139; 145 and 147; 137, 145, 139 and 147; 141, 145, 143 and 147; 141, 145, 149 and 147; 151, 145, 139 and 147.

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 EGFR in this application). The antigen-binding fragment (Fab) is a region (Fab region) on an antibody that binds to antigens. 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 (WO2019191120A1, incorporated herein by reference in its entirety). 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 an immune cell) and at least one target cell (such as a tumor cell, an immune cell, or a 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.

The term “affinity” refers to a measure of the attraction between two polypeptides, such as antibody/antigen, receptor/ligand, etc. The intrinsic attraction between two polypeptides can be expressed as the binding affinity equilibrium dissociation constant (KD) of a particular interaction. A KD binding affinity constant can be measured, e.g., by Bio-Layer Interferometry, where KD is the ratio of kdis (the dissociation rate constant) to kon (the association rate constant), as $KD = kdis/kon$.

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 the equilibrium dissociation constant 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 K_A or K_a 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 K_A or K_a refers to an association rate of a particular antibody-antigen interaction.

A potential shortcoming of cetuximab is that its variable regions were discovered in mice, and these regions retain non-human sequences. It has been demonstrated that chimeric antibodies may have increased capacity for immunogenicity when compared to humanized or human antibodies.⁶ On the other hand, humanization can increase the stability of antibodies by making the framework regions more compatible.⁷ Another concern is the occupied glycan site at VH N85 (Kabat), where Fab glycosylation could affect the biological properties of the antibody, as well as introduce glycan heterogeneity that must be well-controlled during manufacturing.^{8,9} While immunogenicity of cetuximab appears low based on low incidence of anti-cetuximab IgG response (5%), hypersensitivity is a common occurrence due largely to pre-existing IgE antibodies against the galactose- α -1,3-galactose oligosaccharide that modifies the VH when expressed in SP2/O cells.¹⁰⁻¹²

To overcome these liabilities, cetuximab was humanized with the goals of removing post-translational modification sites, stabilizing the antibody, and reducing the potential for immunogenicity while retaining high affinity for EGFR. Strategies for humanization included a straight CDR graft onto a stable human framework, sequence-guided grafting onto the most similar germline or consensus framework, and a structure-guided approach based on predicted stability effects of humanizing mutations. The result is a panel of humanized cetuximab sequences with superior biophysical properties, where the structural modeling approach was the most successful in generating stable binders with no loss in EGFR affinity.

Humanization of antibodies discovered in non-human species is a common practice not only to decrease the immunogenicity, but also to increase stability and remove sequence liabilities. In this study, cetuximab scFv was humanized using three distinct strategies including unbiased CDR grafting, sequence-guided humanization, and model-guided humanization (**Table 2**). Although each approach was successful in generating EGFR binders with increased humanness, there was a clear trend in stability and affinity retention across the humanization strategies. Whereas the simple CDR graft resulted in destabilization and the largest (4-fold) loss in antigen affinity, the sequence homology approach resulted in stabilization and a more modest (2-fold) decrease in affinity, and the model-guided approach was the most successful with significant stabilization and no change in antigen affinity.

When expressed as a mAb, the humanized version H7 had increased titer and thermal stability relative to cetuximab, unchanged binding kinetics, and similar TDCC potency when transformed to bispecific α EGFR x α CD3 format (**Table 8**).

In addition to superior biophysical properties, the humanized versions removed sequence liabilities associated with the mouse variable regions of cetuximab. The humanness of VH and

VL were significantly increased for all humanizations, and the presence of immunogenic peptides appeared to be reduced based on predicted affinity for MHCII alleles (**Table 1**). Although it is difficult to predict immunogenicity of therapeutic antibodies, the increased humanness and decreased number of T cell epitopes could feasibly reduce incidence of immunogenicity.^{17,18,20} Furthermore, the removal of glycosylation and deamidation sites reduces the complexity of lot-to-lot characterization and eliminates the potential for immunogenic Fab saccharides, even when expressed in non-human cells.

After humanization, additional modification of the three C-terminal residues of VL was attempted as a means to decrease aggregation of scFvs.^{13,15,16} Due to absence of the CH1/CL domains, scFvs have surfaces unnaturally exposed to the solvent. As human V λ has a more hydrophobic C-terminus with fewer charged residues than V κ (LTVL vs. LEIK), it may have superior packing of its last beta sheet. Indeed, this modification decreased aggregation in all three cases (on average by 8%), and increased titer and thermal stability in two of three cases (**Table 6**).

Furthermore, IgG antibodies have a conserved N-glycosylation site at N297, located in the CH2 domain within the upper Fc domain. In addition, a minority of antibodies are glycosylated in the Fab region, due to N-glycosylation motifs that are sometimes present within the variable regions (8). The glycan profile of antibody therapeutics must be routinely characterized batch-to-batch in order to ensure consistent and homogeneous protein is obtained during large-scale expression and purification. A challenge arises when glycan sites are located both within the Fab and the Fc of an antibody, as the molecule must be digested or otherwise deconvoluted to clearly identify the glycan profiles at each site. However, removal of the glycan within the Fab domain often compromises its affinity for the targeted antigen, as the glycan can stabilize the active antigen-binding conformation. In the case of cetuximab, the antibody is glycosylated at N99 (AHo) of the VH domain (9), glycosylation increases the cost of goods due to the need for additional quality control steps to characterize its glycan sites. Removal of the Fab glycan while retaining the original affinity for EGFR represents a major leap forward for the generation of antibodies that are easier to characterize and still retain full efficacy.

Cetuximab has been humanized previously using other strategies. One CDR grafting study of cetuximab generated an antibody that could bind to cells overexpressing EGFR, though the affinity was decreased 9-fold.^{21,22} This increase in K_D mirrors the affinity change observed for CDR grafting in the present study. Also, cetuximab has been glycoengineered to remove α -1,3-galactose epitopes, demonstrating an alternate approach to decrease the immunogenicity of this antibody.²³ Collectively, the data presented here demonstrate that protein engineering of cetuximab can improve its stability and immunogenicity properties, and more generally suggest that sequence-, and especially structure-guided methods can be used to generate humanized antibodies with superior stability and binding properties.

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. Humanized EGFR binding sequences

The humanness of the sequences was calculated using the Lake Pharma Antibody Analyzer (<https://dm.lakepharma.com/bioinformatics/>), which provides a T20 score (range 0 to 100, with 100 being the most human) (**Table 1, Figure 2C**). Notably, the wild-type mouse sequences had low scores of 66.44 (VH) and 70.38 (VK) when calculating a score for the framework regions only. In contrast, the sequences for humanized variants (e.g. H1-H11) had significantly higher T20 humanness scores, ranging from 76.95 to 88.10 (VH) and from 81.44 to 91.04 (VK). Thus, the sequences for humanized variants are predicted to have lower immunogenicity than the mouse sequences due to lower MHCII binding and higher degree of humanness.

To increase the humanness of the cetuximab variable regions and decrease the potential for immunogenicity, the mouse VH and Vk domains were converted to a more human framework (**Figure 1**). Version H1 was based on a simple graft of Kabat CDR residues onto a stable human framework.¹³ Versions H8, H9, H10, and H11 were designed based on sequence homology to human germline sequences. In particular, for versions H10 and H11, the framework residues were mutated in order to match the most similar human germline sequences. For versions H8 and H9, the framework residues were mutated to the consensus residue in human antibodies. The rest of the humanized versions (H2, H3, H4, H5, H6, H7) were designed based on structural analysis of cetuximab, by mutating framework residues to those residues occurring with a frequency of at least 5% in the human germline that caused the most stable structure *in silico*. Because the energy analysis for this type of humanization depends on the input model, several input structures were examined. Version H2 used the cetuximab crystal structure 1YY9.¹⁴ Versions H3, H4, H5, H6, and H7 used scFv models generated from the antibody modeling feature of Discovery Studio, based on the sequence of cetuximab *variable* domains. Versions H4, H5, H6, and H7 incorporated changes in the input sequence to increase similarity of the VH C-terminus to the consensus sequence in humans, or to make the Vk C-terminus more V λ -like. After humanization in Discovery Studio, H7, H9, and H11 were further modified by converting the last three residues of the Vk domain into their corresponding residues from the λ J-gene. This change was evaluated due to the known importance of the last VL beta strand in determining scFv stability and aggregation propensity, and the more hydrophobic nature of the V λ terminus, which could provide packing energy to stabilize the interaction.^{13,15,16} All humanization strategies are summarized in **Table 2**.

For humanized version H1, the cetuximab Kabat CDRs were grafted onto a stable framework described previously.¹³ All other humanized versions were designed using Discovery

Studio 2020 suite. Versions H8-H11 were designed using the Predict Humanizing Mutations protocol based exclusively on the amino acid sequence of cetuximab as the Query Sequence. Identity Threshold was set to 50, Frequent Residue Substitution Tolerance was set to 20, Germline Substitution Tolerance was set to 0, and substitutions of Kabat CDR residues, IMGT CDR residues, Vernier Zone residues, and human germline residues were excluded. Versions H10 and H11 were generated based on Germline substitutions, while versions H8 and H9 used Frequent Residue Substitutions. Versions H2-H7 were designed using different input models for cetuximab with Calculate Mutation Energy set to True (CHARMM forcefield) in order to generate Best Single Mutations sequences. The Query Structure was various models for cetuximab, as shown in **Table 2**. Version H2 used the cetuximab component of PDB 1YY9 (cetuximab in complex with EGFR) in order to capture the poses of CDRs in the bound state. Versions H3-H7 used cetuximab models generated by Discovery Studio's Antibody Modeling Cascade. The Input Sequences were cetuximab VH and VL for H3, cetuximab VH (ending TVSS instead of TVSA) and VL for H4 and H7, cetuximab VH and VL (ending LTVL instead of LELK) for H5, and cetuximab VH (ending TVSS instead of TVSA) and VL (ending LTVL instead of LELK) for H6. The Top 5 Framework Templates were used with Sequence Similarity Cutoff of 10. CDR loop definition was set to Honegger and Maximum Templates Per Loop was set to 3 with Optimization Level set to High. After generating humanized sequences, versions H10, H8, and H4 were modified to H11, H9, and H7, respectively, by substituting the last four residues of the VL to LTVL to mimic the stable FR4 of lambda antibodies.

Sequences for cetuximab variable domains and their humanized versions are shown in (**Figure 1**). Panels A and B show alignments of the VH and VL sequences, respectively. Vernier zone residues flanking the CDR region, and in structurally important framework regions, were also conserved to maintain antigen binding. Examination of amino acid identity between the sequences (**Table 3**) revealed that the humanized VH sequences had 84-87% identity with cetuximab, and 79-100% identity with each other. Excluding comparison of versions with modified lambda J region, which by definition have 100% VH identity to their corresponding unmodified humanization, the maximum identity between humanized VH sequences was 95%. The humanized VL sequences had 79-86% identity with cetuximab, and 76-98% identity with each other. Notably, the sequence identity was reduced when comparing only the framework regions (70-82% identity for cetuximab VH and humanized VH, and 60-82% identity for cetuximab VL and humanized VL).

Besides the Fc glycans, wild-type cetuximab has 2 potential glycosylation sites in the VH domain (Kabat N85, known to be glycosylated) and the VK domain (Kabat N41, part of NGS glycosylation motif), respectively. In addition, this same VK N49 may be deamidated, as it forms an NG deamidation motif. In order to remove liabilities associated with stability and manufacturing assessment of these post-translational modification sites, all 3 liabilities (2 glycosylation and 1 deamidation) were removed in all humanized sequences, H1-H11 (**Figure 1**).

In particular, Kabat residue VH N85, comprising an occupied NDT glycosylation motif in cetuximab, was modified to A, D, or E amino acids in the humanizations, eliminating this known glycan site. Similarly, VL N41, comprising an NGS glycosylation motif in cetuximab, was changed to the more typical G residue in all humanizations

The humanness of wild-type cetuximab and humanized variable regions was calculated using the T20 humanness score based on the sequence of the framework regions.¹⁷ Cetuximab, which is a chimeric antibody with mouse variable regions, had low T20 scores of 66.44 (VH) and 70.38 (Vk). The T20 score of humanized VH domains increased from 66.44 to a range of 76.95-88.10 (Table 1, **Figure 2A**), while the score of humanized Vk domains increased from 70.38 to a range of 81.44-91.04 (Table 1, **Figure 2B**). Thus, humanization of cetuximab variable regions significantly improved the humanness of these sequences, which could reduce immunogenicity based on increased sequence homology to human germlines.

While presence of non-human sequences in biologics can cause immunogenicity in the form of anti-drug antibodies (ADAs), robust high-affinity ADA can only occur if the offending B cell is activated to undergo class-switch recombination to the IgG subtype. This B cell activation requires binding of presented MHCII-peptide to a compatible T cell receptor on CD4+ T cells. Thus, an undesired ADA response is more likely to occur if the therapeutic antibody contains peptides that bind stably to MHC class II.

The MixMHC2pred algorithm (<https://github.com/GfellerLab/MixMHC2pred>) was used to predict MHCII-binding ligands within the antibody sequences.¹⁸ 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 stable T cell epitope. The higher the number of MHCII-binding peptides identified in a sequence, the more potential T cell epitopes the sequence contains. Notably, the algorithm cannot distinguish immunogenic versus tolerogenic peptides; however, a high number of core peptides increases the likelihood of containing some peptides that are pro-immunogenic. The MixMHC2pred algorithm was purchased and downloaded from its GitHub repository. After running the algorithm on VL/VH scFv sequences containing (G₄S)₄ linker, the number of core peptides was calculated and tabulated for the different sequences. Scoring was performed across multiple alleles, allowing sequences to be evaluated for the presence of strong ligands to any allele of MHCII. 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.

In order to evaluate the presence of MHCII epitopes within cetuximab variable regions, the VH and VL sequences were run through a calculator that predicts MHCII binding affinity. The algorithm, MixMHC2pred, is based on binding of ~100,000 peptides to different HLA-II alleles.¹⁸ Based on an input sequence, MixMHC2pred evaluates binding of each peptide within the sequence to each HLA-II allele, and returns a ranked score for each residue based on its strongest interaction with any allele. The number of core peptides binding to MHC was calculated based on the number of unique peptides ranking within the top 0.2% of all interactions. To simplify the

scoring system into a single value per VH-VL pair, sequences were run as scFv [VL-(G₄S)₃-VH], which accounts for peptides within both VH and VL. Using this system, the number of MHCII core peptides was calculated for cetuximab and the humanized sequences (**Table 1, Figure 2C**). Although MHCII binding was not used as a criterion for humanization, all of the humanized sequences had a reduced number of peptides scoring within 0.2% of interactions. While cetuximab had 12 core peptides, the humanized sequences had 7-11 core peptides. This reduction in MHCII binding, combined with more human sequence, may lessen the likelihood of immunogenicity for the humanized variable regions. Additionally, 12 residues within CDRs were identified in the mouse sequence that are predicted to be part of MHCII-binding peptides. In many humanized variants, including H2, H3, H4, H5, H6, H7, H10, and H11, the number of CDR residues in MHCII-binding peptides was reduced.

Example 2. Methods of making and characterizing humanized EGFR binding peptides, domains, antibodies, and antibody-like proteins

To characterize humanized anti-EGFR variable regions in the form of various single therapeutics, i.e. EGFR binding complex, α huEGFR variants (α huEGFR), His-tagged scFv protein (scFv-6His), recombinant scFv-monoFc monomer (scFv-monoFc), monoclonal antibody (mAb), bispecific antibody (bispecific), penta-GNC antibody (pentaGNC), hexa-GNC antibody (HexaGNC), and penta-miniGNC antibody (miniGNC) were generated and characterized, as listed in **Table 4**, by the following methods.

2a. Expression and purification of EGFR binding complex

Protein stability is a key parameter defined by the difference in free energy between the folded and unfolded states. For protein therapeutics, stability may impact immunogenicity, pharmacokinetics, and even efficacy (7), and reduction of aggregation can help to develop therapeutics that are easier to manufacture and safer for patients. In addition, expression efficiency and protein yield directly determine the cost of protein therapeutics. If proteins can be more efficiently expressed to reach higher titers and increased yield of purified protein, manufacturing costs can be reduced significantly.

Proteins were expressed by transfecting the expression plasmids for His-tagged scFv or scFv-monoFc (single plasmid) or co-transfecting heavy and light chains (for other formats) in the ExpiCHO system (Thermo Fisher), collectively called EGFR binding complex. Briefly, 10 μ g of each expression plasmid (or 20 μ g of an unpaired plasmid) was brought to 1ml with OptiPRO SFM medium. 1ml of OptiPRO SFM medium containing 80ul Expifectamine CHO reagent was added to the DNA and incubated at room temperature for 2.5 minutes. The resulting mixture was then added to 25ml ExpiCHO cells at 6×10^6 cells/ml in a 125ml Erlenmeyer flask and incubated at 37°C, 5% CO₂, 150rpm. Cells were fed with 8.75ml ExpiCHO feed and 150 μ l of CHO enhancer at 24 hours post-transfection and shifted to 32°C, 5% CO₂, 150rpm. Cells were fed again at 48 hours post-transfection with 8.75ml ExpiCHO feed. Culture supernatant was harvested 8 days post-

transfection, spun for 1 hour at 4500rpm to pellet the cells and then passed through a 0.2mm filter.

Fc-containing proteins were purified from the harvested supernatant using a 1-ml MabSelect Prisma protein A column (GE Healthcare). The column was equilibrated with phosphate-buffered saline. The supernatant was then passed through the column at a flow rate of 2 ml/min. The column was washed with 10ml PBS + 0.1% Triton X-100, followed by 10ml PBS + 300mM NaCl, and finally 10ml PBS. Protein was then eluted by passing 5ml of 50 mM sodium acetate, pH 3.5 through the column. The eluted protein was immediately neutralized by addition of 0.5ml 1M Tris-Cl, pH8.0.

His-tagged scFv proteins were purified from the harvested supernatant using a 1-ml HisTrap HP column or 1-ml protein L (CaptoL) column (GE). The column was equilibrated with phosphate-buffered saline containing 0.5 M NaCl and 20 mM imidazole, pH 7.4 (HisTrap) or PBS (protein L). The supernatant was spiked with 10x binding buffer to reach 0.5 M NaCl and 20 mM imidazole (His trap only) and run over the column at a flow rate of 2 ml/min. The column was washed with 10 column volumes of PBS containing 0.5 M NaCl and 20 mM imidazole (HisTrap) or PBS (protein L), and the protein was eluted using PBS containing 0.5 M NaCl and 500 mM imidazole, pH 7.4 (HisTrap) or 50 mM sodium acetate pH 3.5, later neutralized with 0.5 ml 1M Tris pH 8.0 (protein L).

Immediately after first-step protein A or His tag purification, scFv-monoFc proteins were analyzed by analytical SEC using Waters Acquity UPLC H-Class with ACQUITY UPLC® Protein BEH SEC 200Å, 4.6mm x 150mm, 1.7 µm column. PBS (125 mM sodium phosphate, 137 mM sodium chloride, pH 6.8) was used as mobile phase for 10-minute runs at 0.3 ml/min, injecting 10 µg protein. For higher resolution, mAbs were instead analyzed by analytical SEC using an Acquity Arc Waters HPLC with XBridge BEH SEC 300Å, 7.8 x 300 mm, 3.5 µm column. PBS (150 mM sodium phosphate, 100 mM sodium chloride, pH 6.8) was used as mobile phase for 20-minute runs at 0.714 ml/min, injecting 50 µg protein. Two separate purifications were assessed for each protein, with % peak of interest values reported as average ± standard deviation.

2b. Assays for characterizing the binding specificity and affinity of EGFR binding complex

Biolayer interferometry (Octet) binding assays were performed on an Octet96 or Octet384 instrument to ensure that proteins containing humanized cetuximab binding domains retain binding to their cognate antigens. Fc-containing protein was captured to anti-human Fc (AHC) sensor tips by loading for 180 seconds at 10 µg/ml. Alternatively, His-tagged proteins were covalently coupled at 10 µg/ml to AR2G tips using manufacturer protocol. After a 60-second baseline step, a 180- to 300-second association phase with serial dilutions (0-200 nM; 1:2.5 dilution factor) or a single 100 nM concentration of purified human EGFR in assay buffer (phosphate-buffered saline containing 0.1% BSA, 0.05% Tween20) was performed, followed by a 300- to 600-second dissociation phase in assay buffer. Regeneration was achieved using 10 mM glycine, pH 1.5. Binding curves were globally fit to a 1:1 model to extract the dissociation

constants, K_D . Binding kinetics for each protein were assessed in duplicate, with tabulated values reported as average $\pm$ standard deviation.

2c. Assays for characterizing TDCC of EGFR binding complex

The tumor-targeting properties of the humanized anti-EGFR domain in multi-specific antibodies, collectively known as GNC antibodies, were evaluated by testing their ability to induce tumor-specific cytotoxicity while engaging T-cell activation, redirecting T-cell mediated cytotoxicity, and ultimately killing the target cells. A luminescence-based T cell-dependent cellular cytotoxicity (TDCC) assay was used to measure the extent of antibody-induced cellular cytotoxicity by quantification of cell viability via constitutive expression of luciferase.

Luciferized BXPC3 tumor cells (ATCC) were cultured at 37°C, 5% CO₂ in the RPMI 1640 media containing 10% fetal bovine serum. Cell viability was monitored with a Vi-CELL automated cell counter (Beckman Coulter). 500 tumor cells (20 μ L) per well were plated into a 384-well, white, flat-bottom polystyrene TC-treated microplate (Corning) and incubated at 37 °C, 5% CO₂. After 24 hours, human pan T-cells were added to reach an effector-to-target (E–T) ratio of 5:1 and antibody was added with a 5-fold dilution series (0 – 30 nM). Cells were dispensed using a Multidrop bulk liquid dispenser (BIOTEK). Antibody dilutions were added (10 μ L/well) and plates were incubated for an additional 72 hrs at 37°C, 5% CO₂ before luminescence-based cell viability quantification.

To quantify the luminescence produced by constitutively expressed firefly luciferase, the Bright-Glo Luciferase Assay System (Promega) was used. BrightGlo reagent was added (20 μ L per well) at room temperature and luminescence was quantified with a luminescence detecting plate reader (BMG Labtech). Antibody EC₅₀ was determined by transforming the data in Microsoft Excel and analyzing with GraphPad Prism 6 software “log(agonist) vs. response — variable slope (four parameters)”. The resulting EC₅₀ value is reported. The TDCC assay was done in quadruplicate with good inter-plate reproducibility, and no significant variability was seen from different locations on the plate.

Example 3. His-tagged-EGFR binding scFv proteins.

The sequences encoding humanized (H1) anti-EGFR binding domains were cloned into His-tagged scFv expression format containing the residues GSHHHHHH at the C-terminal of the scFv. The expression vectors were transfected into 25 mL of ExpiCHO and expressed for 8 days before harvesting and purifying via protein L affinity chromatography. The H1 variant had significantly higher titer than the mouse version (**Table 5**).

Analytical SEC data after protein L purification demonstrates that the humanized scFv had significantly less aggregation than the scFv encoded by wild-type mouse sequence (**Figure 3**, **Table 5**). Additionally, the main peak was shifted to the right, consistent with modification of the glycosylation site and resulting aglycosylation of the VH.

Octet was used to verify that the humanized scFv protein can bind to human EGFR (**Figure 4**). His-tagged scFv proteins were loaded via covalent coupling onto AR2G sensors at 10 μ g/ml

and bound to a serial dilution (highest 200 nM, 1:2.5 dilutions) of His-tagged human EGFR. The resulting global fit to a 1:1 binding model demonstrated that both wild-type mouse scFv and humanized scFv proteins bind to EGFR with affinities in the low nanomolar range (**Table 5**).

Dynamic light scattering was used to compare thermal stability of the scFv proteins (**Figure 5**). The temperature was ramped from 25 °C to 75 °C at 0.5 °C/min while the radius of the scFv proteins (1 mg/ml) was monitored by a Wyatt DynaPro Plate Reader III. The data revealed that the H1 version has a significantly higher T_m value (**Table 5**), consistent with increased stability.

The stability toward chemical denaturation was also examined using guanidine and urea unfolding assays (**Figure 6**). Proteins at a concentration of 0.1 mg/ml were incubated with 24 guanidine HCl concentrations from 0 to 5.4 M or urea concentration from 0 to 7.2 M overnight. Fluorescence intensity (excitation 295 nm, emission 360 nm) was measured on a CLARIOstar plate reader, fluorescence intensity was normalized to represent fraction unfolded protein, and sigmoidal fits were used to extract EC50 values for stability comparison. The humanized variant H1 was more resistant than wild-type to unfolding by guanidine denaturation according to resulting EC50 values (**Table 5**).

Example 4. Humanized EGFR binding scFv-monoFc fusion proteins

To assess of the biophysical properties of humanized cetuximab VH and VL domains, sequences were cloned into scFv format and fused to a monoFc to facilitate purification and Octet analysis.¹⁹ The scFv domain was in VL-VH orientation, and included a (G₄S)₄ linker between VH and VL domains. Notably, generation of the scFv panel was more efficient than generating the corresponding mAb panel, which requires separate cloning for heavy and light chains. As controls, the wild-type cetuximab scFv and an aglycosylated version generated by mutation of the modified asparagine residue (VH N85E) were also generated.

Plasmids encoding wild-type, aglycosylated (N85E), and humanized scFv-monoFc proteins were transiently transfected in ExpiCHO cells, and protein was purified from the cell supernatant using protein A affinity chromatography. As shown in **Table 6**, the majority of humanized proteins had superior expression titer to the wild-type and simple aglycosylated versions of cetuximab despite containing the same monoFc domain and using the same algorithm for codon optimization. While the average titers for wild-type and aglycosylated cetuximab were 163 and 116 µg/ml, respectively, the average titer for the humanized versions ranged from 220 to 506 µg/ml for H8 and H7, respectively.

After the first step protein A purification, analytical size-exclusion chromatography (SEC) was used to assess aggregation of the scFv-monoFc proteins (**Figure 7A, Table 6**). The wild-type and aglycosylated cetuximab had 93.6% and 94.9% protein of interest, respectively, due to a small amount of aggregation, and the humanized versions had on average similar levels of aggregation. The version with the least aggregation (H9) had 97.4% protein of interest, while the most aggregated version (H4) had 82.6% protein of interest. The modification of V_k C-terminus

to include the sequence from V λ appeared to decrease aggregation. Humanized versions containing these V λ residues (H11, H9, and H7) had less aggregation than the corresponding versions where the original V κ residues were used (H10, H8, and H4, respectively). Preparative SEC was performed for all proteins in order to remove aggregate, exchange into storage buffer, and ensure accuracy of subsequent biophysical assays which benefit from using highly pure protein. SDS-PAGE of purified scFv-monoFc proteins demonstrated increased mobility of N85E and all humanized versions relative to wild-type cetuximab, confirming lack of glycosylation for these variants (**Figure 7C**).

The scFv-monoFc proteins were analyzed by SDS-PAGE using NuPAGE 4-12% Bis-Tris gels (Thermo Fisher, NP0323BOX) and MES running buffer (Thermo Fisher, NP0002). 3 μ g of each protein was prepared in LDS sample buffer (Thermo Fisher, NP0007) with or without 10 mM DTT and heated for 10 min at 70 °C. Gels were run for 50 minutes at 150 V, stained with SimplyBlue (Thermo Fisher, LC6065), and destained with water before imaging.

Binding of scFv-monoFc proteins to human EGFR was assessed by biolayer interferometry to reveal whether the humanization process altered binding kinetics (**Table 6, Figure 8A**). The monoFc domain was used to load proteins onto anti-human Fc (AHC) sensors, followed by binding of scFv to serial dilutions of the extracellular domain of human EGFR. Wild-type cetuximab scFv had an affinity of 3.18 nM, consistent with previous reports. The aglycosylated variant (N85E) had very similar binding kinetics with a K_D of 3.16 nM, indicating that glycosylation is not imperative for antigen binding.

The K_D values for the humanized versions fell into three main categories. For the humanized version using a straight CDR graft onto a stable human framework (H1), there was a 4-fold decrease in binding affinity which was driven by increased rate of dissociation. For humanizations based on sequence homology to a single human germline (H10, H11) or the global dataset of human germlines (H8, H9), there was a consistent 2-fold decrease in binding affinity where faster dissociation was again the kinetic determinant. Finally, for humanizations based on structural homology (H2 through H7), there was no significant decrease in binding affinity.

Thermal stability of scFv-monoFc proteins was assessed by dynamic light scattering (**Table 6, Figure 9A**) by observing the increase in hydrodynamic radius as the temperature was ramped from 25 °C to 85 °C.

Since the shapes of the unfolding curves were complex and not uniform for the different samples, the temperature at which the radius surpassed 10 nm was used to objectively compare protein stabilities. Using this metric, the wild-type cetuximab protein unfolded at 47.2 °C, while the aglycosylated N85E variant appeared slightly less stable, unfolding at 44.5 °C. Thus, the occupied glycosylation site may help to stabilize the folded conformation of wild-type cetuximab scFv.

Similar to the binding results, three categories of stability were observed. For the humanization based on CDR grafting to an unrelated human framework, the stability was slightly

decreased relative to wild-type cetuximab. Five humanized versions showed similar or slightly enhanced stability relative to cetuximab. Two of these were based on sequence homology to the global dataset of human germlines (H8, H9) while three were based on structural modeling (H4, H5, H7). Lastly, five humanized versions appeared to be significantly more stable than the other proteins. H10 and H11 were generated by CDR grafting onto the most sequentially homologous human framework, while H2, H3, and H6 were based on homology models. In contrast to SEC data showing systematic reduction in aggregation by using C-terminal residues from λ J genes, the DLS data did not show a consistent impact of these residues on stability. Whereas versions H11 and H7 showed subtle increases in stability relative to H10 and H4, respectively, H9 actually appeared less stable than its relative H8.

Example 5. Humanized anti-EGFR monoclonal antibodies

To understand if the properties of scFv-monoFc proteins would translate to IgG format, mAbs were generated for wild-type cetuximab, the aglycosylated variant N85E, and a humanized version of cetuximab. Based on the highest protein expression, low aggregation, improved thermal stability, and unchanged binding affinity, humanized version H7 was selected for conversion to mAb format. The three mAb proteins were produced by transient transfection in ExpiCHO cells and harvested after 9 days of expression.

Mirroring the scFv-monoFc results, the expression titer of humanized H7 was increased relative to that of wild-type or aglycosylated cetuximab (**Table 8**), although the difference in titer was not as pronounced as for the scFv-mFc format. After protein A purification, all proteins were >99% pure as assessed by analytical SEC (**Table 8, Figure 7B**). Notably, there was significantly less aggregation of the mAbs than the corresponding scFv-mFc proteins, which could be attributed to the intrinsic stability of the IgG backbone relative to scFv and monoFc domains. The SEC data also demonstrates that wild-type cetuximab had a significantly shorter retention time than either the aglycosylated N85E or humanized H7 versions. This difference in apparent molecular size can be attributed to the glycosylation of cetuximab, which is absent in N85E and humanized versions.

Binding kinetics of mAbs to human EGFR were assessed by biolayer interferometry (**Table 8, Figure 8B**) and demonstrated no difference in binding affinity or kinetics between versions. These results confirmed the results of the scFv-monoFc proteins, which demonstrated that the aglycosylating mutation N85E and the humanization mutations of H7 did not disrupt the interaction of cetuximab CDRs with its antigen. Binding affinity of the mAbs was similar to that of the corresponding scFv-monoFc proteins.

Finally, the DLS experiment was repeated to characterize the stability of the mAbs (**Table 8, Figure 9B**). Whereas wild-type and aglycosylated cetuximab had very similar stabilities (unfolding at 68.3 and 68.1 °C, respectively), the H7 version had an elevated unfolding temperature of 72.5 °C. Thus, humanized version H7 appears to be more stable than wild-type cetuximab whether in scFv or mAb format.

Example 6: Bispecific antibodies with T cell engager and humanized EGFR binding

As a final evaluation of functional activity, bispecific versions of cetuximab were generated and used in a T cell-dependent cellular cytotoxicity (TDCC) assay. The three versions of cetuximab mAb (wild-type, N85E, H7) contained the K409R mutation in the CH3 domain, which allowed for controlled Fab-arm exchange to occur when incubated with an anti-CD3 antibody containing the complementary F405L mutation. The formation of α EGFR x α CD3 bispecific antibodies from the complementary anti-EGFR and anti-CD3 mAbs was confirmed by cation exchange chromatography (**Figure 10**). Antibodies were analyzed by cation exchange chromatography using Agilent 1260 Infinity Quaternary HPLC with Thermo Scientific ProPac™ SCX-10 HPLC Column, 4 x 250 mm, 10 μ m at 35°C. Thermo Scientific CX-1 pH Gradient Buffers were used as mobile phases (**Table 7** contains gradient steps). 50 μ g of protein sample was loaded and separated with flow rate of 0.5 ml/min, eluted at gradient shown in table below over 35 minutes.

To assess TDCC activity, serial dilutions of bispecific antibodies and control mAbs were incubated with activated T cells and luciferized EGFR-bearing BxPC3 target cells at an effector:target ratio of 5:1 in a 384-well plate (**Figure 11, Table 8**). After 3-day incubation at 37 °C, BrightGlo reagent was added to read out luminescence, which is proportional to the number of remaining target cells. The bispecific cetuximab x α CD3 antibody showed potent tumor cell killing with an EC50 value of 24.6 nM. Aglycosylated N85E and humanized H7 showed similar EC50 values (30.7 and 20.3 pM, respectively) with overlapping 95% confidence intervals. In contrast, none of the control mAbs (α CD3, cetuximab, or cetuximab H7) showed any BxPC3 killing up to 30 nM, indicating that cytotoxicity required simultaneous targeting of both tumor cells and T cells. Thus, the humanized version of cetuximab retained the biological functionality of cetuximab when tested in a TDCC assay.

Example 7. Penta-GNC antibodies having a humanized anti-EGFR scFv or Fab domain

Humanized EGFR binding variants, H1, H4, and H7, were configured and cloned into PentaGNC format in either one of four scFv positions or the Fab position (**Figure 12**, D1 or D2 position). Proteins were transfected into 25 mL of ExpiCHO and expressed for 8 days before harvesting and purifying via protein A affinity chromatography. The proteins were expressed with good titer (**Table 9**).

Analytical SEC data after protein A purification demonstrates that the penta-GNC antibodies comprising a humanized anti-EGFR domain, as either a scFv or Fab, can be expressed with low aggregation (**Figure 13, Table 9**).

Octet was used to verify that the penta-GNC antibodies having a humanized anti-EGFR domain (e.g. H1, H4, H7) can bind to human EGFR (**Figure 14**). The penta-GNC antibodies were loaded via AHC sensors at 10 μ g/ml and bound to a serial dilution (highest 200 nM, 1:2.5 dilutions)

or a single 100-nM concentration of His-tagged human EGFR. The resulting global fit to a 1:1 binding model demonstrated that the penta-GNC antibodies bind to EGFR with affinities in the low nanomolar range (**Table 10**).

Two penta-GNC antibodies were tested for their TDCC activity using luciferized BxPC3 cells as target cells (**Figure 15**). 5-fold serial dilutions (0-30 nM) of pentaGNC antibodies were dosed to a mixture of 500 BxPC3 cells and 2500 activated T cells (effector:target at 5:1), which were incubated for 72 hours before measuring the luminescence readout corresponding to viability of the target cells. Resulting fits to a sigmoidal function revealed that the EGFR-binding domains (H7) of the penta-GNC antibodies efficiently targeted the BxPC3 tumor cells for killing by co-incubated T cells, as demonstrated by EC50 values in the sub-picomolar range (**Table 9**).

Example 8. Hexa-GNC antibodies having a humanized anti-EGFR scFv or Fab domain

The humanized anti-EGFR binding variant, H7, was configured and cloned into the hexa-GNC format in either one of five scFv positions or the Fab position (**Figure 12**, D1 or D2 position). Proteins were transfected into 25 mL of ExpiCHO and expressed for 8 days before harvesting and purifying via protein A affinity chromatography. The proteins were expressed with good titer (**Table 11**).

Analytical SEC data after protein A purification demonstrates that the hexa-GNC molecules containing a humanized anti-EGFR domain, either a scFv or a Fab can be expressed with low aggregation (**Figure 16**, **Table 11**). Notably, both proteins containing version H7 had significantly less aggregation than the protein with cetuximab.

Octet was used to verify that the hexa-GNC antibodies containing a humanized anti-EGFR domain can bind to human EGFR (**Figure 17**). The hexa-GNC proteins were loaded via AHC sensors at 10 ug/ml and bound to a serial dilution (highest 200 nM, 1:2.5 dilutions) or a single 100-nM concentration of His-tagged human EGFR. The resulting global fit to a 1:1 binding model demonstrated that the hexaGNC antibodies bind to EGFR with affinities in the low nanomolar range (**Table 11**).

One HexaGNC was tested for activity in a TDCC bioassay using luciferized BxPC3 cells as target cells (**Figure 18**). 5 -fold serial dilutions (0-30 nM) of the hexa-GNC antibodies were dosed to a mixture of 500 BxPC3 cells and 2500 activated T cells, which were incubated for 72 hours before measuring the luminescence readout corresponding to viability of the target cells. Resulting fits to a sigmoidal function revealed that the EGFR-binding domain (H7) of the hexa-GNC antibody efficiently targeted the BxPC3 tumor cells for killing by co-incubated T cells, as demonstrated by an EC50 value in the sub-picomolar range (**Table 11**).

Example 9. Penta-miniGNC antibodies having a humanized anti-EGFR scFv or Fab domain

Humanized EGFR binding variants, H1, H4, and H7, were configured and cloned into the penta-miniGNC format (PCT/US2021/022847, incorporated herein by reference in its entirety) at either one of four scFv positions (mD1, mD2, mD4, mD5) or the Fab (mD3) position (**Figure 19**).

Proteins were transfected into 25 mL of ExpiCHO and expressed for 8 days before harvesting and purifying via protein A affinity chromatography. The proteins were expressed with good titer (**Table 12**).

Analytical SEC data after protein A purification demonstrates that penta-miniGNC molecules containing a humanized anti-EGFR domain can be expressed with low aggregation (**Figure 20, Table 12**).

Octet was used to verify that the penta-miniGNC antibodies containing humanized anti-EGFR domains (H4, H7) can bind to human EGFR (**Figure 21**). The penta-miniGNC antibodies were loaded via AHC sensors at 10 ug/ml and bound to a serial dilution (highest 200 nM, 1:2.5 dilutions) or a single 100-nM concentration of His-tagged human EGFR. The resulting global fit to a 1:1 binding model demonstrated that the penta-miniGNC antibodies bind to EGFR with affinities in the low nanomolar range (**Table 12**).

Two penta-miniGNC antibodies were tested for TDCC activity using luciferized BxPC3 cells as target cells (**Figure 22**). 5-fold serial dilutions (0-30 nM) of penta-miniGNC antibodies were dosed to a mixture of 500 BxPC3 cells and 2500 activated T cells (effector:target at 5:1), which were incubated for 72 hours before measuring the luminescence readout corresponding to viability of the target cells. Resulting fits to a sigmoidal function revealed that the EGFR-binding variant, H7, of the penta-miniGNC antibody efficiently targeted the BxPC3 tumor cells for killing by co-incubated T cells, as demonstrated by EC50 values in the sub-picomolar range (**Table 12**).

TABLES

Table 1. Humanization of VH/VK regions predicts reduced immunogenicity and increased humanness scores (framework regions only)

Version	Core peptides	CDR residues in core peptide	Sequence length	VH T20 score	VK T20 score
Cetuximab	13	12	241	66.44	70.38
H1	9	12	241	88.10	87.69
H2	10	6	241	77.07	81.44
H3	11	6	241	76.95	82.56
H4	11	6	241	77.47	86.26
H5	8	10	241	78.56	82.88
H6	9	10	241	77.30	83.63
H7	11	6	241	77.47	84.04
H8	11	12	241	81.09	86.31
H9	11	12	241	81.09	82.63
H10	7	10	241	85.11	91.04
H11	7	10	241	85.11	87.44

Table 2. Methods for generating humanized cetuximab variants

Humanized version	Method	Basis	Starting sequence/model	Modification
H1	CDR graft onto stable framework	Sequence	Cetuximab, FW1.4gen	None
H2	DS Best Single Mutations	Model	PDB 1YY9	None
H3	DS Best Single Mutations	Model	Cetuximab model	None
H4	DS Best Single Mutations	Model	Cetuximab model (TVSS)	None
H5	DS Best Single Mutations	Model	Cetuximab model (LTVL)	None
H6	DS Best Single Mutations	Model	Cetuximab model (TVSS-LTVL)	None
H7	DS Best Single Mutations	Model	Cetuximab model (TVSS)	Lambda J
H8	DS Frequent Residue Substitutions	Sequence	Cetuximab	None
H9	DS Frequent Residue Substitutions	Sequence	Cetuximab	Lambda J
H10	DS Germline Substitutions	Sequence	Cetuximab	None
H11	DS Germline Substitutions	Sequence	Cetuximab	Lambda J

Table 3. The sequence identity matrices of the entire VH domain (**A**), VH framework regions (entire VH domain, except Kabat CDR residues) (**B**), the entire VL domain (**C**), and the VL framework regions (entire VL domain, except Kabat CDR residues) (**D**), for wild-type cetuximab, aglycosylated cetuximab (N85E), and humanized cetuximab versions (H1-H11), respectively.

VH identity matrix -- all residues													
	WT	N85E	H1	H10	H11	H8	H9	H2	H3	H4	H7	H5	H6
WT		99.2	78.2	84.9	84.9	85.7	85.7	86.6	84.9	84.9	84.9	84.9	84.0
N85E	99.2		79.0	84.9	84.9	86.6	86.6	87.4	85.7	84.9	84.9	85.7	84.9
H1	78.2	79.0		84.9	84.9	92.4	92.4	82.4	82.4	79.8	79.8	81.5	79.8
H10	84.9	84.9	84.9		100.0	92.4	92.4	87.4	85.7	86.6	86.6	89.1	86.6
H11	84.9	84.9	84.9	100.0		92.4	92.4	87.4	85.7	86.6	86.6	89.1	86.6
H8	85.7	86.6	92.4	92.4	92.4		100.0	89.9	89.9	87.4	87.4	89.1	87.4
H9	85.7	86.6	92.4	92.4	92.4	100.0		89.9	89.9	87.4	87.4	89.1	87.4
H2	86.6	87.4	82.4	87.4	87.4	89.9	89.9		95.0	96.6	96.6	95.0	94.1
H3	84.9	85.7	82.4	85.7	85.7	89.9	89.9	95.0		95.0	95.0	94.1	94.1
H4	84.9	84.9	79.8	86.6	86.6	87.4	87.4	96.6	95.0		100.0	93.3	95.8
H7	84.9	84.9	79.8	86.6	86.6	87.4	87.4	96.6	95.0	100.0		93.3	95.8
H5	84.9	85.7	81.5	89.1	89.1	89.1	89.1	95.0	94.1	93.3	93.3		94.1
H6	84.0	84.9	79.8	86.6	86.6	87.4	87.4	94.1	94.1	95.8	95.8	94.1	
VH identity matrix -- framework residues													
	WT	N85E	H1	H10	H11	H8	H9	H2	H3	H4	H7	H5	H6
WT		98.9	70.1	79.3	79.3	80.5	80.5	81.6	79.3	79.3	79.3	79.3	78.2
N85E	98.9		71.3	79.3	79.3	81.6	81.6	82.8	80.5	79.3	79.3	80.5	79.3
H1	70.1	71.3		79.3	79.3	89.7	89.7	75.9	75.9	72.4	72.4	74.7	72.4
H10	79.3	79.3	79.3		100.0	89.7	89.7	82.8	80.5	81.6	81.6	85.1	81.6
H11	79.3	79.3	79.3	100.0		89.7	89.7	82.8	80.5	81.6	81.6	85.1	81.6
H8	80.5	81.6	89.7	89.7	89.7		100.0	86.2	86.2	82.8	82.8	85.1	82.8
H9	80.5	81.6	89.7	89.7	89.7	100.0		86.2	86.2	82.8	82.8	85.1	82.8
H2	81.6	82.8	75.9	82.8	82.8	86.2	86.2		93.1	95.4	95.4	93.1	92.0
H3	79.3	80.5	75.9	80.5	80.5	86.2	86.2	93.1		93.1	93.1	92.0	92.0
H4	79.3	79.3	72.4	81.6	81.6	82.8	82.8	95.4	93.1		100.0	90.8	94.3
H7	79.3	79.3	72.4	81.6	81.6	82.8	82.8	95.4	93.1	100.0		90.8	94.3
H5	79.3	80.5	74.7	85.1	85.1	85.1	85.1	93.1	92.0	90.8	90.8		92.0
H6	78.2	79.3	72.4	81.6	81.6	82.8	82.8	92.0	92.0	94.3	94.3	92.0	
VL identity matrix -- all residues													
	WT	N85E	H1	H10	H11	H8	H9	H2	H3	H4	H7	H5	H6
WT		100.0	70.1	83.2	81.3	85.0	83.2	86.0	85.0	82.2	79.4	82.2	84.1
N85E	100.0		70.1	83.2	81.3	85.0	83.2	86.0	85.0	82.2	79.4	82.2	84.1
H1	70.1	70.1		79.4	82.2	80.4	83.2	77.6	80.4	80.4	83.2	76.6	78.5
H10	83.2	83.2	79.4		97.2	95.3	92.5	88.8	87.9	91.6	89.7	88.8	88.8
H11	81.3	81.3	82.2	97.2		92.5	95.3	86.9	86.0	89.7	92.5	87.9	86.9
H8	85.0	85.0	80.4	95.3	92.5		97.2	87.9	88.8	89.7	87.9	86.9	88.8
H9	83.2	83.2	83.2	92.5	95.3	97.2		86.0	86.9	87.9	90.7	86.0	86.9
H2	86.0	86.0	77.6	88.8	86.9	87.9	86.0		95.3	95.3	92.5	90.7	90.7
H3	85.0	85.0	80.4	87.9	86.0	88.8	86.9	95.3		95.3	92.5	88.8	91.6
H4	82.2	82.2	80.4	91.6	89.7	89.7	87.9	95.3	95.3		97.2	93.5	90.7
H7	79.4	79.4	83.2	89.7	92.5	87.9	90.7	92.5	92.5	97.2		93.5	89.7
H5	82.2	82.2	76.6	88.8	87.9	86.9	86.0	90.7	88.8	93.5	93.5		91.6
H6	84.1	84.1	78.5	88.8	86.9	88.8	86.9	90.7	91.6	90.7	89.7	91.6	
VL identity matrix -- framework residues													
	WT	N85E	H1	H10	H11	H8	H9	H2	H3	H4	H7	H5	H6
WT		100.0	60.0	77.5	75.0	80.0	77.5	81.3	80.0	76.3	72.5	76.3	78.8
N85E	100.0		60.0	77.5	75.0	80.0	77.5	81.3	80.0	76.3	72.5	76.3	78.8
H1	60.0	60.0		72.5	76.3	73.8	77.5	70.0	73.8	73.8	77.5	68.8	71.3
H10	77.5	77.5	72.5		96.3	93.8	90.0	85.0	83.8	88.8	86.3	85.0	85.0
H11	75.0	75.0	76.3	96.3		90.0	93.8	82.5	81.3	86.3	90.0	83.8	82.5
H8	80.0	80.0	73.8	93.8	90.0		96.3	83.8	85.0	86.3	83.8	82.5	85.0
H9	77.5	77.5	77.5	90.0	93.8	96.3		81.3	82.5	83.8	87.5	81.3	82.5
H2	81.3	81.3	70.0	85.0	82.5	83.8	81.3		93.8	93.8	90.0	87.5	87.5
H3	80.0	80.0	73.8	83.8	81.3	85.0	82.5	93.8		93.8	90.0	85.0	88.8
H4	76.3	76.3	73.8	88.8	86.3	86.3	83.8	93.8	93.8		96.3	91.3	87.5
H7	72.5	72.5	77.5	86.3	90.0	83.8	87.5	90.0	90.0	96.3		91.3	86.3
H5	76.3	76.3	68.8	85.0	83.8	82.5	81.3	87.5	85.0	91.3	91.3		88.8
H6	78.8	78.8	71.3	85.0	82.5	85.0	82.5	87.5	88.8	87.5	86.3	88.8	

Table 4. EGFR binding complex in the forms of humanized EGFR binding sequence variants (variable regions H1-H11), His-tagged scFv protein (scFv-6His), recombinant scFv-monoFc monomer (scFv-monoFc), monoclonal antibody (mAb), bispecific antibody (bispecific), penta-GNC antibody (pentaGNC), hexa-GNC antibody (hexaGNC), and penta-miniGNC antibody (miniGNC).

Cetuximab version	scFv-6His	scFv-monoFc	mAb	Bispecific	PentaGNC	HexaGNC	miniGNC
Wild-type	SI-79R1	SI-79SF1	SI-79C1	SI-79X1		SI-77H5	
Aglycosylated (N85E)		SI-79SF2	SI-79C5	SI-79X5			
H1	SI-79R2	SI-79SF3			SI-55P3 SI-55P4		SI-68P7
H2		SI-79SF12					
H3		SI-79SF10					
H4		SI-79SF4	SI-79C2	SI-79X2	SI-79P2 SI-79P3		SI-79P1
H5		SI-79SF11					
H6		SI-79SF9					
H7		SI-79SF6	SI-79C3	SI-79X3	SI-55P9 SI-77P1	SI-55H11 SI-77H4	SI-68P13 SI-68P17
H8		SI-79SF5					
H9		SI-79SF7					
H10		SI-79SF8					
H11		SI-79SF13					

Table 5. Characterization of His-tagged humanized anti-EGFR scFv.

Protein	α huEGFR	Titer (ug/ml)	aSEC %POI	DLS Tm (°C)	Gdn EC50 (M)	huEGFR KD (nM)
SI-79R1	Cetuximab	13.8	39.5	47.87	1.42	2.08
SI-79R2	H1	108.2	84.5	71.37	2.92	12.0

Table 6. Biophysical properties of cetuximab-derived scFv-monoFc proteins. Values are average and standard deviation of two independent experiments.

Version	Titer ($\mu\text{g/ml}$)	aSEC %POI	DLS Temp ($^{\circ}\text{C}$)	EGFR K_D (nM)	k_a [$1/(\text{M}\cdot\text{s})$] $\times 10^5$	k_d (1/s) $\times 10^{-3}$
WT	163 $\pm$ 39	93.6 $\pm$ 2.6	47.2 $\pm$ 1.0	3.18 $\pm$ 0.18	4.44 $\pm$ 1.13	1.42 $\pm$ 0.44
N85E	116 $\pm$ 6	94.9 $\pm$ 3.1	44.5 $\pm$ 1.3	3.16 $\pm$ 0.35	4.44 $\pm$ 0.91	1.42 $\pm$ 0.44
H1	309 $\pm$ 26	91.5 $\pm$ 7.1	46.2 $\pm$ 0.9	13.1 $\pm$ 1.2	7.18 $\pm$ 1.68	9.27 $\pm$ 1.34
H2	411 $\pm$ 59	86.8 $\pm$ 2.1	52.4 $\pm$ 2.1	3.08 $\pm$ 0.68	4.81 $\pm$ 0.91	1.51 $\pm$ 0.61
H3	418 $\pm$ 8	88.1 $\pm$ 2.7	52.3 $\pm$ 2.0	3.45 $\pm$ 0.81	5.04 $\pm$ 0.92	1.77 $\pm$ 0.73
H4	412 $\pm$ 5	82.6 $\pm$ 5.5	49.7 $\pm$ 1.4	3.05 $\pm$ 0.62	4.50 $\pm$ 0.54	1.39 $\pm$ 0.44
H5	394 $\pm$ 23	85.6 $\pm$ 6.2	50.2 $\pm$ 1.5	2.27 $\pm$ 0.38	4.74 $\pm$ 1.31	1.10 $\pm$ 0.48
H6	372 $\pm$ 73	88.0 $\pm$ 3.4	52.2 $\pm$ 2.0	3.42 $\pm$ 0.36	4.76 $\pm$ 1.33	1.65 $\pm$ 0.62
H7	506 $\pm$ 14	92.7 $\pm$ 2.3	50.5 $\pm$ 2.4	3.14 $\pm$ 0.53	4.47 $\pm$ 0.97	1.43 $\pm$ 0.54
H8	220 $\pm$ 3	92.2 $\pm$ 0.0	51.3 $\pm$ 1.1	6.79 $\pm$ 1.35	5.71 $\pm$ 0.78	3.93 $\pm$ 1.30
H9	211 $\pm$ 22	97.4 $\pm$ 0.9	48.7 $\pm$ 1.3	6.92 $\pm$ 1.58	5.63 $\pm$ 0.67	3.95 $\pm$ 1.35
H10	308 $\pm$ 3	83.7 $\pm$ 1.9	52.6 $\pm$ 1.3	6.77 $\pm$ 2.10	6.65 $\pm$ 0.73	4.58 $\pm$ 1.89
H11	376 $\pm$ 12	88.6 $\pm$ 2.4	53.0 $\pm$ 1.3	6.74 $\pm$ 1.61	6.61 $\pm$ 1.11	4.54 $\pm$ 1.81

Table 7: Gradient method for cation exchange separation of αEGFR and αCD3 antibodies.

Gradient	Time (min)	%B
	0.00	0.0
	3.00	0.0
	5.00	25.0
	20.00	70.0
	20.01	100.0
	25.00	100.0
	25.01	0.0
	35.00	0.0

Table 8. Biophysical properties of cetuximab-derived monoclonal antibodies. Values are average and standard deviation of two independent experiments.

Version	Titer ($\mu\text{g/ml}$)	aSEC %POI	DLS Temp ($^{\circ}\text{C}$)	EGFR KD (nM)	k_a [$1/(\text{M}\cdot\text{s})$] $\times 10^5$	k_d (1/s) $\times 10^{-4}$	*EC50 (pM)
WT	203 $\pm$ 13	99.9 $\pm$ 0.2	68.3 $\pm$ 0.1	2.68 $\pm$ 0.07	3.46 $\pm$ 0.27	9.26 $\pm$ 0.48	24.6 [10.4-58.4]
N85E	209 $\pm$ 9	99.4 $\pm$ 0.3	68.1 $\pm$ 0.9	2.46 $\pm$ 0.28	3.26 $\pm$ 0.41	7.96 $\pm$ 0.09	30.7 [11.3-83.8]
H7	249 $\pm$ 1	99.1 $\pm$ 0.4	72.5 $\pm$ 1.2	2.41 $\pm$ 0.15	3.37 $\pm$ 0.20	8.12 $\pm$ 0.05	20.3 [13.9-29.9]

*EC50 value for depleting EGFR+ BxPC3 cells using $\alpha\text{CD3} \times \alpha\text{EGFR}$ bispecific antibody, with 95% confidence interval shown in brackets.

Table 9. Characterization of the penta-GNC antibodies comprising a humanized anti-EGFR scFv domain or a humanized anti-EGFR Fab region.

GNC Ab	αEGFR Variant	GNC Domain	GNC binding domains	Titer ($\mu\text{g/ml}$)	aSEC %POI	huEGFR K_D (nM)	TDCC EC50 (pM)
SI-55P3	H1	scFv (1)	αCD3 (2), $\alpha\text{PD-L1}$ (3), $\alpha 4\text{-1BB}$ (4), αCD19 (6)	175.9	86.13	18.1	nd
SI-55P4	H1	scFv (1)	αCD3 (2), $\alpha\text{PD-L1}$ (3), 41BBLT (4), αCD19 (6)	59.6	93.22	nd	nd
SI-79P2	H4	scFv (1)	αCD3 (2), $\alpha\text{PD-L1}$ (3), $\alpha 4\text{-1BB}$ (4), αCD19 (6)	68.9	87.74	4.30	nd
SI-79P3	H4	scFv (1)	αCD3 (2), $\alpha\text{PD-L1}$ (3), 41BBLT (4), αCD19 (6)	70.3	92.80	5.21	nd
SI-55P9	H7	scFv (1)	αCD3 (2), $\alpha\text{PD-L1}$ (3), $\alpha 4\text{-1BB}$ (4), αCD19 (6)	118.0	85.96	6.88	0.5727
SI-77P1	H7	Fab (2)	αCD3 (1), $\alpha\text{PD-L1}$ (3), $\alpha 4\text{-1BB}$ (4), αCD19 (6)	98.1	77.94	2.17	0.0826

Table 10. Octet binding analysis of EGFR binding complex.

Protein	Octet Binding Kinetics		
	K _D (nM)	k _a (M ⁻¹ s ⁻¹)	k _d (s ⁻¹)
SI-79R1	2.08	657000	0.00137
SI-79R2	12.00	894000	0.01070
SI-55P3	18.10	601000	0.01090
SI-79P2	4.30	328000	0.00141
SI-79P3	5.21	284000	0.00148
SI-55P9	6.88	297000	0.00204
SI-77P1	2.17	212000	0.00046
SI-77H5	3.39	286000	0.00097
SI-55H11	4.65	268000	0.00125
SI-77H4	3.29	214000	0.00122
SI-79P1	3.03	425000	0.00158
SI-68P13	5.64	389000	0.00219
SI-68P17	2.46	259000	0.00064

Table 11. Characterization of the hexaGNC antibodies comprising a humanized anti-EGFR scFv domain or a humanized anti-EGFR Fab region.

GNC Ab	αEGFR Variant	GNC Domain	GNC binding domains	Titer (μg/ml)	aSEC %POI	huEGFR K _D (nM)	TDCC EC50 (pM)
SI-77H5	Cetuximab	Fab (2)	αCD3 (1), αPD-L1 (3), α4-1BB (4), αHER3 (5), αCD19 (6)	35.0	72.02	3.39	nd
SI-77H4	H7	Fab (2)	αCD3 (1), αPD-L1 (3), α4-1BB (4), αHER3 (5), αCD19 (6)	61.1	77.25	3.29	nd
SI-55H11	H7	scFv (1)	αCD3 (2), αPD-L1 (3), α4-1BB (4), αHER3 (5), αCD19 (6)	30.0	84.42	4.65	0.09387

Table 12. Characterization of the penta-miniGNC antibodies comprising a humanized anti-EGFR scFv domain or a humanized anti-EGFR Fab domain.

GNC Ab	αEGFR Variant	miniGNC Domain	GNC binding domains	Titer (μg/ml)	aSEC %POI	huEGFR K _D (nM)	TDCC EC50 (pM)
SI-68P7	H1	scFv (1)	αCD19 (2), αCD3 (3), 41BBLT (4), αPD-L1 (5)	85.2	84.60	nd	nd
SI-79P1	H4	scFv (1)	αCD19 (2), αCD3 (3), α4-1BB (4), αPD-L1 (5)	75.3	72.61	3.03	nd
SI-68P13	H7	scFv (1)	αCD19 (2), αCD3 (3), α4-1BB (4), αPD-L1 (5)	76.6	87.69	5.64	0.259
SI-68P17	H7	Fab (3)	αCD3 (1), αCD19 (2), α4-1BB (4), αPD-L1 (5)	62.0	54.87	2.46	0.322

SEQUENCE LISTING

Sequences of humanized EGFR binding sequence variants (H1-H11)

Sequence	Amino acid seq. ID	Nucleotide seq. ID
H1 VH	1	2
H1 VL	3	4
H2 VH	5	6
H2 VL	7	8
H3 VH	9	10
H3 VL	11	12
H4 VH	13	14
H4 VL	15	16
H5 VH	17	18
H5 VL	19	20
H6 VH	21	22
H6 VL	23	24
H7 VH	25	26
H7 VL	27	28
H8 VH	29	30
H8 VL	31	32
H9 VH	33	34
H9 VL	35	36
H10 VH	37	38
H10 VL	39	40
H11 VH	41	42
H11 VL	43	44

Sequences of antibody constant regions, linker motifs, and tags

Sequence	Amino acid seq. ID	Nucleotide seq. ID
MonoFc	45	46
Human IgG1	47	48
Human C kappa	49	50
(G4S) ₄ linker	51	52
His tag	53	54

Sequences of α EGFR scFv-His proteins

Sequence	Amino acid seq. ID	Nucleotide seq. ID
SI-79R1	55	56
SI-79R2	57	58

Sequences of α EGFR scFv-monoFc proteins

Sequence	Amino acid seq. ID	Nucleotide seq. ID
SI-79SF1	59	60
SI-79SF2	61	62
SI-79SF3	63	64
SI-79SF4	65	66
SI-79SF5	67	68
SI-79SF6	69	70
SI-79SF7	71	72
SI-79SF8	73	74
SI-79SF9	75	76
SI-79SF10	77	78
SI-79SF11	79	80
SI-79SF12	81	82
SI-79SF13	83	84

Sequences of pentaGNC proteins containing a humanized EGFR binding domain

Sequence	Amino acid seq. ID	Nucleotide seq. ID
SI-55P3 HC	85	86
SI-55P3 LC	87	88
SI-55P4 HC	89	90
SI-55P4 LC	91	92
SI-79P2 HC	93	94
SI-79P2 LC	95	96
SI-79P3 HC	97	98
SI-79P3 LC	99	100
SI-55P9 HC	101	102
SI-55P9 LC	103	104
SI-77P1 HC	105	106
SI-77P1 LC	107	108

Sequences of hexaGNC proteins containing a humanized EGFR binding domain

Sequence	Amino acid seq. ID	Nucleotide seq. ID
SI-77H5 HC	109	110
SI-77H5 LC	111	112
SI-55H11 HC	113	114
SI-55H11 LC	115	116
SI-77H4 HC	117	118
SI-77H4 LC	119	120

Sequences of penta-miniGNC proteins containing a humanized EGFR binding domain

Sequence	Amino acid seq. ID	Nucleotide seq. ID
SI-68P7 HC	121	122
SI-68P7 LC	123	124
SI-79P1 HC	125	126
SI-79P1 LC	127	128
SI-68P13 HC	129	130
SI-68P13 LC	131	132
SI-68P17 HC	133	134
SI-68P17 LC	135	136

Sequences of α EGFR mAbs and α CD3 mAbs

Sequence	Amino acid seq. ID	Nucleotide seq. ID
SI-79C1 HC	137	138
SI-79C1 LC	139	140
SI-79C2 HC	141	142
SI-79C2 LC	143	144
SI-79C3 HC	141	142
SI-79C3 LC	149	150
SI-79C5 HC	151	152
SI-79C5 LC	139	140
SI-9C21 HC	145	146
SI-9C21 LC	147	148

Sequences of α EGFR x α CD3 bispecific antibodies

Sequence	Amino acid seq. ID	Nucleotide seq. ID
SI-79X1 HC1	137	138
SI-79X1 HC2	145	146
SI-79X1 LC1	139	140
SI-79X1 LC2	147	148
SI-79X2 HC1	141	142
SI-79X2 HC2	145	146
SI-79X2 LC1	143	144
SI-79X2 LC2	147	148
SI-79X3 HC1	141	142
SI-79X3 HC2	145	146
SI-79X3 LC1	149	150
SI-79X3 LC2	147	148
SI-79X5 HC1	151	152
SI-79X5 HC2	145	146
SI-79X5 LC1	139	140
SI-79X5 LC2	147	148

>Sequence ID 1: Cetuximab H1 VH amino acid sequence
EVQLVESGGGLVQPGGSLRLSCKVSGFSLTNYGVHWVRQAPGKGLEWVGVIWSGGNTDYNTPFTSRFTISRDTSKNTVYLMNSLR
AEDTAVYYCARALTYDYEFAYWGQGLVTVSS

>Sequence ID 2: Cetuximab H1 VH nucleotide sequence
GAAGTTCAGCTGGTGGAAATCCGGCGGAGGATTGGTTCACCTGGCGGCTCTCTGAGACTGTCTGTAGGTGTCTGGCTTCTCCCT
GACCAACTACGGCGTGCAGTGGGTCCGACAGGCACCTGGAAAAGGACTGGAATGGGTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTCACCATCTCTCGGACACCTCCAAGAACCAGGTGTACCTGCAGATGAACTCCCTGAGA
GCCGAGGACACCGCGTGTACTATTGTGTAGAGCCCTGACCTACTATGACTACGAGTTCGCCTATTGGGGCCAGGGAACCCTGGT
CACAGTCTCTCT

>Sequence ID 3: Cetuximab H1 VL amino acid sequence
EIVMTQSPSTLSASVGDRIITCRASQSIGTNIHWYQQKPKAPKLLIYASESISGIPSRFSGSGSGAEFTLTISLQPDFATY
YCQQNNWPPTTFGQGTKLV

>Sequence ID 4: Cetuximab H1 VL nucleotide sequence
GAGATCGTGATGACCCAGTCTCCTTCCACACTGTCCGCCTCTGTGGGCGACAGAGTGATCATCACCTGTAGAGCCAGCCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGCAAGGCCCTAAGCTGCTGATCTACTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGATCTGGCGCTGAGTTACCTGACAATCTCCAGCCTGCAGCCTGACGACTTCGCCACCTAC
TACTGCCAGCAGAACAACAACTGGCCACACCTTTGGCCAGGGCACCAAACTGACAGTTCTT

>Sequence ID 5: Cetuximab H2 VH amino acid sequence
QVQLQSGPGLVKPSQTLSTCTVSGFSLTNYGVHWIRQAPGKLEWLVGIWSGGNTDYNTPFTSRFTISKDNSKNQVYFKLRSLR
AEDTAIYYCARALTYDYEFAYWGQGLVTVSS

>Sequence ID 6: Cetuximab H2 VH nucleotide sequence
CAAGTTCAGTGCAGCAGTCTGGCCCTGGCCTCGTGAAGCCTTCTCAGACCCTGTCTATCACCTGTACCGTGTCCGGCTTCTCCCT
GACCAATTACGGCGTGCAGTGGATCAGACAGGCCCTGGCAAAGGACTGGAATGGGTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTCACCATCTCCAAGGACAACCTCCAAGAACCAGGTGTACTTCAAGCTGCGGTCCCTGAGA
GCCGAGGACACCGCATCTACTACTGTGTAGAGCCCTGACCTACTACGACTACGAGTTCGCCTATTGGGGCCAGGGCACACTGGT
CACAGTCTCTCT

>Sequence ID 7: Cetuximab H2 VL amino acid sequence
EIVLTQSPSILSVSPGERATFSCRASQSIGTNIHWYQQRPGKPPRLIKYASESISGIPSRFSGSGSGTEFTLTITSVQSEDIAYV
YCQQNNWPPTTFGPGTKLELK

>Sequence ID 8: Cetuximab H2 VL nucleotide sequence
GAGATCGTGCTGACCCAGTCTCCTTCCATCCTGTCTGTGTCTCCCGGCGAGAGGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGCGGCCTGGCAAGCCTCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGATCTGGCACCAGTTACCTGACCATCACCTCCGTGCAGTCCGAGGATATCGCCGTGTAC
TACTGCCAGCAGAACAACAACTGGCCACACCTTTGGACCCGGCACCAAGCTGGAATTGAAA

>Sequence ID 9: Cetuximab H3 VH amino acid sequence
QVQLVQSGPGLVKPSQTLSTCTVSGFSLTNYGVHWIRQAPGKLEWLVGIWSGGNTDYNTPFTSRFTITKDNSKNQVYFKLRSVR
SEDTAVYYCARALTYDYEFAYWGQGLVTVSS

>Sequence ID 10: Cetuximab H3 VH nucleotide sequence
CAAGTTCAGCTGGTTCAGTCTGGCCCTGGCCTCGTGAAGCCTTCTCAGACCCTGTCTCTGACCTGCACCGTGTCTGGCTTCTCCCT
GACCAATTACGGCGTGCAGTGGATCAGACAGGCCCTGGCAAAGGACTGGAATGGGTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTCACCATCACCAGGACAACCTCCAAGAACCAGGTGTACTTCAAGCTGAGATCCGTGCGG
AGCGAGGACACCGCGTGTACTATTGTGCTAGAGCCCTGACCTACTACGACTACGAGTTCGCCTATTGGGGCCAGGGCACACTGGT
CACAGTCTCTCT

>Sequence ID 11: Cetuximab H3 VL amino acid sequence
EIVLTQSPSILSVSPGERVTFSCRASQSIGTNIHWYQQRPGKPPRLIKYASESISGIPARFSGSGSGTEFTLTISVQSEDFATY
YCQQNNWPPTTFGPGTKLELK

>Sequence ID 12: Cetuximab H3 VL nucleotide sequence
GAGATCGTGCTGACCCAGTCTCCTTCCATCCTGTCTGTGTCTCCCGGCGAGAGAGTGACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGCGGCCTGGCAAGCCTCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGCCAGATTTCCGGCTCTGGCTCTGGCACCAGTTACCTGACCATCTCCTCCGTGCAGTCCGAGGATTTGCCACCTAC
TACTGCCAGCAGAACAACAACTGGCCACACCTTTGGACCCGGCACCAAGCTGGAATTGAAA

>Sequence ID 13: Cetuximab H4 VH amino acid sequence
QVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGLEWLGVWSGGNTDYNTPFTSRFTITKDNSKNQVYFKLRSVR
ADDTAIYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 14: Cetuximab H4 VH nucleotide sequence
CAAGTTCAGTTGCAGCAGTCTGGCCCTGGCCTGGTCAAGCCTTCTGAGACACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCT
GACCAATTACGGCGTGCACTGGATCAGACAGGCCCTGGCAAAGGACTGGAATGGCTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTACCATCACCAAGGACAACCTCCAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGCGG
GCTGATGACACCGCATCTACTACTGTGCTCGGGCCCTGACCTACTACGACTACGAGTTTGCTTACTGGGGCCAGGGCACCTGGT
CACAGTTTCTTCT

>Sequence ID 15: Cetuximab H4 VL amino acid sequence
EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDAFVY
YCQQNNWPPTTFGPQTKLELK

>Sequence ID 16: Cetuximab H4 VL nucleotide sequence
GAGATCGTGCTGACCCAGTCTCCTTCCACACTGTCTGTCTCTCCGGCGAGAGAGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAAGCCCGGCAAGCCTCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTACCTGACCATCTCCTCCGTGCAGTCCGAGGATTCGCCGTGTAC
TACTGCCAGCAGAACAACTGGCCACACCTTTGGACCCGGCACCAAGCTGGAATTGAAA

>Sequence ID 17: Cetuximab H5 VH amino acid sequence
QVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGLEWIGVIWSGGNTDYNTPFTSRFTISKDNSKNQVYFKLRSLT
SEDTAIYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 18: Cetuximab H5 VH nucleotide sequence
CAAGTTCAGTGTTCAGTCTGGCCCTGGCCTGGTCAAGCCTTCCGAAACACTGTCTCTGACCTGCACCGTGTCCGGCTTCTCCCT
GACCAATTATGGCTGCACTGGATCAGACAGGCCCTGGCAAAGCCTGGAATGGATCGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTACCATCTCCAAGGACAACCTCCAAGAACCAGGTGTACTTCAAGCTGCGGTCCCTGACC
TCTGAGGACACCGCATCTACTACTGCGCTAGAGCCCTGACCTACTACGACTACGAGTTGCGCTATTGGGGCCAGGGCACACTGGT
CACAGTCTCTTCT

>Sequence ID 19: Cetuximab H5 VL amino acid sequence
EIQLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDAFVY
YCQQNNWPPTTFGPQTKLEIL

>Sequence ID 20: Cetuximab H5 VL nucleotide sequence
GAGATCCAGCTGACCCAGTCTCCTTCCACACTGTCTGTGTCTCCGGCGAGAGAGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAAACCGGCCAGCCTCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTACCTGTCTATCACCTCCGTGCAGTCCGAGGACTTCGCCGTGTAC
TACTGCCAGCAGAACAACTGGCCACACCTTTGGACCCGGCACCAAGCTGGAAATTCTT

>Sequence ID 21: Cetuximab H6 VH amino acid sequence
QVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGLEWIGVIWSGGNTDYNTPFTSRFTITKDNSKNQVFFKLRSVR
AEDTALYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 22: Cetuximab H6 VH nucleotide sequence
CAAGTTCAGTGTTCAGTCTGGCCCTGGCCTGGTCAAGCCTTCCGAGACACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCT
GACCAATTACGGCGTGCACTGGATCAGACAGGCCCTGGCAAAGCCTGGAATGGATCGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTACCATCACCAAGGACAACCTCCAAGAACCAGGTGTTCTTCAAGCTGCGGAGCGTGCGC
GCTGAGGATACCGCTCTGTACTATTGCGCTCGGGCCCTGACCTACTACGACTACGAGTTTGCTTACTGGGGCCAGGGAACCTGGT
CACCGTTTCTTCT

>Sequence ID 23: Cetuximab H6 VL amino acid sequence
EIVLTQSPSTLSVSPGERVFSRASQSIGTNIHWYQQRTGQPPRLLIKYASESISGIPARFSGSGSGTEFTLTITSVQSEDAFVY
YCQQNNWPPTTFGQTKLDIK

>Sequence ID 24: Cetuximab H6 VL nucleotide sequence
GAGATCGTGCTGACCCAGTCTCCTTCCACACTGTCTGTGTCTCCGGCGAGAGAGTGCTCCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAGAACCGGCCAGCCTCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGCCAGATTTCCGGCTCTGGCTCTGGCACCGAGTTACCTGACCATCACCTCCGTGCAGTCTGAGGACTTCGCCGTGTAC
TACTGCCAGCAGAACAACTGGCCACACCTTTGGCCAGGGCACCAAGCTGGATATCAA

>Sequence ID 25: Cetuximab H7 VH amino acid sequence
QVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGLEWLGVWSGGNTDYNTPFTSRFTITKDNSKNQVYFKLRSVR
ADDTAIYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 26: Cetuximab H7 VH nucleotide sequence
CAAGTTCAGTTGCAGCAGTCTGGCCCTGGCCTGGTCAAGCCTTCTGAGACACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCT
GACCAATTACGGCGTGCATGGATCAGACAGGCCCTGGCAAAGGACTGGAATGGCTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTCACCATCACCAGGACAACCTCCAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGCGG
GCTGATGACACCGCATCTACTACTGTGCTCGGGCCCTGACCTACTACGACTACGAGTTTGCTTACTGGGGCCAGGGCACCCCTGGT
CACAGTTTCTTCT

>Sequence ID 27: Cetuximab H7 VL amino acid sequence
EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDAFVY
YCQQNNWPPTTFGPGTKLTVL

>Sequence ID 28: Cetuximab H7 VL nucleotide sequence
GAGATCGTGCTGACCCAGTCTCCTTCCACACTGTCTGTCTCTCCCGGCGAGAGGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCCGGCAAGCCTCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTACCTGACCATCTCCTCCGTGCAGTCCGAGGATTCGCCGTGTAC
TACTGCCAGCAGAACAACACTGGCCACACCTTTGGACCCGGCACCAAGCTGACAGTTCTT

>Sequence ID 29: Cetuximab H8 VH amino acid sequence
QVQLVESGPGGLVQPSGSLTCTVSGFSLTNYGVHWVRQAPGKGLEWVGVIWSGGNTDYNTPFTSRFTISKDNSKNQVYLMNSLR
AEDTAVYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 30: Cetuximab H8 VH nucleotide sequence
CAAGTTCAGTGGTGAATCTGGCCCTGGCCTGGTTCAGCCTTCTGGCTCTCTGTCTGACCTGCACCGTGTCTGGCTTCTCCCT
GACCAATTACGGCGTGCATGGGTTCGACAGGCTCCAGGCAAAGGACTGGAATGGGTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTCACCATCTCCAAGGACAACCTCCAAGAACCAGGTGTACCTGAAGATGAACCTCCCTGAGA
GCCGAGGACACCGCTGTGTATTACTGTGCTAGAGCCCTGACCTACTACGACTACGAGTTCGCCTATTGGGGCCAGGGAACCCCTGGT
CACAGTCTCTCT

>Sequence ID 31: Cetuximab H8 VL amino acid sequence
DIVLTQSPSSLSVSPGERVTISCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTISVSEDAFVY
YCQQNNWPPTTFGQGTKLEIK

>Sequence ID 32: Cetuximab H8 VL nucleotide sequence
GACATCGTGCTGACCCAGTCTCCATCCAGCCTGTCTGTGTCTCCTGGCGAGAGAGTGACCATCTCTTGCCGGGCTCTCAGAGCAT
GGCACCAACATCCACTGGTATCAGCAGAAGCCTGGACAGGCCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACAGACTTTACCTGACCATCAGCTCCGTGGAATCCGAGGACTTCGCCGTGTAC
TACTGCCAGCAGAACAACACTGGCCACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAA

>Sequence ID 33: Cetuximab H9 VH amino acid sequence
QVQLVESGPGGLVQPSGSLTCTVSGFSLTNYGVHWVRQAPGKGLEWVGVIWSGGNTDYNTPFTSRFTISKDNSKNQVYLMNSLR
AEDTAVYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 34: Cetuximab H9 VH nucleotide sequence
CAAGTTCAGTGGTGAATCTGGCCCTGGCCTGGTTCAGCCTTCTGGCTCTCTGTCTCTGACCTGCACCGTGTCTGGCTTCTCCCT
GACCAATTACGGCGTGCATGGGTTCGACAGGCTCCAGGCAAAGGACTGGAATGGGTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCAGCCGGTTCACCATCTCCAAGGACAACCTCCAAGAACCAGGTGTACCTGAAGATGAACCTCCCTGAGA
GCCGAGGACACCGCTGTGTATTACTGTGCTAGAGCCCTGACCTACTACGACTACGAGTTCGCCTATTGGGGCCAGGGAACCCCTGGT
CACAGTCTCTCT

>Sequence ID 35: Cetuximab H9 VL amino acid sequence
DIVLTQSPSSLSVSPGERVTISCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTISVSEDAFVY
YCQQNNWPPTTFGQGTKLTVL

>Sequence ID 36: Cetuximab H9 VL nucleotide sequence
GACATCGTGCTGACCCAGTCTCCATCCAGCCTGTCTGTGTCTCCTGGCGAGAGAGTGACCATCTCTTGCCGGGCTCTCAGAGCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGACAGGCCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACAGACTTTACCTGACCATCAGCTCCGTGGAATCCGAGGACTTCGCCGTGTAC
TACTGCCAGCAGAACAACACTGGCCACACCTTTGGCCAGGGCACCAAGCTGACAGTTCTT

>Sequence ID 37: Cetuximab H10 VH amino acid sequence
QVQLQESGPGLVKPSSESLTCTVSGFSLTNYGVHWVRQPPGKLEWIGVIWSGGNTDYNTPFTSRVTISKDNSKNQVSLKMNSLT
AADTAVYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 38: Cetuximab H10 VH nucleotide sequence
CAAGTTCAGCTGCAAGAGTCTGGCCCTGGCCTGGTCAAGCCTTCCGAATCTCTGTCTCTGACCTGCACCGTGTCCGGCTTCTCCCT
GACCAATTATGGCGTGCACCTGGGTTTCGACAGCCTCCAGGCAAAGGCCTGGAATGGATCGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCTCTAGAGTGACCATCAGCAAGGACAACCTCCAAGAACCAGGTGTCCCTGAAGATGAACAGCCTGACC
GCTGCCGACACCGTGTGTACTATTGTGTAGAGCCCTGACCTACTACGACTACGAGTTCGCCTATTGGGGCCAGGGAACCTGGT
CACAGTCTCCTCT

>Sequence ID 39: Cetuximab H10 VL amino acid sequence
DIVLTQSPATLSVSPGERATLSCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTISVQSEDAFVY
YCQQNNWPTTFGQGTKLEIK

>Sequence ID 40: Cetuximab H10 VL nucleotide sequence
GACATCGTGTGACCCAGTCTCCAGCCACACTGAGTGTCTCTCCAGGCGAGAGCTACCTGTCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGACAGGCCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCAGAGCTTTACCTGACCATCTCCTCCGTGCAGTCCGAGGATTTCCGCGGTGTAC
TACTGCCAGCAGAACAACTGGCCACACCTTTGGCCAGGGCACCAAGCTGGAAATCAA

>Sequence ID 41: Cetuximab H11 VH amino acid sequence
QVQLQESGPGLVKPSSESLTCTVSGFSLTNYGVHWVRQPPGKLEWIGVIWSGGNTDYNTPFTSRVTISKDNSKNQVSLKMNSLT
AADTAVYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 42: Cetuximab H11 VH nucleotide sequence
CAAGTTCAGCTGCAAGAGTCTGGCCCTGGCCTGGTCAAGCCTTCCGAATCTCTGTCTCTGACCTGCACCGTGTCCGGCTTCTCCCT
GACCAATTATGGCGTGCACCTGGGTTTCGACAGCCTCCAGGCAAAGGCCTGGAATGGATCGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTACCTCTAGAGTGACCATCAGCAAGGACAACCTCCAAGAACCAGGTGTCCCTGAAGATGAACAGCCTGACC
GCTGCCGACACCGTGTGTACTATTGTGTAGAGCCCTGACCTACTACGACTACGAGTTCGCCTATTGGGGCCAGGGAACCTGGT
CACAGTCTCCTCT

>Sequence ID 43: Cetuximab H11 VL amino acid sequence
DIVLTQSPATLSVSPGERATLSCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTISVQSEDAFVY
YCQQNNWPTTFGQGTKLVL

>Sequence ID 44: Cetuximab H11 VL nucleotide sequence
GACATCGTGTGACCCAGTCTCCAGCCACACTGAGTGTCTCTCCAGGCGAGAGCTACCTGTCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGACAGGCCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCAGAGCTTTACCTGACCATCTCCTCCGTGCAGTCCGAGGATTTCCGCGGTGTAC
TACTGCCAGCAGAACAACTGGCCACACCTTTGGCCAGGGCACCAAACTGACAGTTCTT

>Sequence ID 45: MonoFc amino acid sequence
GSGGSPVAGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWL
NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQPENNYKTTPKPVLD
SGSFLYSLTLDKSRWQQGNVFSVLSLHEALHNHYTQKSLSLSPGK

>Sequence ID 46: MonoFc nucleotide sequence
GGATCCGGCGGCTCTCCCGTCGCTGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCC
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA
ATGCCAAGACAAAGCCGCGGAGGAGCAGTACGCTAGCAGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACACGAGCTGGCTG
AATGGCAAGGAGTACAAGTGCAAGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCC
CCGAGAACCACAGGTGTACCCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCTGAGATGCCACGTCAAAGGCT
TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGAGCCGAGAGAACAACTACAAGACCACGAAGCCCGTGTGGACTCC
GACGGCTCCTTCTTCTTACAGCACCCCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCA
TGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCTGTCTCCGGGCAAATGA

>Sequence ID 47: Human IgG1 amino acid sequence
ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN
HKPSNTKVDKRVPEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTPPVLDSDGSFLYSKLTVDKSRWQQGNVFSVMSVHEALHNHYTQKSLSLSPG

>Sequence ID 48: Human IgG1 nucleotide sequence

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACC
TGAAGTCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACAT
GCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTACGCGTCTCACCCTCTGCACCCAGGACTGGCTGAATGGCAAGGA
GTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC
AGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCAGC
GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTT
CTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGTTAA

>Sequence ID 49: Human C kappa amino acid sequence

RTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKKHYA
CEVTHQGLSSPVTKSFNRGEC

>Sequence ID 50: Human C kappa amino acid sequence

CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTGTGTGCCTGCT
GAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAG
AGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCACCCATCAGGCGCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

>Sequence ID 51: (G4S)4 linker amino acid sequence

GGGSGGGSGGGSGGGSGGGSG

>Sequence ID 52: (G4S)4 linker nucleotide sequence

GGCGCGGAGGATCTGGCGGAGGTGGAAGCGGAGCGGAGGAAGCGGTGGCGGCGGATCT

>Sequence ID 53: His tag amino acid sequence

GSHHHHHH

>Sequence ID 54: His tag nucleotide sequence

GGATCCCATCATCACCATCACCATTGA

>Sequence ID 55: SI-79R1 amino acid sequence

DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIADY
YCQQNNWPTTFGAGTKLELKGSGSGGGSGGGSGGGSGVQLVQSPGLVQPSQSLITCTVSGFSLTNYGVHWVRQSPGKGL
EWLGVWISGNGTDYNTFPFTRLSINKDNSKSVFFKMNSLQSNDAIYYCARALTYDYEFAYWGQGLVTVSSGSHHHHHH

>Sequence ID 56: SI-79R1 nucleotide sequence

GACATCTTGCTGACTCAGTCTCAGTCATCTGTCTGTGAGTCCAGGAGAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGAGTAT
TGGCACAACATACACTGGTATCAGCAAGAACAATGGTTCTCAAGGCTTCTCATAAAGTATGCTTCTGAGTCTATCTCTGGGA
TTCTTCCAGGTTTGTGAGTGGATCAGGGACAGATTTACTCTTAGCATCAACAGTGTGGAGTCTGAAGATATTGCAGATTAT
TACTGTCAACAAAATAATACTGGCCAACCACGTTCCGCTGCTGGGACCAAGCTGGAGCTGAAAGGCGGTGGCGGTAGTGGGGGAGG
CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGGTCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGA
GCCTGTCCATCACCTGCACAGTCTCTGGTTCTCATTAACTAATATGGTGTACACTGGGTTCCGAGTCTCCAGGAAAGGCTCTG
GAGTGGCTGGGAGTGATATGGAGTGGTGGAAACACAGACTATAATACACCTTTCACATCCAGACTGAGCATCAACAAGGACAATTC
CAAGAGCCAAGTTTCTTTAAATGAACAGTCTGCAATCTAATGACACAGCCATATATTACTGTGCCAGAGCCCTCACCATTATG
ATTACGAGTTTGCTTACTGGGCGCAAGGACTCTGGTCACTGTCTCGAGTGGATCCCATCATCACCATCACCATTGA

>Sequence ID 57: SI-79R2 amino acid sequence

EIVMTQSPSTLSASVGRVITCRASQSIGTNIHWYQQKPKAPKLLIYYASESISGIPSRFSGSGSGAEFTLTISLQPDFFATY
YCQQNNWPTTFGQGTKLTVLGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCTVSGFSLTNYGVHWVRQAPGKGL
EWVGVWISGNGTDYNTFPFTRFTISRDTSKNTVYLMNSLRAEDTAVYYCARALTYDYEFAYWGQGLVTVSSGSHHHHHH

>Sequence ID 58: SI-79R2 nucleotide sequence

GAAATCGTTATGACACAGTCCCATCCACTCTTAGCGCTTCTGTAGGGGATCGAGTGATTATCAGTCCGGGGCTCCCAATCCAT
AGGAACCAACATACACTGGTATCAACAAAACAGGCAAGCGCCAAACTGCTTATCTACTACGCTCCGAGAGTATTTCTGGAA
TCCCGAGTCGCTTCTCAGGTTCTGGAAGCGGCGTGAGTTTACCCTCAAAATTTCTTCACTCCAACCGGATGACTTCGTACATAT
TACTGCCAACAAAATAAATGGCCGACGACCTTTGGCCAGGGCAGAACTTACGGTACTTGGCGGTGGCGGTAGTGGGGGAGG
CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAAGTACAGCTTGTCTGAGTCCGGTGGGGGGCTTGTTCAGCCAGGGGGTT

CCTTGAGGCTTTCCTGCACCGTCTCTGGGTTTAGCTTGACGAATTACGGCGTTCACTGGGTTAGACAAGCACCGGGGAAGGGGCTG
GAATGGGTCGGTGTGATATGGTCCGGGGTAATACGGATTACAATACACCTTTACGTACGCTTACGATTAGCAGGGACACGTC
AAAAAATACAGTCTACTTGCAGATGAACCTCTTAGGGCGGAAGATACTGCAGTTTATTACTGCGCAAGGGCTCTGACATACTACG
ATTATGAATTGCAATATTGGGGCCAGGGGACTTTGGTCACGGTCTCGAGTGGATCCCATCATCACCATCACCATTGA

>Sequence ID 59: SI-79SF1 amino acid sequence

DILLTQSPVILSVSPGERVVSFSCRASQSIGTNIHWYQQRNNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLINSVESEDIADY
YCQQNNNWPTTFGAGTKLELKGGGSGGGSGGGSGGGSGVQLKQSGPLVQPSQSLITCTVSGFSLTNYGVHWRQSPGKGL
EWLGVWISGNTDYNTPFTSRLSINKDMSKQVFFKMNSLQSNDAIYYCARALTYDYEFAYWQGTLLTVSAGSGSPVAGPSV
FLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPDSIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLT
DKSRWQQGNVFSVSLHEALHNHYTQKSLSLSPGK

>Sequence ID 60: SI-79SF1 nucleotide sequence

GACATCCTGCTGACCCAGTCTCCAGTGATCCTGTCCGTGTCTCTGGCGAGAGAGTGTCTTCAGTGCAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGCGGACCAACGGCTCCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACCGACTTCACCTGTCCATCAACTCCGTGGAATCCGAGGATATCGCCGACTAC
TACTGCCAGCAGAACAACTGGCCACCACTTTGGCGCTGGCACCAAGCTGGAATTGAAAGCGCGCGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGCGGATCTCAAGTTCAAGTCAAGCAGTCTGGCCCTGGCTTTCAGCCTTCTCAGA
GCCTGAGCATCACCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGGTTTCGACAGAGCCCTGGCAAAGGACTG
GAATGGCTGGGAGTGATTTGGAGCGCGGCAACACCGACTACAACACCCCTTTACCTCTCGGCTGTCTATCAACAAGGACAACTC
CAAGAGCCAGGTGTTCTTCAAGATGAACCTCCCTGCAGTCCAACGACACCGCCATCTACTACTGTCTCGGGCCCTGACCTACTACG
CTACGAGTTTGTCTTACTGGGGCCAGGGCACCTGGTCAAGTTTCTGCTGGATCCGGCGGCTCTCCCTCGCTGGACCGTCACTC
TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTA
GCACGTACCGTGTGGTCAAGTCTCCCTGACCGTCTGCACCGAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCGAGCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCAGCTCAAAGGCTTCTATCCCGAGCAGATCGCCGTGGAGTGGGAGAGCA
ATGGGCAGCGGAGAACAACTACAAGACCACGAAGCCCGTGGTGGACTCCGACGGCTCCTTCTTCTCTACAGACCCCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCTGTCTCCGGCAAAATGA

>Sequence ID 61: SI-79SF2 amino acid sequence

DILLTQSPVILSVSPGERVVSFSCRASQSIGTNIHWYQQRNNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLINSVESEDIADY
YCQQNNNWPTTFGAGTKLELKGGGSGGGSGGGSGGGSGVQLKQSGPLVQPSQSLITCTVSGFSLTNYGVHWRQSPGKGL
EWLGVWISGNTDYNTPFTSRLSINKDMSKQVFFKMNSLQSEDAIYYCARALTYDYEFAYWQGTLLTVSAGSGSPVAGPSV
FLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPDSIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLT
DKSRWQQGNVFSVSLHEALHNHYTQKSLSLSPGK

>Sequence ID 62: SI-79SF2 nucleotide sequence

GACATCCTGCTGACCCAGTCTCCAGTGATCCTGTCCGTGTCTCTGGCGAGAGAGTGTCTTCAGTGCAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGCGGACCAACGGCTCCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACCGACTTCACCTGTCCATCAACTCCGTGGAATCCGAGGATATCGCCGACTAC
TACTGCCAGCAGAACAACTGGCCACCACTTTGGCGCTGGCACCAAGCTGGAATTGAAAGCGCGCGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGCGGATCTCAAGTTCAAGTCAAGCAGTCTGGCCCTGGCTTTCAGCCTTCTCAGA
GCCTGAGCATCACCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGGTTTCGACAGAGCCCTGGCAAAGGACTG
GAATGGCTGGGAGTGATTTGGAGCGCGGCAACACCGACTACAACACCCCTTTACCTCTCGGCTGTCTATCAACAAGGACAACTC
CAAGAGCCAGGTGTTCTTCAAGATGAACCTCCCTGCAGTCCGAGGACACCGCCATCTACTACTGTCTCGGGCCCTGACCTACTACG
ACTACGAGTTTGTCTTACTGGGGCCAGGGCACCTGGTCAAGTTTCTGCTGGATCCGGCGGCTCTCCCTGCTGGACCGTCACTC
TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTA
GCACGTACCGTGTGGTCAAGTCTCCCTGACCGTCTGCACCGAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCGAGCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCAGCTCAAAGGCTTCTATCCCGAGCAGATCGCCGTGGAGTGGGAGAGCA
ATGGGCAGCGGAGAACAACTACAAGACCACGAAGCCCGTGGTGGACTCCGACGGCTCCTTCTTCTCTACAGACCCCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCTGTCTCCGGCAAAATGA

>Sequence ID 63: SI-79SF3 amino acid sequence

EIVMTQSPSTLSASVGDRIITCRASQSIGTNIHWYQQKPKAPKLLIYYASESISGIPSRFSGSGSGAEFTLTISLQPDDEFATY
YCQQNNNWPTTFGQTKLTVLGGGSGGGSGGGSGGGSEVQLVPGGSLRLSKVSGFSLTNYGVHWRQAPGKGL
EWVGVWISGNTDYNTPFTSRFTISRDTSKNTVYLLQMSLRAEDTAVYYCARALTYDYEFAYWQGTLLTVSSGSGSPVAGPSV

FLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPDSIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLTIV
DKSRWQQGNVFSVSLHEALHNHYTQKSLSLSPGK

>Sequence ID 64: SI-79SF3 nucleotide sequence

GAGATCGTGATGACCCAGTCTCCTTCCACACTGTCCGCCCTCTGTGGGCGACAGAGTGATCATCACCTGTAGAGCCAGCCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGCAAGGCCCTAAGCTGCTGATCTACTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGATCTGGCGGTGAGTTTACCCTGACAATCTCCAGCCTGCAGCCTGACGACTTCGCCACCTAC
TACTGCCAGCAGAAACAACAACTGGCCACCACCTTTGGCCAGGGCACCAACTGACAGTTCTTGGCGGCGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTGAAGTTTCAAGTGGTGAATCCGGCGGAGGATTGGTTCAACCTGGCGGCT
CTCTGAGACTGTCTGTAAGGTGTCTGGCTTCTCCCTGACCAACTACGGCGTGCACTGGGTCCGACAGGCACCTGGAAAAGGACTG
GAATGGGTCCGAGTGATTTGGAGCGGCGCAACACCGACTACAACACCCCTTTTACCAGCGGTTTACCATTCTCTCGGGACACCTC
CAAGAACACCGTGTACCTGCAGATGAACCTCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTCTAGAGCCCTGACCTACTATG
ACTACGAGTTCCGCTATTGGGGCCAGGGAACCCCTGGTACAGTCTCCTCTGGATCCGGCGGCTCTCCCGTCGCTGGACCGTCACTC
TTCCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTGACATGCGTGGTGGTGGTGGTGGTGGTGGTGGT
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTA
GCACGTACCGTGTGGTCAAGCTCCTCACCCTCCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCAGTCAAGGCTTCTATCCCAGCGACATCGCGGTGGAGTGGGAGAGCA
ATGGGCAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCACCTCACCCTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCCGGGCAATGA

>Sequence ID 65: SI-79SF4 amino acid sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNNWPTTFGPGTKLELKGSGSGSGSGSGSGSGSQVQLQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGVIWSSGNTDYNTPFTSRFTITKDNSKNQVYFKLRVSRADDTAIYYCARALTYDYEFAYWGQGLVTVSSGSGSPVAGPSV
FLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPDSIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLTIV
DKSRWQQGNVFSVSLHEALHNHYTQKSLSLSPGK

>Sequence ID 66: SI-79SF4 nucleotide sequence

GAGATCGTGATGACCCAGTCTCCTTCCACACTGTCTGTGCTCTCCCGCGAGAGAGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCCGGCAAGCCTCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTTACCCTGACCATCTCCTCCGTGCAGTCCGAGGATTTCGCCGTGTAC
TACTGCCAGCAGAAACAACAACTGGCCACCACCTTTGGACCCGGCACCAGCTGGAATTGAAAGCGCGCGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTTCAAGTGGTGCAGCAGTCTGGCCCTGGCCTGGTCAAGCCTTCTGAGA
CACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCACTGGATCAGACAGGCCCCCTGGCAAAGGACTG
GAATGGCTGGGAGTGATTTGGAGCGGCGCAACACCGACTACAACACCCCTTTTACCAGCCGGTTCACCATCACCAGGACAACTC
CAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGGCGGCTGATGACACCGCCATCTACTACTGTGCTCGGGCCCTGACCTACTACG
ACTACGAGTTTGTCTACTGGGGCCAGGGCACCCTGGTCAAGTTTCTTCTGGATCCGGCGGCTCTCCCGTCGCTGGACCGTCACTC
TTCCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTGACATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
AGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGACATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTA
GCACGTACCGTGTGGTCAAGCTCCTCACCCTCCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCAGTCAAGGCTTCTATCCCAGCGACATCGCGGTGGAGTGGGAGAGCA
ATGGGCAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCACCTCACCCTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCCGGGCAATGA

>Sequence ID 67: SI-79SF5 amino acid sequence

DIVLTQSPSSLSVSPGERVTISCRASQSIGTNIHWYQQKPKQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTISVSEDFAVY
YCQQNNNWPTTFGQGTKEIKGGGSGGGSGGGSGGGSGSQVLVESGPGLVQPSGSLTCTVSGFSLTNYGVHWIRQAPGKGL
EWVGVWSSGNTDYNTPFTSRFTISKDNSKNQVYLMNSLRADDTAVYYCARALTYDYEFAYWGQGLVTVSSGSGSPVAGPSV
FLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPDSIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLTIV
DKSRWQQGNVFSVSLHEALHNHYTQKSLSLSPGK

>Sequence ID 68: SI-79SF5 nucleotide sequence

GACATCGTGATGACCCAGTCTCCATCCAGCCTGTCTGTGCTCTTCCGGCGAGAGAGTGACCATCTCTTCCCGGGCCTCTCAGAGCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGACAGGCCCCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACAGACTTACCCTGACCATCAGCTCCGTGGAATCCGAGGACTTCGGCTGTAC
TACTGCCAGCAGAAACAACAACTGGCCACCACCTTTGGCCAGGGCACCAGCTGGAAATCAAAGCGCGGAGGATCTGGCGGAGG

TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTCAGCTGGTGAATCTGGCCCTGGCCTGGTTCAGCCTTCTGGCT
CTCTGTCTCTGACCTGCACCGTGTCTGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGGTTTCAGAGGCTCCAGGCAAAGGACTG
GAATGGGTCGAGTGATTTGGAGCGGCGGCAACCCGACTACAACACCCCTTTACCAGCCGGTTCACCATCTCCAAGGACAACCTC
CAAGAACCAAGGTGACCTGAAGATGAACCTCCCTGAGAGCCGAGGACACCGCTGTGTATTACTGTGCTAGAGCCCTGACCTACTACG
ACTACGAGTTGCGCTATTGGGGCCAGGGAACCTGGTCACAGTCTCCTCTGGATCCGGCGGCTCTCCCTGCGTGGACCGTCAGTC
TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACGCTA
GCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA
ATGGGCGAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCACCCCTACCCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCCGGGCAATGA

>Sequence ID 69: SI-79SF6 amino acid sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNWPPTTFGPQKLTVLGGGSGGGGSGGGGSGGGGSGVQLQQSGPLVKPSETLSITCTVSGFLTNYGVHWIRQAPGKGL
EWLGVWISGNTDYNTPFTSRFTITKDNSKNQVYFKLRVSRADDTAIYYCARALTYDYEFAYWQGTLLVTVSSGSGGSPVAGPSV
FLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLTV
DKSRWQQGNVFSCSVLHEALHNHYTQKSLSLSPGK

>Sequence ID 70: SI-79SF6 nucleotide sequence

GAGATCGTGTGACCCAGTCTCCTTCCACACTGTCTGTCTCTCCGGCGAGAGAGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCCGGCAAGCCTCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTTACCCTGACCATCTCCTCCGTGCAGTCCGAGGATTTCCGGCTGTAC
TACTGCCAGCAGAAACAACACTGGCCACACCTTTGGACCCGGCACCAAGCTGACAGTTCTTGGCGGGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTCAGTTGCAGCAGTCTGGCCCTGGCCTGGTCAAGCCTTCTGAGA
CACTGTCCATCACCCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGATCAGACAGGCCCTTGGCAAAGGACTG
GAATGGCTGGGAGTGATTTGGAGCGGCGGCAACCCGACTACAACACCCCTTTACCAGCCGGTTCACCATCACCAGGACAACCTC
CAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGCAGGCTGATGACACCGCCATCTACTACTGTCTCGGGCCCTGACCTACTACG
ACTACGAGTTTGTCTACTGGGGCCAGGGCACCTGGTCACAGTTTCTTCTGGATCCGGCGGCTCTCCCTGCGTGGACCGTCAGTC
TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACGCTA
GCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA
ATGGGCGAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCACCCCTACCCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCCGGGCAATGA

>Sequence ID 71: SI-79SF7 amino acid sequence

DIVLTQSPSSLSVSPGERVTISCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTISVSEDFAVY
YCQQNNWPPTTFGQGTKLTVLGGGSGGGGSGGGGSGGGGSGVQLVSGPLVQPSGSLTCTVSGFLTNYGVHWVRQAPGKGL
EWVGVWISGNTDYNTPFTSRFTISKDNSKNQVYLMNLSRAEDTAVYYCARALTYDYEFAYWQGTLLVTVSSGSGGSPVAGPSV
FLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLTV
DKSRWQQGNVFSCSVLHEALHNHYTQKSLSLSPGK

>Sequence ID 72: SI-79SF7 nucleotide sequence

GACATCGTGTGACCCAGTCTCCATCCAGCCTGTCTGTCTCTCTGGCGAGAGAGTACCATCTCTTGGCGGGCCTCTCAGAGCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGACAGGCCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTTCCAGATTCTCCGGCTCTGGCTCTGGCACAGACTTTACCCTGACCATCAGCTCCGTGGAATCCGAGGACTTCGCGGTGTAC
TACTGCCAGCAGAAACAACACTGGCCACACCTTTGGCCAGGGCACCAAGCTGACAGTTCTTGGCGGGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTTCAGCTGGTGAATCTGGCCCTGGCCTGGTTTACGCTTCTGGCT
CTCTGTCTCTGACCTGCACCGTGTCTGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGGTTTCAGAGGCTCCAGGCAAAGGACTG
GAATGGGTCGAGTGATTTGGAGCGGCGGCAACCCGACTACAACACCCCTTTACCAGCCGGTTCACCATCTCCAAGGACAACCTC
CAAGAACCAGGTGTACTGAAGATGAACCTCCCTGAGAGCCGAGGACACCGCTGTGTATTACTGTGCTAGAGCCCTGACCTACTACG
ACTACGAGTTTCGCTATTGGGGCCAGGGAACCTGGTCACAGTCTCCTCTGGATCCGGCGGCTCTCCCTGCGTGGACCGTCAGTC
TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACGCTA
GCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG

GGATGAGCTGACCAAGAACCAGGTCAGCCTGAGATGCCACGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA
ATGGGCAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGACCCTCACCCTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCCGGGCAATGA

>Sequence ID 73: SI-79SF8 amino acid sequence

DIVLTQSPATLSVSPGERATLSCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTITSSVQSEDFAVY
YCQQNNNWPTTFGQGTKEIKGGGSGGGSGGGSGGGSGVQLQESGPLVKPSESLSLTCTVSGFLTNYGVHWVRQPPGKGL
EWIGVIWSGGNTDYNTPFTSRVTISKDNSKNQVSLKMNLSLAADTAVYYCARALTYDYEFAYWQGTILVTVSSGSGSPVAGPSV
FLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPDSIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLT
DKSRWQQGNVFCSVLHEALHNHYTQKSLSLSPGK

>Sequence ID 74: SI-79SF8 nucleotide sequence

GACATCGTGTGACCCAGTCTCCAGCCACACTGAGTGTCTCCAGCGGAGAGAGCTACCTGTCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCTGGACAGGCCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCAGACACTTACCTGACCATCTCCTCCGTGACGTCCGAGGATTTCGCGCTGTAC
TACTGCCAGCAGAACAACTGGCCACCACTTTGGCCAGGGCACCAGCTGGAATCAAAGCGCGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTCAGTTCAGTGCAGAGTCTGGCCCTGGCCCTGGTCAAGCCTCCGAAT
CTCTGTCTCTGACCTGCACCGTGTCCGGCTTCTCCCTGACCAATTATGGCGTGCAGTGGGTTCGACAGCCTCCAGGCAAAGGCCTG
GAATGGATCGGAGTGATTTGGAGCGGCGGCAACACCGACTACAACACCCCTTTACCTCTAGAGTGACCATCAGCAAGGACAACCTC
CAAGAACAGGTGTCCCTGAAGATGAACAGCCTGACCGCTGCCGACACCGCTGTGTACTATTGTGCTAGAGCCTGACCTACTACG
ACTACGAGTTCGCGCTATTGGGGCAGGGAAACCTGGTCAAGTCTCCTCTGGATCCGGCGGCTCTCCCTCGCTGGACCGTCACTC
TTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTA
GCAGTACCGTGTGGTCAAGTCTCACCCTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCCAAGCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCCTGAGATGCCACGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA
ATGGGCAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGACCCTCACCCTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCCGGGCAATGA

>Sequence ID 75: SI-79SF9 amino acid sequence

EIVLTQSPSTLSVSPGERVFSFSCRASQSIGTNIHWYQQRTGQPPRLLIKYASESISGIPARFSGSGSGTEFTLTITSSVQSEDFAVY
YCQQNNNWPTTFGQGTKEIKGGGSGGGSGGGSGGGSGVQLQSGPLVKPSETLSITCTVSGFLTNYGVHWIRQAPGKGL
EWIGVIWSGGNTDYNTPFTSRFTITKDNSKNQVFFKLRVRAEDTALYYCARALTYDYEFAYWQGTILVTVSSGSGSPVAGPSV
FLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPDSIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLT
DKSRWQQGNVFCSVLHEALHNHYTQKSLSLSPGK

>Sequence ID 76: SI-79SF9 nucleotide sequence

GAGATCGTGTGACCCAGTCTCCTTCCACACTGTCTGTGTCTCCCGCGAGAGAGTGTCTTCTCAGTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAGAACCAGCCAGCTCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGCCAGATTTTCCGGCTCTGGCTCTGGCACCAGGTTACCTGACCATCACCTCCGTGACGTCTGAGGACTTCGCGCTGTAC
TACTGCCAGCAGAACAACTGGCCACCACTTTGGCCAGGGCACCAGCTGGATATCAAAGCGCGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTCAGTGTGTCAGTCTGGCCCTGGCCCTGGTCAAGCCTCCGAGA
CACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGATCAGACAGGCCCTGGCAAAGGCCTG
GAATGGATCGGAGTGATTTGGAGCGGCGGCAACACCGACTACAACACCCCTTTTACCAGCGGTTACCATCACAAGGACAACCTC
CAAGAACAGGTGTCTTCAAGCTGCGGAGCGTGCAGCTGAGGATACCGCTCTGTACTATTGCGCTCGGGCCCTGACCTACTACG
ACTACGAGTTTGTCTACTGGGCGCAGGGAACCCCTGGTCAACGTTTCTTCTGGATCCGGCGGCTCTCCCTGCGTGGACCGTCACTC
TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTA
GCAGTACCGTGTGGTCAAGTCTCACCCTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
GCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTGAGCCTGAGATGCCACGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA
ATGGGCAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGACCCTCACCCTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCCGGGCAATGA

>Sequence ID 77: SI-79SF10 amino acid sequence

EIVLTQSPSILSVSPGERVTFSCRASQSIGTNIHWYQQRPGLPRLLIKYASESISGIPARFSGSGSGTEFTLTITSSVQSEDFATY
YCQQNNNWPTTFGPTKLEIKGGGSGGGSGGGSGGGSGVQLVQSGPLVKPSQTLSTCTVSGFLTNYGVHWIRQAPGKGL
EWLGVWISGNTDYNTPFTSRFTITKDNSKNQVYFKLRVRS EDTAVYYCARALTYDYEFAYWQGTILVTVSSGSGSPVAGPSV

GAGATCGTGTCTGACCCAGTCTCCTTCCATCCTGTCTGTGTCTCCCGCGAGAGAGCCACCTTCAGCTGTAGACCTCTCAGTCCA
CGGACCAACATCCATCGGTATCAGCAGCGGCTGGCAGGCTCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCTATCAGCGGCA
TCCCCCTCAGGATTTCCGGCTCTGGATCTGGCCACCGAGTTCACCTGACCATCGCTGCGATCCGAGGATATCGCGGTGAC
TACTGCCAGCAGAACACAACCTGGCCCAACCACTTTGGACCCGGCACAAGCTGGAATTGAAAGGCGGCGGAGGATCTGGCGGTAG

TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTTCAGTTGCAGCAGTCTGGCCCTGGCCTCGTGAAGCCTTCTCAGAC
 CCCTGTCTATCACCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGATCAGACAGGCCCTGGCAAAGGACTG
 GAATGGCTGGGAGTGATTTGGAGCGGCGGCAACCCGACTACAACACCCCTTTACCAGCCGGTTCACCATCTCCAAGGACAATC
 CAAGAACCAGGTGTACTTCAAGCTGCGGTCCCTGAGAGCCGAGGACACCGCCATCTACTACTGTGCTAGAGCCCTGACCTACTACG
 ACTACGAGTTTCGCTATTGGGGCCAGGGCACACTGGTCACAGTCTCTTCTGGATCCGGCGGCTCTCCCTCGCTGGACCGTCAGTC
 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
 AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACGCTA
 GCACGTACCGTGTGGTTCAGCGTCTCACCCTCTGCACACGAGTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
 GCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
 GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA
 ATGGGCGAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCACCCCTACCCGTG
 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
 CTCCTGTCTCCGGGCAATGA

>Sequence ID 83: SI-79SF13 amino acid sequence

DIVLTQSPATLSVSPGERATLSCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPSRFSGSGSGTDFTLTISVQSEDFAVY
 YCQQNNWPPTFFGQTKLTVLGGGSGGGGSGGGGSGGGGSGVQLQESGPGLVKPSSESLTCTVSGFLTNYGTVHVVQPPGKGL
 EWIGVIWSGNTDYNTPFTSRVTISKDNSKNQVSLKMNSLTAADTAVYYCARALTYDYEFAYWQGTLVTVSSGSGSGSPVAGPSV
 FLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDLNKGKEYCKVSNK
 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLT
 VDKSRWQQGNVFSVCSVLHEALHNHYTQKSLSLSPGK

>Sequence ID 84: SI-79SF13 nucleotide sequence

GACATCGTGTGACCCAGTCTCCAGCCACACTGAGTGTGTCTCCAGGCGAGAGAGCTACCCGTGCTGTAGAGCCTCTCAGTCCAT
 CGGCACCAACATCCACTGGTATCAGCAGAAAGCCTGGACAGGCCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCTATCAGCGCA
 TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACAGACTTTACCTGACCATCTCTCCGTGCAGTCCGAGGATTTCCGGGTGTAC
 TACTGCCAGCAGAAACAACTGGCCACACCTTTGGCCAGGGCACCAACTGACAGTCTTGGCGGGGAGGATCTGGCGGAGG
 TGGAAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTTCAGTGCAGAGTCTGGCCCTGGCCTGGTCAAGCCTTCCGAAT
 CTCTGTCTCTGACCTGCACCGTGTCCGGCTTCTCCCTGACCAATTATGGCGTGCAGTGGGTTTCGACAGCCTCCAGGCAAGGCCTG
 GAATGGATCGGAGTGATTTGGAGCGGCGGCAACCCGACTACAACACCCCTTTACCTCTAGAGTGACCATCAGCAAGGACAATC
 CAAGAACCAGGTGTCCCTGAAGATGAACAGCCTGACCGCTGCCGACACCGCTGTGTACTATTGTGCTAGAGCCCTGACCTACTACG
 ACTACGAGTTTCGCTATTGGGGCCAGGGAACCTGGTCACAGTCTCTCTGGATCCGGCGGCTCTCCCTCGCTGGACCGTCAGTC
 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGA
 AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACGCTA
 GCACGTACCGTGTGGTTCAGCGTCTCACCCTCTGCACACGAGTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
 GCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
 GGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA
 ATGGGCGAGCCGGAGAACAACTACAAGACCACGAAGCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCACCCCTACCCGTG
 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGCTCCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
 CTCCTGTCTCCGGGCAATGA

>Sequence ID 85: SI-55P3 heavy chain amino acid sequence

EIVMTQSPSTLSASVGDRIITCRASQSIGTNIHWYQQKPGKAPKLLIYYASESISGIPSRFSGSGSGAEFTLTISLQPDFFATY
 YCQQNNWPPTFFGQTKLTVLGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCSVSGFLTNYGTVHVVQAPGKGL
 EWVGVWSGNTDYNTPFTSRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARALTYDYEFAYWQGTLVTVSSGGGSGGGGSGV
 QLQESGGRVLQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSRSED
 AIYYCARGGYSIDIWQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
 LYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPKPKDLMISRTPEVTCVVV
 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNKGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCSVMHEALHNHY
 TQKSLSLSPGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWIIACIAAGSAGITYDANWA
 KGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARSAFSDYAMDLDWQGTLVTVSSGGGSGGGGSGGGGSGGGGSDIQTQSPST
 LSASVGDRTITCQASQSISSHLNHYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQGYSGN
 VDNVFGGTVKEIKGGGSGGGGSGRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEIYIGTISGGNVYYASS
 ARGRTISRSSKNTVDLQMNLSRAEDTAVYYCARDGYSYDPMWQGTLVTVSSGGGSGGGGSGGGGSGGGGSDVMTQSPSSVS
 ASVGDRTITCQASQNIIRTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTDYV
 GGAFFGGTKVEIK

>Sequence ID 86: SI-55P3 heavy chain nucleotide sequence

GAAATCGTTATGACACAGTCCCCATCCACTCTTAGCGCTTCTGTAGGGGATCGAGTGATTATCACATGCCGGGCTCCCAATCCAT
 AGGAACCAACATACACTGGTATCAACAAAACAGGCAAGCGCCAAACTGCTTATCTACTACGCCTCCGAGAGTATTTCTGGAA
 TCCCGAGTCGCTTCTCAGTTCTGGAAGCGGCGTGAAGTTACCTCACAAATTTCTTACTCCAACCGGATGACTTCGTACATAT
 TACTGCCAACAAAACAATAATTGGCCGACGACCTTTGGCCAGGGCAGAAACTTACGGTACTTGGCGGTGGCGGTAGTGGGGGAGG

CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAAGTACAGCTTGTGAGTCCGGTGGGGGGCTTGTTCAGCCAGGGGGTT
CCTTGAGGCTTTCCTGCTCCGTCTCTGGGTTTAGCTTGACGAATTACGGCGTTCACTGGGTTAGACAAGCACCGGGGAAAGGGGTG
GAATGGGTCGGTGTGATATGGTCCGGGGTAATACGGATTACAATACACCTTTCACGTACGCTTTACGATTAGCAGGGACACGTC
AAAAATACAGTCTACTTGGAGATGAACCTCTTAGGGCGGAAGATACTGCAAGTTTATTACTGCGCAAGGGCTCTGACATACTACG
ATTATGAATTTGCATATTGGGGCCAGGGGACTTTGGTCACGGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAGTG
CAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCTTGTCACTGACGTGTAACCAAGCGGCATTGATCTGTCCCTC
TAACGCCATCGGATGGGTCGACAGGCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACG
CAAGCTGGGCAAAAGGGCGATTTACGATATCAGGAGCACCTCTACAGTTTATTTGAAAATGAACCTCCCTCCGGTCCGAGGATACC
GCGATATATTACTGTGCCAGAGGGGGGTACTCCTCTGATATCTGGGGGACAGGTACACTGGTTACAGTTTCATCCGCTAGCACCAA
GGGCCCATCGGTCTTCCCTCCGACCCCTCCTCCAAGAGACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTCTCTACAGTCTCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAAACTCTTGACAAAACCTCACACATGCCACCCGTGCCAGCACCTGAAGCCGGGG
GGGCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTG
GAGGTGAGGCCAGCAAGGACCGGAGAACCACTACAAGCACGCGCTCCCGTGGTGGTGCATGCAAGCAAGCAAGCCGCGGGA
GGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCG
CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAGAGGTGTACACC
CTGCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT
GGAGTGGGAGGAGCACTGGGAGCCGAGAACCACTACAAGCACGCGCTCCCGTGGTGGTGGTGCATGCAAGCAAGCAAGCCGCGG
GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGG
AGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGG
CTGCTGCGATCTGTAGGAGACAGAGTCACCATCACTTGGCAGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAA
AAAGGCCGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGT
ATATTACTGTGCGAGATCGCGCTTTTCGTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCTGGTCACCGTGTGAGCGGTG
GAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACC
GAGTCTGGGGAGGCGCTTCTGGCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACTGCTTGGATTCAACATCAGTAGCTACACAA
TGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGTGGAGTACATCGGAACCATTAGTAGTGGTGGTAATGTATACTACGCAAGCTCC
GCTAGAGGCAGATTACCATCTCCAGACCCCTCGTCCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGC
TGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCTATGTGGGGCCAGGGAACCTGGTCACCGTCTCTTCAGGCGGTGGCG
GTAGTGGGGGAGGCGCTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCT
GCATCTGTAGGAGACAGAGTCACCATCACCTGTGAGGCCAGTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACAGG
GAAAGCCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTGAGTCTACCTATCTTGGTACTGATTATGTT
GGCGGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAATGA

>Sequence ID 87: SI-55P3 light chain amino acid sequence

ENVLTSQSPASLSASPERVITITCSASSSVSYMHWYQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTQKVTVLGGGSGGGGSGGGSGGGGQVTLKESGPGLVQPGQTLRLTCAFSGFSLSTSGMGVGVIRQPPGKG
LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGQGLVTVSSGGGSGGGGSDP
VLTQSPSSLSASVGRVITISCSQSSQSVAKNNNLAWFQKPGQAPKLLIYASSTLAAGVPSRFSGSGSGDFTLTISSVQPEDFATY
YCSARDSGNIQSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 88: SI-55P3 light chain nucleotide sequence

GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCAATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTCCGGCTCAGGCAACGATCACACCTTACGATTTCCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGGTACCCATTCACTTTCGGGACAGGGACAAAAGTGACGGTACTGGGTGGAGGCGGTTACGGCGGAGGTGG
TTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTCAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTCAGCAGGACAGACCC
TTAGGCTCAGCTGTGCTTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGTCCGGTGGATTCCGGCAGCCTCCCGCAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCCGGCTGACCATAGTAAGGATAC
CTCAAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTTGGGGCAGGGGACTCTCGTCACGGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGATCCA
GTTCTGACACAAAAGTCCATCCAGCCTGTCTGCCTCAGTCGGCGACAGAGTGACCATCAGTTGCCAGAGCTCACAGCTCTGGCTAA
GAACAACAACCTGGCGTGGTTCACACAGAAACCTGGACAGGCTCCGAAATTGCTGATCTATTCTGCTTCCACGCTTCTGCTGGTG
TTCTTCCCGCTTTTCAGGTAGTGGTAGCGGGACAGACTTCACCTTGAATATAAGCAGCGTGCAGCCTGAAGATTTTGCACCTAC
TATTGTTCTGTAGAGACAGTGGAAATATTAGTCTTTGGGGGGGGAACGAAGGTGCAATAAAGCGTACCGTGGCTGCACCTATC
TGCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGCTGCTGAATACTTCTATCCAGAG

AGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC
ACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGG
CCTGAGCTCGCCCCGCACAAAGAGCTTCAACAGGGGAGAGTGTGA

>Sequence ID 89: SI-55P4 heavy chain amino acid sequence

EIVMTQSPSTLSASVGDRIITCRASQSIGTNIHWYQQKPKAPKLLIYYASESISGIPSRFSGSGSGAEFTLTISLQPDFFATY
YCQNNNWPPTTFGQGTKLQMLVGGGSGGGGSGGGGSEVQLVDSGGGLVQPGGSLRLSCVSGFSLTNYGVHWRQAPGKGL
EWVGVIWGGNTDYNTPFTSRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARALTYDYEFAYWQGTTLVTSSGGGSGGGGSGV
QLQESGGRLVQPGPELSLTCKTSGIDLSSNAIGWVRQAPGKGLEWIGVIFSGNTYYASWAKGRFTISRSTSTVYLMKNSLRSED
AIYYCARGGYSSDIWQGTTLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGKEYKCAVSNKALPAPIEKTSKAKGQPREPQVYT
LPFPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHY
TQKLSLSLSPGGGGSGGGGSEVQLLESGLLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIIACIAAGSAGITYDANWA
KGRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARSAFSDYAGMDLWGQGTTLVTSSGGGSGGGGSGGGGSGGGGDIQMTQSPST
LSASVGDRIITCQASQSISSHLNHWYQQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYICQQGYSGWN
VDNVFGGGTVEIKGGGSGGGGSGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGPLSWYSDPGLAGVSLTGGLSYKEDTK
ELVVAKAGVYVFFQLELRRVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAGQRLGVHLH
TEARARHAWQLTQAGATVGLFRVTPEIPAGLGGGSGGGGSGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGPLSWYSDPGLAGV
SLTGGLSYKEDTKELVVAKAGVYVFFQLELRRVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNSAFGFQGRLLHLSAG
QRLGVHLHTEARARHAWQLTQAGATVGLFRVTPEIPAGL

>Sequence ID 90: SI-55P4 heavy chain nucleotide sequence

GAAATCGTTATGACACAGTCCCCATCCACTCTTAGCGCTTCTGTAGGGGATCGAGTGATTATCACATGCCGGGCTCCCAATCCAT
AGGAACCAACATACACTGGTATCAACAAAACAGGCAAGGCGCCAAAACCTGCTTATCTACTACGCTCCGAGAGTATTTCTGGAA
TCCCGAGTCTGCTTCTCAGGTTCTGGAAGCGGCGCTGAGTTTACCCTCACAATTTCTTCACTCCAACCGGATGACTTCGTACATAT
TACTGCCAACAAAACAATAATTGGCCGACGACCTTTGGCCAGGGCACGAACTTACGGTACTTGGCGGTGGCGGTAGTGGGGGAGG
CGGTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAAGTACAGCTTGTCGAGTCCGGTGGGGGGCTTGTTCAGCCAGGGGGT
CCTTGAAGCTTTCTGCTCCGTCTCTGGGTTTACGTTGACGAATACGCGCTTCACTGGGTAGACAAAGCAGCGGCAAGGGGTG
GAATGGGTCTGATATGGTCCGGGGTAATACGGATTACAATACACCTTTTACGTCACGCTTTACGATTAGCAGGGACACGTC
AAAAATACAGTCTACTTGCAGATGAACCTCTTAGGGCGGAAGATACTGCAGTTTATTACTGCGCAAGGGCTCTGACATACTACG
ATTATGAATTTGCATATTGGGGCCAGGGGACTTTGGTCAAGCTTCTGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAGTG
CAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCTTGTCACTGACGTGTAAACAAAGCGCATTGATCTGTCCTC
TAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACG
CAAGCTGGGCAAAAGGGCGATTTACGATATCACGGAGCACCTCTACAGTTTATTGAAATGAACCTCCCTCCGGTCCGAGGATACC
CGCATATATTACTGTGCGAGAGGGGGTACTCCTCTGATATCTGGGGGCGGGTACACTGGTTACAGTTTCATCCGCTAGCACCAA
GGGCGCATCGGTCTTCCCCCTGGCACCTCTCCAAGGACCTTCTGGGGCACAGCGGCTTGGGTGCTCAAGGCTACT
TCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGGCTGCACACCTTCCCGGTGTCTTACAGTCTCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGCTGAATCACAGCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAAGCCGCGG
GGGCACCGTCTTCTCTTCCCCCAAAACCAAGGACCTCATGATCTCCCGGACCCCTGAGGTGCTGCGTGGTGGTGGTGGT
GACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
GGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGGC
CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAAGAAACATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
CTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCGCGGT
GGAGTGGGAGAGCAATGGGCGAGCCGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTATA
GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGG
AGGCTTGGTACAGCTTGGGGGTCCCTGAGACTCTCCTGTGACGCTCTGGATTCTCCTTCACTAGCGGGTACGACATGTGCTGGG
TCCGCCAGGCTCCAGGAAGGGGTGGAGTGGATCGCATGCATTGCTGCTGGTAGTCTGGTATCACTTACGACCGCAACTGGGCG
AAAGCCGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGATCTGCAATGAACAGCTGAGAGCCGAGGACACGGCGT
ATATTACTGTGCGAGATCGGCGTTTCTGTTGACTACGCCATGGACCTCTGGGGCAGGGAACCTGGTCAACCTGTCTGAGCGGTG
GAGCGGATCTGGCGGAGGTGGTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTGACATCCAGATGACCCAGTCTCTTCTCCACC
CTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCAGGCCAGTCAGAGCATTAGTTCCTCACTTAACTGGTATCAGCAGAA
ACCAGGGAAGGCCCTAAGCTCCTGATCTATAAGGCATCACTCTGGCATCTGGGTCCCATCAAGGTCAGCGGCAGTGGATCTG
GGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTGCAACTTATTACTGCCAACAGGTTATAGTTGGGGTAAT
GTTGATAATGTTTTCCGGCGAGGGACCAAGGTGGAGATCAAAGGCGGTGGAGGGTCCGGCGGTGGTGGTCCGGACGAGAGGCC
CGAGTGTCTCTGATGACCCAGCAGGCTCTTGGACTTGGCGAGGGTATGTTGCTCAACTTGTGGCTCAGAATGTTCTGCTCA
TTGATGGACCACTCTCTTGGTATAGTGACCCGGTCTGGCGGGGTGAGTCTGACCGCGGGCTCTCTTATAAAGAGGATAGTAAG
GAACGTGCTGAGCAAGAGCGGCTTTATACGTTTTTTTTCAGCTGGAGCTCAGGCGGTGGTGGCGGCGAGGCGGCTGCTC
TGTGTCCTGGCCCTGCACTTACAGCCCTTGAGAAGCGCTGCAAGTGTGCGGCACTGGCTTTAACTGTTGACCTCCCTCCGGCT

CTTCTGAAGCTAGAAACAGCGCTTTCGGCTTCCAAGGGCGCCTGCTGCACCTGAGCGCAGGCCAGCGCTTAGGTGTGCACCTTCAT
 ACAGAGGCCAGGGCCGACACGCTTGGCAGCTCACACAGGGTGCCACGGTTCTCGGACTTTCCGCGTTACTCCCGAGATCCCCGC
 TGGCCTCGGAAGTACTGGTCTGGGTCTAAACCCGGTTCGGCGAAGGTAGTACTAAAGGACGAGAAGGGCCAGAGTTAAGTCCAG
 ATGACCTGCTGGGCTTTTGGACCTGCGGCAGGGCATGTTCTGCTCAACTGGTGGCTCAGAACGTGCTGCTGATCGATGGCCCCCTG
 AGTTGGTACAGCGATCCCGGGCTGGCAGGCGTGTCACTTACAGGGGGCCTCTCTTACAAGGAAGACACCAAGGAGTTAGTGGTGC
 TAAGGCTGGCGTGTATTACGTGTTCTTCCAAGTGGAGCTGAGAAAGGTTGTGGCAGGAGAGGGTAGCGGCAGCGTGTCTTTAGCCC
 TTCACTTGCATGCCCTGAGGTCTGCTGCAGGTGCAGCCGCTCTCGCGCTCACCGTGGATCTCCCCCAGCCTCATCTGAAGCTAGG
 AACAGTGCATTTGGCTTTTCAAGGACGCTTGTGACCTCTCCGCTGGACAGAGGCTGGGCGTGCACCTTACACAGAGGCCCGTGC
 CAGGATGTCATGGCAGCTCACTCAGGGGGCAACAGTGTGGGTCTCTTCCGCGTGAATACAGCTGGACTTGGCGGTG
 GAGGCGCGCGGAGGAGGATCTCGTGGGGGCCAGAACTGTCCCCGATGACCCAGCCGAGCTGCTCGATCTCAGACAGGGCATG
 TTCGCTCAGCTTGTAGCCCAAATGTCTCTGATTGACGCGCTTTGAGCTGGTATAGTGATCCCGGCTTGGCGGGGTATCTCT
 GACCGGAGGCTCTCTACAAGGAAGACACCAAGAGCTGGTGGTGGCAAAAGCGGGGTGTATTATGTGTTCTTTAGCTCGAGC
 TGCGGAGAGTTGTGGCGGGGAAGGCTCTGGGAGCGTATCTCTTGCACCTTACCTGACAGCCCTGCGCAGCGCGCTGGAGCCGCC
 GCCCTTGTCTTACTGTGGATCTGCCTCTGCTTCTCAGAAGCAGCAACAGCGCCTTCGGCTTTCAAGGACGTCTCTGCACTT
 YCSARDSGNTQSFGGGTKEIKRTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
 TGGGACTCTTTAGAGTGACACCCGAGATCCCGCTGGCTTGTGA

>Sequence ID 91: SI-55P4 light chain amino acid sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHVYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
 CFQGSVYPFTFGQGTQVTVLGGGGSGGGSGGGSGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTGMGVGWRQPPGKG
 LEWLAIHWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGQGLVTVSSGGGGSGGGSDP
 VLTQSPSSLSASVGRVITISQSSQSVAKNNNLAWFQQKPGQAPKLLIYASASTLAAGVPSRFSGSGSGTDFTLTISVQPEDFATY
 YCSARDSGNTQSFGGGTKEIKRTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
 TYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

>Sequence ID 92: SI-55P4 light chain nucleotide sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGTAACATCACTTGTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCTTACGATTTCAGTATGGAACCCGAAGATTTTGCACTTATTAT
 TGTTTCCAGGGAGCGTGTACCCATTCACTTTCCGGCAGGGGACAAAAGTGACGGTACTGGGTGGAGGCGGTTTCCAGCGGAGGTGG
 TTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTCAGTGCATTTGAAGGAATCTGGCCCCGGCTTGTTCAGCCAGGACAGACCC
 TTAGGCTCACCTGTGCCTTCACTGGTCTTTCTCTAGCACTAGCGGTATGGGGGTCGGCTGGATTCCGCGAGCCTCCCGCAAAGGT
 CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCCGGCTGACCATTAGTAAGGATAC
 CTCAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAAGTCTGGT
 CTTACTTTGATATTATTTGGGGGAGGGGACTCTCGTACGCTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGATCCA
 GTTCTGACACAAAGTCCATCCAGCCTGTCTGCCTCAGTGGCGACAGAGTGACCATCAGTTGCCAGAGCTCACAGTCTGTGGCTAA
 GAACAACAACCTTGGCGTGGTTCACACAGAAACCTGGACAGGCTCCGAAATTGCTGATCTATTCTGCTTCCACGCTTGTCTGTGGT
 TTCCTTCCGCTTTTTCAGGTAGTGGTAGCGGGACAGACTTCACTTTGACTATAAGCAGCGTGCAGCCTGAAGATTTTGGCACCTAC
 TATTGTTCTGCTAGAGACAGTGAAATATTCAGTCTTTGGGGGGGAACGAAGGTGAAATAAAGCGTACGGTGGCTGCACCATC
 TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAG
 AGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC
 ACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGG
 CCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGA

>Sequence ID 93: SI-79P2 heavy chain amino acid sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
 YCQQNNWPTTFPGTKLELKGSGSGGGSGGGSGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
 EWLGVWISGNTDYNTPFTSRFTITKDNKSNQVYFKLRVSRADDTAIYYCARALTYDYEFAYWGQGLVTVSSGGGGSGGGSGV
 QLQESGGRIVQPGPELSLTCTSGIDLSSNAIGWVRQAPGKLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLMNSLRSED
 AIYYCARGGYSSDIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
 LYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHCTCPPEAFAAGAPSVFLFPPKPKDTLMISRTPEVTCV
 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQLDNLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFVMHEALHNHY
 TQKSLSLSPGGGGSGGGSEVQLLESGLLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWIAIAGSAGITYDANWA
 KGRFTISRDNSTNTLYLQMNSLRAEDTAVYYCARSAFSDYAMDWLWGQGLVTVSSGGGGSGGGSGGGSGGGSGGGSDIQTQSPST
 LSASVGRVITITCQASQSISSHLNHYQQKPKGAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQGYSGW
 VDNVFGGGTKVEIKGGGGSGGGSGRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGGNVYYASS
 ARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARDSDYSDPMWGQGLVTVSSGGGGSGGGSGGGSGGGSGGGSDVVMQSPSSVS
 ASVGRVITITCQASQNIQRTYLSWYQQKPKGAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTDYV
 GGAFFGGTKVEIK

>Sequence ID 94: SI-79P2 heavy chain nucleotide sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACGCGCGACTTTCTCTTGCAAGGGCAAGTCAATCCAT
AGGGACTAATATACATTTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAAGTATGCAAGTGAGTCTATTTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
TACTGCCAACAGAATAAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGTTGGAAGTGAAGGCGGTGGCGGTAGTGGGGGAGG
CGGTCTTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
CGCTTAGTATAACGTGTAAGTTTTCAGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGCGAGGACCCCGGCAAGGTTT
GAATCGGTGCGGTGTTATTTTTCAGTTGAGATCCGTCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
CAAAAATCAAGTTTATTTTCAAGTTGAGATCCGTCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAACAGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAGTG
CAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTTGCTACTGACGTGTAACCAAGCGGCAATGGATCTGTCCCTC
TAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACG
CAAGCTGGGCAAAAGGGCGATTTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAAGTCCCTCCGGTCCGAGGATACC
GCGATATATTACTGTGCCAGAGGGGGGTACTCCTCTGATATCTGGGGGACAGGTTACACTGGTTACAGTTTCATCCGCTAGCACCAA
GGGCCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCGGAACCGGTGACGGTCTCGTGGAACTCAGGCGCCCTGACACGCGCGGTGCACACCTTCCCGGTCTCCTACAGTCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGGCCAAATCTTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAAGCCGCGG
GGGACCCGTGAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTG
GAGTGGAGGAGCAATGGGAGCGGAGTCAAGTTCACTGAGTCAAGACCGCGGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
GGAGCAGTACAACAGCACGTACCGTGTGGTCCAGCGTCTCACCCTGCTGCACAGGAGTGGTGAATGGCAAGGAGTACAAGTGGC
CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGGAGCCCCGAGAACCAGAGGTGTACACC
CTGCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT
GGAGTGGAGAGCAATGGGAGCGGAGGAGCAACTACAAGACCGCCCTCCCGTCTGGACTCCGACGGCTCCTTCTTCTCTATA
GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGG
AGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGTACGACATGTGCTGGG
TCCGCGAGGTCTCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGGTAGTGCCTGGTATCACTACGACGCAACTGGCG
AAAGGCCGGTTACCATCTCCAGAGACAATTCCAAGAACCGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCCGT
ATATTACTGTGCGAGATCGCGCTTTCTGTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCCTGGTCACCGTGTGAGCGGTG
GAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACC
CTGTCTGCATCTGTAGGAGACAGAGTACCATCACTTGCCAGGCCAGTCAGAGCATTAAGTTCCCACTTAACTGGTATCAGCAGAA
ACCAGGGAAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTG
GGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCTTATTACTGCCAACAGGTTATAGTTGGGGTAAT
GTTGATAATGTTTTCGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGGAGGGTCCGGCGGTGGTGGCTCCGGACGGTCTGGTGGT
GGAGTGGGGAGGCGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCT
GCATCTGTAGGAGACAGAGTACCATCACCTGTCCAGGCCAGTCAGAACATTAGGACTTACTTATCTCTGGTATCAGCAGAAACAGG
GAAAGCCCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTGAGTCTACCTATCTTGGTACTGATTATGTT
GGCGGTGCTTTCGGCGGAGGACCAAGGTGGAGATCAAATGA

>Sequence ID 95: SI-79P2 light chain amino acid sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHWYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVIRQPPKKG
LEWLAHIWDDDKRYPALKSRLTISKDTSKNQVYLQMSLDAEDTAVYYCARMELWSYFDYWQGTLLVTVSSGGGSGGGGSDP
VLTQSPSSLSASVGRVITISQSSQSVAKNNNLAWFQQKPGQAPKLLIYASSTLAAGVPSRFSGSGSGDFTLTISSVQPEDFATY
YCSARDSGNIQSFGGGKKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 96: SI-79P2 light chain nucleotide sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAAGTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGGTGTACCCATTCACTTTCGGGCGAGGGACAAAAGTGACGGTACTGGGTGGAGGCGGTTTCAGGCGGAGGTGG
TTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTCAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGGCGGACAGACCC
TTAGGCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGGTCCGGCTGGATTCGGCAGCCTCCCGCAAGGT
CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCCGGCTGACCATTAGTAAGGATAC
CTCAAAAAATCAAGTGTACTTGCAAAATGAATAGCCTTGACGCGGAGGATACGGCTGTATATTATGCGCGCGGATGGAATCTGGT
CTTACTACTTTGATTATTGGGGGAGGGGACTCTGTCACGGTCTCAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGATCCA
GTTCTGACACAAAGTCCATCCAGCCTGTCTGCCTCAGTCCGCGACAGAGTGACCATCAGTTGCCAGAGCTCACAGTCTGTGGCTAA

GAACAACAACCTTGGCGTGGTTCCAAACAGAAACCTGGACAGGCTCCGAAATTGCTGATCTATTCTGCTTCCACGCTTCTGCTGCTGGTG
TTCCTTCCCCTTTTCAGGTAGTGGTAGCGGGACAGACTTCACTTTGACTATAAGCAGCGTGCAGCCTGAAGATTTTGCAGCCTAC
TATTGTTCTGCTAGAGACAGTGGAAATATTCACTCCTTTGGGGGGGGAACGAAGGTGAAATAAAGCGTACGGTGGCTGCACCATC
TGTCTTCATCTTCCCCTCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGTGCTGCTGCTGAATAACTTCTATCCCAGAG
AGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC
ACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACAAAAGTCTACGCTGCGAAGTCAACCATCAGGG
CCTGAGCTCGCCCTCACAAAGAGCTTCAACAGGGGAGAGTGTGA

>Sequence ID 97: SI-79P3 heavy chain amino acid sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNWPTTFPGTKLELKGSGSGSGSGSGSGSQVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGVIWSGGNTDYNTPFTSRFTITKDN SKNQVFKLRVSRADTAIYYCARALTYDYEFAYWQGTLTVTSSGGGSGGGGSGV
QLQESGGRLVQPGPELSLTCTKTSGLDLSNAIGWVRQAPGKGLEWIGVIFGSGNTYYASWAKGRTISRSTSTVYLMKNSLRSED
AIYYCARGGYSSDIWQGTLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVTPSSSLGTLYICNVNHNKPSNTKVDKRVKPSKCDKTHTCPPCPAPEAAGAPSVFLFPKPKDTLMISRTPEVTVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
LPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCVSMHEALHNHY
TQKSLSLSPGGGGSGGGGSEVQLLESGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIIACIAAGSAGITYDANWA
KGRFTISRDNKSTLYLQMLSLRAEDTAVYYCARSAFSGSGSGESTKGRGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGFL
LSASVGRVITITCQASQSISSHLNHYQQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQGYSGW
VDNVFGGGTVEIKGGGSGGGSGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGFLSWYSDPGLAGVSLTGGLSYKEDTK
ELVVAAGVYVFFQLELRRVAGEGSGSVSLALHLQPLRSAAGAAALALTVLDPFASSEARNSAFGFQGRLLHLSAGQRLGVHLH
TEARARHAWQLTQGTATVGLFRVTPEIPAGLSTGSGSKPGSGESTKGRGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGFL
SWYSDPGLAGVSLTGGLSYKEDTKELVVAAGVYVFFQLELRRVAGEGSGSVSLALHLQPLRSAAGAAALALTVLDPFASSEAR
NSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGTATVGLFRVTPEIPAGLGGGSGGGSGREGPELSPDDPAGLLDLRQGM
FAQLVAQNVLIDGFLSWYSDPGLAGVSLTGGLSYKEDTKELVVAAGVYVFFQLELRRVAGEGSGSVSLALHLQPLRSAAGAA
ALALTVLDPFASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGTATVGLFRVTPEIPAGL

>Sequence ID 98: SI-79P3 heavy chain nucleotide sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACGCGCGACTTTCTCTTGACGGGCAAGTCAATCCAT
AGGGACTAATATACATTGGTATCAACAAAGCCAGGTAAACACCCAGGCTTTTGATTAAAGTATGCAAGTGAGTCTATTTCGGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACTACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
TACTGCCAACAGAAATAAATACTGGCCGACTACCTTCGGACCCGGTACAAAGTTGGAACGTAAAGGCGGTGGCGGTAGTGGGGGAGG
CGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
CGRTTAGTATAACGTGTACTGTTTTCAGGCTTTAGCCTTACGAACCTATGGAGTTCACTGGATTTCGCGAGGCGACCCGCAAGGTTT
GAATGGCTGGGTGTTATTTGGTCAAGTGGAAATACAGACTATAACACCCCTTTTACAAGTCCGGTTCACAATTACGAAAGATAATTC
CAAAATCAAGTTTATTTCAAGTTGAGATCCGTCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAAAGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAAGTG
CAGTTGCAAGAAAGTGGGTAGACTGGTTCAGCCTGGTGAACCTTGTCACTGACGTGTAAGAACAGCGGCAATGATCTGTCCCTC
TAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACG
CAAGCTGGGCAAAAGGGCGATTTACGATATCACGGAGCAGCTCTACAGTTTATTTGAAATGAAGTCCCTCCGGTCCGAGGATACC
CGGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGCGGGTACACTGGTTACAGTTTCATCCGCTAGCACCAA
GGGCCCCATCGGTCTTCCCTTGGCACCTCCTCCAAGAGCACCTTGGGGGACAGCGGCCCTGGGCTGCCTCAAGGACTACT
TCCCGCAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGTGTCTTACAGTCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAACGTGAATCACAGCCAG
CAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAAGCCGCGG
GGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGT
GACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
GGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGGC
CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
CTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGACCTGGTCAAGGCTTCTATCCCAGGACATCGCCGT
GGAGTGGGAGAGCAATGGGCGCCGAGAAACATAAGAACACGCTCCCGTGTGACTCCGACGGCTCTTCTTCTCTATA
GCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCAAGAGGCTCTCCTGTCTCCGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGG
AGGCTTGGTACAGCTGGGGGTCCTGAGACTCTCTGTGAGGCTTGGATTCTCCTTCAAGTACGGGTACGACATGTGCTGG
TCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTCTGGTATCACTTACGACGCAACTGGGCG
AAAGCCCGTTACCATCTCCAGAGACAATTCAGAACACGCTGATCTGCAATGAACAGCTGAGAGCCGAGGACACGGCGT
ATATTACTGTGCGAGATCGGCTTTTCTGTTGACTACGCACTGACCTTGGGGCCAGGAAACCTGGTCAACCTGTGCGAGCGGTG
GAGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGTTGGAGGCGGCTTGACATCCAGATGACCCAGTCTCTTCCACC
CTGTCTGCATCTGTAGGAGACAGAGTCAACATCACTTGCAGGCGAGTCAAGCATTAGTTCCTCACTTAACTGGTATCAGCAGAA
ACGAGGGAAGCCCTAAGCTCCTGATCTATAAGGCATCACTCTGGCATCTGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTG
GGACAGAAATTTACTCTCACCATCAGCAGCTGCAGCTGATGATTTTCAACTTATTACTGCCAAGGCTTATAGTTGGGGAAT
GTTGATAATGTTTTCCGGCGAGGACCAAGGTGGAGATCAAAGGCGGTGGAGGTCGGCGGTGGTGGCTCCGGACGAGAGGCCCC

CGAGCTGTCTCTGATGACCCAGCAGGCCTCTTGGACTTGCGGCAGGGTATGTTGCTCAACTTGTGGCTCAGAATGTTCTGCTCA
TTGATGGACCACTCTCTTGGTATAGTGACCCCGGTCTGGCCGGGGTGTGCTGACCCGGCGGGCTCTCTTATAAAGAGGATACTAAG
GAAGTGGTCTGAGCAAAAGCGGGCGTTTATTACGTTTTTTTTCAGCTGGAGCTCAGGCGCTGGTGGCCGGCAGGGCAGTGGCTC
TGTGTCCCTGGCCCTGCACCTTACAGCCCTTGAGAAGCGCTGCAGGTGCTGCGGCACTGGCTTTAACTGTTGACCTCCCTCCGGCT
CTTCTGAAGCTAGAAACAGCGCTTTCGGCTTCCAAGGGCGCTGCTGCACCTGAGCGCAGGCCAGCGCTTAGGTGTGCACCTTCAT
ACAGAGGCCAGGGCCGACACGCTTGGCAGCTCACACAGGTGCCACGGTTCTCGGACTTTTCCGCTTACTCCCGAGATCCCCGC
TGGCTCGGAAGTATCTGGTTCTGGTCTAAACCCGTTACCGGCGAAGGTAGTACTAAAGGACGAGAAGGGCCAGAGTTAAGTCCAG
ATGACCTGCTGGGCTTTTGGACCTGCGGCAGGGCATGTTGCTCAACTGGTGGCTCAGAACGTGCTGCTGATCGATGGCCCCCTG
AGTTGGTACAGCATCCCGGGCTGGCAGGCGTGTCACTTACAGGGGGCTCTCTTACAAGGAAGACACCAAGGAGTTAGTGGTGC
TAAGGCTGGCGTGTATTACGTGTTCTTCCAAGTGGAGCTGAGAAGGGTGTGGCAGGAGAGGGTAGCGGCAGCGTGTCTTTAGCCC
TTCCTTGGACGCCCTGAGGTCTGCTGCAGGTGCAGCCGCTCTCGGCTACCGTGGATCTCCCCCAGCCTCATCTGAAGCTAGG
AACAGTGCATTTGGCTTTAGGGACGCTTGTGTCACCTCTCCGCTGGACAGAGGCTGGCGGTGCACCTTCACACAGAGGCCCGTGC
CAGGCATGCATGGCAGCTCACTCAGGGGGCAACAGTGTGGGTCTCTTCCGCTGACTCCTGAAATACAGCTGGACTTGGCGGTG
GAGGCAGCGCGGAGGAGGATCTCGTGGGGGCCAGAACTGTCCCCGATGACCCAGCCGACTGCTCGATCTCAGACAGGGCATG
TTCCGCTGAGTGTAGCCCAAAATGCTCTGATTGAGGCCCTTTGAGCTGGTATAGTGATCCCGGCTTGGCCGGGTATCTCT
GACCGGAGGCTCTCTACAAGGAAGACACCAAGAGCTGGTGGTGGCAAAAGCGGGGTGTATTATGTGTTCTTTAGCTCGAGC
TGCGGAGAGTTGTGGCCGGGAAGGTCTGGGAGCGTATCTCTTGCACCTTACCTGTCAGCCCCCTGCGCAGCGCGCTGGAGCCGCC
GCCCTTGTCTTACTGTGGATCTGCCTCTGCTTCTCAGAAGCACGCAACAGCGCCTTCGGCTTTCAAGGACGTCTCTGCACTT
YCSARDSGNTQSFGGGTKEIKRTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TGGGACTCTTTAGAGTGACACCCGAGATCCCCGCTGGCTTGTGA

>Sequence ID 99: SI-79P3 light chain amino acid sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHWYQQKPKQAPKLWIYDTSKLASGVPSRFSGSGSGNDHTLTITSSMEPEDFATYY
CFQGSVYPFTFGQGTQKVTVLGGGSGGGSGGGSGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVWIRQPPGKG
LEWLAIHWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYDYWGQGLVTVSSGGGSGGGGSDP
VLTQSPSSLSASVGRVITISQSSQSVAKNNNLAWFQQKPGQAPKLLIYASASTLAAGVPSRFSGSGSGTDFTLTISVQPEDFATY
YCSARDSGNTQSFGGGTKEIKRTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 100: SI-79P3 light chain nucleotide sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGTCTGCATCAAGCAGCGT
CTCATAACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGTACCCATTCACTTTCCGGCAGGGGACAAAAGTGACGGTACTGGGTGGAGGCGGTTTCAGGCGGAGGTGG
TTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTCAGGTACATTTGAAGGAATCTGGCCCGGCTTGTTCAGCCAGGACAGACCC
TTAGGCTCACCTGTGCCTTCACTGGTCTTTCTCTTAGCACTAGCGGTATGGGGTTCGGCTGGATTTCGGCAGCCTCCCGGCAAGGT
CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCCGGCTGACCATTAGTAAGGATAC
CTCAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCGCAGGATACGGCTGTATATTATTCGCGCGGATGGAACCTCTGGT
TTTACTTCTGATATTATTATTTGGGGGAGGGGACTCTCGTACAGTCTCAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGATCA
GTTCTGACACAAAGTCCATCCAGCCTGTCTGCCTCAGTCGGCGACAGAGTGACCATCAGTTGCCAGAGCTCACAGTCTGTGGCTAA
GAACAACTTGGCGTGGTTCACACAGAAACCTGGACAGGCTCCGAAATTGCTGATCTATTCTGCTTCCACGCTTGTCTGCTGGTG
TTCTTCCCGCTTTTCAGGTAGTGGTAGCGGGACAGACTTCACTTTGACTATAAGCAGCGTGCAGCCTGAAGATTTTGGCAGCTAC
TATTGTTCTGCTAGAGACAGTGGAAATATTCAGTCTTTGGGGGGGGAACGAAGGTGAAATAAAGCGTACGGTGGCTGCACCATC
TGTCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAG
AGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC
ACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGG
CCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGA

>Sequence ID 101: SI-55P9 heavy chain amino acid sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPPRLIKYASEISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNWPTTFPGTKLTVLGGGSGGGSGGGSGGGSGGVQLQQSGPLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGLVWGGNTDYNTPFTSRFTITKDNSKNQVYFKLRVSRADDTAIYYCARALTYDYEFAYWGQGLVTVSSGGGSGGGGSEV
QLVESGGGLVQPGGSLRLSCAASGFTISTNAMSVMVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAE
DTAVYYCARDGGSSAITSNNIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTHTCPCPAPEAAGAPSVFLFPPKPKDLMISRTF
EVTCTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMH
EALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWIAIAGSAGI
TYDANWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMDLDWGQGLVTVSSGGGSGGGGSGGGGSGGGSDIQ
MTQSPSTLSASVGRVITITQASQSISSHLNHWYQQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQ
QGYSGWNVNDFGGGTKEIKGGGSGGGGSGRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGG
NYYYASSARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARDSSGSDPMWQGLVTVSSGGGSGGGGSGGGGSGGGSDVMT

QSPSSVSASVGDRTITCQASQNIIRTYLSWYQKPKGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTI SDLEPGDAATYYCQST
YLGTDYVGGAFGGGKVEIK

>Sequence ID 102: SI-55P9 heavy chain nucleotide sequence
GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAAGCGCGACTTTCTCTTGCAGGGCAAGTCAATCCAT
AGGGACTAATATACATTTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAAGTATGCAAGTGAGTCTATTTCCGGTA
TCCCTGACCCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGAT
TACTGCCAACAGAAATAAATACTGGCCGACTACCTTCGGACCCCGGTACAAAGCTGACCGTTTTAGGCGGTGGCGGTAGTGGGGAGG
CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
CGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCTTACGAATATGGAGTTCAGTGGATTCCGGCAGGCACCCGGCAAAGGTTTG
GAATGGCTGGGTGTTATTTGGTTCAGGTGGAAATACAGACTATAACACCCCTTTACAAGTCGGTTCACAAATACGAAAGATAATTC
CAAAATCAAGTTTATTTCAAGTTGAGATCCGTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAACAGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCGAGCCTCTGGATTCAACATCAGTAC
CAATGCAATGGTCCGCGCAGGCTCCAGGGAAGGGGTCTGGTGGAACTCAGGCGCCTGACCAGCGGCGTGCACACTTCCCG
CGAGCTGGGCGAAAGGCAGATTCAACATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTGCAC
CGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG
GAGGTACATGCGTGGTGGTGGACGTGAGCCAGCAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGGTGGAGGTGCATAA
TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCTCACCGTCTGCACACAGGACTGGCTGA
ATGGCAAGGAGTACAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTT
CTATCCCGACGACATCGCGGTGGAGTGGGAGAGCAATGGGCAGCGGGAACAACACTACAAGACCACGCTCCCGTGTCTGGACTCCG
ACGGCTCCTTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGTCTGTGCAACCACTACACGAGAGCCTCTCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGT
GCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCGAGCCTCTGGATTCTCCTTACGTA
ATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGTCAACATCACTTGCAGGCCAGTCAAGACATTAGTTCCTCA
ACTTACGACGCGAACTGGGCGAAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCT
GAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTTTCTGTTGACTACGCCATGACCTCTGGGGCCAGGGAACCC
TGGTACCGTGTGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGTCCGGTGGAGGGCGCTCTGCATCCAG
ATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGTCAACATCACTTGCAGGCCAGTCAAGACATTAGTTCCTCA
CTTAAACTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAA
GGTTGAGCGGCGAGTGGATCTGGGACAGAAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAA
CAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGGAGGGTCCGGCGGTGG
TGGCTCCGACCGTCTGCTGGTGGAGTCTGGGGGAGGCTTCTGCGCGCGGAGGGTCCGCGGTGGAGGATCAGACGTTGTGATGACC
TCACCATCAGTAGTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGTGGAGTACATCGGAACCATTAGTAGTGGTGGT
AATGTATACTACGCAAGCTCCGCTAGAGGCAGATTCACCATCTCCAGACCCTCGTCCAAGAACCGGTGGATCTTCAAATGAACAG
CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCCTATGTGGGGCCAGGGAACCTGGTCA
CCGTCTCTTCAGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGCGCGCGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACC
CAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTACCATCACCTGTGAGGCCAGTCAAGACATTAGGACTTACTTATC
CTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGGTCCCATCAAGGTTCA
GCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTGAGTCTACC
TATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAATGA

>Sequence ID 103: SI-55P9 light chain amino acid sequence
ENVLTQSPASLSASPERVTITCSASSSVSYMHWYQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFLSTSGMGVGVIRQPPGKG
LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWQGTLLTVSSGGGSGGGGSDV
VMTQSPSTLSASVGDRTITCQASESISWLAHYQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYC
QGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNFPYPRKQVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 104: SI-55P9 light chain nucleotide sequence
GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATATCATGATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAAGTGGTCCGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGTGTACCATTTCACTTTCGGGCGAGGGACAAAAGTGACGGTACTGGGTGGAGGCGGTTTCAGGCGGAGGTGG
TTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTCAGTACATGAAGGAATCGGCCCGGCTTGTTCAGGCGGACAGACCC
TTAGGCTACCTGTGCTTCAAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTGGGCTGGATTCCGGCAGCCTCCCGCAAAGGT

CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGCAGGGGACTCTCGTCACGGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
 GTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
 TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGGTCCCAT
 CAAGGTTACGCGGAGTGGATCTGGGACAGAATCACTCTACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCTTATCTGTC
 CAAGGCTATTTTATTATTATAGTCTGTAATTTCTTTTGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
 ACCATCTGTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGTAATAACTTCTATC
 CCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
 GACAGCACCTACAGCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCCA
 TCAGGGCCTGAGCTCGCCCTCACAAAGAGCTTCAACAGGGGAGAGTGTGTA

>Sequence ID 105: SI-77P1 heavy chain amino acid sequence

EIVMTQSPSTLSASVGRVITTCQASESISWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
 YCQGYFYFISRTYVNSFGQTKLTLVGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTTISTNAMSVMRQA
 PGKLEWVGVITGRDITYYASWAKGRFTISRDTSKNTVYLQMNLSRAEDTAVYYCARDGGSSAITSNNIWGQGLTVTVSSGGGSG
 GGGSVQLQSGSPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKLEWLVWISGGNTDYNTPFTSRFTITKDNSKNQVYFKL
 RSVRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
 VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTCTPCPAPAEAGAPSVFLFPPKPKDITLM
 ISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISK
 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWIIACIAA
 GSAGITYDANWAKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARSAFSDYAMDLDWGQGLTVTVSSGGGSGGGSGGGSGGGSGGG
 GSDIQMTQSPSTLSASVGRVITTCQASQSISSHLNWKYQQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFA
 TYYCQQGYSWGNVDNVFGGGTKEIKGGGSGGGSGSGSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEIYGT
 ISSGGNVYASSARGRFTISRPSKNTVLDQMNLSRAEDTAVYYCARDSGYSDPMWGQGLTVTVSSGGGSGGGSGGGSGGGSGGGSG
 DVVMTQSPSPSVASVGRVITTCQASQNIIRTYLSWYQQKPKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEFGDAATY
 YCQSTYLGTDYVGGAFGGGTKEIK

>Sequence ID 106: SI-77P1 heavy chain nucleotide sequence

GAAATCGTTATGACGAGAGTCCCTCCACGCTCTCCGCTAGTGTGCGGGATCGCGTCATTATCACATGCCAGGCCTCCGAGTCAAT
 CAGCAGCTGGCTTGCATGGTATCAACAGAAGCCGGGAAAAGCTCCTAAATTGCTGATCTATGAAGCGTCAAATTTGGCGTCTGGTG
 TCCCATCTAGGTTCCTCCGGCTCTGGGTCTGGTGCAGAAATTTACTTTGACAATCTCCAGTCTTCAACCAGACGATTTTCGTACCTAC
 TACTGCCAAGGGTATTTCTATTTTATAAGCCGGACATATGTAACTCCTTCGGCCAAGGAACAAAGTTGACTGTTCTTGGTGGCGG
 AGGCAGTGGTGGCGGGGAGCGGAGGTGGTGGTTCAGGGGGTGGTGGAGCGCAAGTCCAATTGGTAGAAAGTGGCGGTGGTCTGG
 TGCAACCTGGTGGATCTCTTCGCTCTCATGCGCGCTAGTGGCTTTACTATTTCAACTAATGCGATGAGCTGGGTTCGCCAGGCC
 CCCGGCAAAGGACTTGAGTGGGTCTGGCGTCTCATCCGCGCAGGGACATTACATACTATGCGAGTTGGGCAAGGGCAGGTTACGAT
 TAGCCGCGTACTTCAAAGAATACCGTTTACCTTCAAATGAATAGCTTGAGGGCGGAAGACACAGCTGTGTATTACTGCGCGAGGG
 ATGAGGTAAGTTCCGCACTAATCTCCAAACATATAGGGACGCTGAGTGGTACTGTCTCGAGTGGCGGTGAGGCTCCGGC
 GGTGGTGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTC
 AGGCTTTAGCTTACGAATCTAGGATTCAGTGGATTCCGCGAGGACCCGGCAAAGGTTTGAATGGCTGGGTGTTATTTGGTCAG
 GTGGAAATACAGACTATAACACCCCTTTACAAGTCGGTTCAAAATACGAAAGATAATTCCAAAAATCAAGTTTATTTCAAGTTG
 AGATCCGTCCGCGCGGACACACTGCGATCTACTATTGTGCGAGGGCTGACCTACTACGATTACGAATTTGCTTGGGGGCA
 AGGGACTCTTGTAACAGTCTCCAGTGCTAGCACCAAGGGCCCATCGGTCTTCCCTTGGCACCTCTCTCAAGAGCACCTCTGGGG
 GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACCAGCGGC
 GTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGGCTCCAGCAGCTTGGGCAC
 CCAGACCTACATCTGCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAAGAGATTGAGCCCAAATCTTGTGACAAAACCTC
 ACACATGCCACCGTGGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCTCATG
 ATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGG
 CGTGAGGAGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGC
 ACCAGGACTGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAGGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGACCTG
 CCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAAGACCAGCCCTC
 CCGTGCTGGACTCCGACGGCTCTTCTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
 TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGG
 TGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTG
 GATTCTCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGTGGAGTGGATCGCATGCAATTGCTGCT
 GGTAGTGTGGTATCACTTACGACGCGAAGTGGGCGAAGGCGGTTTACCATCTCCAGAGACAATCCAAAGAACACGCTGTATCT
 GCAATGAACAGCCTGAGAGCCGAGGACACGCCGTATATCTGTGCGAGATCGGCGTTTTCTGTTGACTACGCCATGGACCTCT
 GGGGCCAGGGAACCTGGTCAACGTGTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTCCGGCGGTGGCGGTCCGGTGGAGGC
 GGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGATCTGTAGGAGACAGAGTACCATCACTTGGCAGGCCAGTCA
 GAGCATTAGTTCCTCACTTAACTGGTATCAGCAGAAACAGGAGGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCAT
 CTGGGGTCCCATCAAGGTTACGCGCAGTGGATCTGGGACAGAAATTTACTCTACCATCAGCAGCCTGCAGCTGATGATTTTGCA

ACTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGG
AGGGTCCGGCGGTGGTGGCTCCGGACGGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCT
GTACTGCCTCTGGATTACCATCAGTAGCTACCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGAACC
ATTAGTAGTGGTGGTAATGTATACTACGCAAGCTCCGCTAGAGGCAGATTACCATCTCCAGACCCTCGTCCAAGAACACGGTGGA
TCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCCTATGTGGGGCC
AGGGAACCCCTGGTCAACGCTCTCTTCAAGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCA
GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTACCATCACCTGTGAGCCAGTCAGAACAT
TAGGACTTACTTATCCTGGTATCAGCAGAAACAGGAAAGCCCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGG
TCCCATCAAGGTTACGCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACTTAC
TATTGTGCTACTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>Sequence ID 107: SI-77Pl light chain amino acid sequence

ENVLTQSPASLSASGERVITCSASSSVSYMHWYQQKPKQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTITSSMEPEDFATYY
CFQGSVYPFTFGQGTQKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGVLVQPGQTLSTLCAFSGFSLSSTGMGVGWRQPPGKG
LEWLAHIIWDDDKRNPALKSRLLTSKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYFDYWGQGLVTVSSGGGSGGGGSEI
VLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPIRFSGSGSGTEFTLTISVQSSEDFAVYYC
QQNNWPTTFPGTKLTVLRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS
LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 108: SI-77Pl light chain nucleotide sequence

GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTTCACTTTCCGGGACGGGACAAAAGTGACCGTCTAGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGTCACTTGAAGGAATCTGGCCCCGGCCTTGTTCAGCCAGGACAGACCC
TTAGCCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTGGCTGGATTCCGGCAGCCTCCCGGCAAGGT
CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCCTTGAAGAGTGGCTGACCATAGTAGAGGATAC
CTCAAAAAATCAAGTGACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGACAGGGGACTCTCGTCAAGGTCTCAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAAATC
GTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACCGCGGACTTTCTCTTGCAAGGCAAGTCAATCCATAGGGAC
TAATATACATTTGGTATCAACAAAAGCCAGGTAAACACCCAGGCTTTTGTATTAAGTATGCAAGTGAAGTCTATTTCCGGTATCCCTG
ACCGCTTCTCTGGATCAGGCAAGTGGCACAGAGTTCACTACCATATCTAGTGTGCAATCAGAGGACTTCGCCGTGTATTACTGC
CAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTACGTACGGTGGCTGCACCATCTGTCTTCAT
CTTCCCGCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAG
TACATGCAAGGTGGATACGCCCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGGACAGCAGCCTACAGC
CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCTGAGCTC
GCGCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG

>Sequence ID 109: SI-77H5 heavy chain amino acid sequence

EIVMTQSPSTLSASVGRVITITQASESISWLAHYQQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDDEFATY
YCQGYFYFISRTYVNSFGQGTKLTVLGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSQVQRQA
PGKLEWVGVITGRDITYYASWAKGRFTISRDTSKNTVYLMNLSRAEDTAVYYCARDGSSSAITSNINWGQGLVTVSSGGGSGG
GGGQVQLKQSGPGLVQPSQSLSTCTVSGFSLTNYGVHWVRQSPGKCLEWLGVIWSSGNTDYNTPFTSRLSINKDNKSQVFFKM
NSLQSNDAIYICARALTYDYEFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLM
ISRTPQVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTI
AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWIAICAA
GSAGITYDANWAKGRFTISRDNKNTLYLMNLSRAEDTAVYYCARSAFSDYAMDLDWGQGLVTVSSGGGSGGGGSGGGGSGGG
GSDIQMTQSPSTLSASVGRVITITQASQISSHLNHYQQKPKGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDDEF
TYYCQGGYSWGNVDNVFGGGTKEIKGGGSGGGGSGRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGT
ISSGNNVYASSARGRFTISRPSKNTVLDQMNLSRAEDTAVYYCARDGSDPMDWGQGLVTVSSGGGSGGGGSGGGGSGGGG
DVVMTQSPSSVSASVGRVITITQASQNIIRTYLSWYQQKPKGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATY
YCQSTYLGTDYVGGAFGGGTKEIK

>Sequence ID 110: SI-77H5 heavy chain nucleotide sequence

GAAATCGTTATGACGAGAGTCCCTCCACGCTCTCCGCTAGTGTGGGGATCGCGTCATTATCACATGCCAGGCCTCCGAGTCAAT
CAGCAGCTGGCTTGATGGTATCAACAGAAGCCGGGAAAGCTCCTAAATTGCTGATCTATGAAGCGTCAAAATTGGCCTCTGGTG
TCCCATTCTAGGTTCTCCGGCTCTGGGTCTGGTGCAGAAATTTACTTTGACAATCTCCAGTCTTCAACGACAGATTTTCGCTACCTAC
TACTGCCAAGGGTATTTCTATTTTATAAGCCGACATATGTAACTCCTTCGGCCAAGGAACAAAGTTGACTGTTCTTGGTGGCGG
AGGCAAGTGGTGGCGGGGGACGCGAGGTGGTGGTTCAGGGGGTGGTGGGAGCGAAGTCCAATTGGTAGAAAGTGGCGGTGGTCTGG
TGCAACCTGGTGGATCTCTTCGCTCTCATGCGCCGCTAGTGGCTTTACTATTTCACTAATGCGATGAGCTGGGTCTGCCAGGCC
CCCGCAAAGGACTTGAGTGGGTCCGCTCATCACCGGACGACATTACATACTATGCGAGTTGGGCAAGGACAGGTTACAGAT

TAGCCGCGATACTTCAAAGAATACCGTTTACCTTCAAATGAATAGCTTGAGGGCGGAAGACACAGCTGTGTATTACTGCGCGAGGG
ATGGAGGTAGTTCGCCATAACTTCCAACAACATATGGGGACAAGGCACGCTGGTTACTGTCTCGAGTGGCGGTGGAGGGTCCGGC
GGTGGTGGATCACAGGTGCAGCTGAAGCAGTCAGGACCTGGCCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTC
TGGTTTCTCATTAACATACTATGGTGTAACACTGGGTTCGCCAGTCTCCAGGAAAGTGTCTGGAGTGGCTGGGAGTGATATGGAGTG
GTGGAAACACAGACTATAATACACCTTTACATCCAGACTGAGCATCAACAAGGACAATTCCAAGAGCCAAAGTTTCTTTAAAAATG
AACAGTCTGCAATCTAATGACACAGCCATATATTACTGTGCCAGAGCCCTCACCCTACTATGATTACGAGTTTGTCTACTGGGGCCA
AGGGAAGTCTGGTCACTGTCTCGAGTGCTAGCACCAAGGGCCCTCGGTCTTCCCCTGGCACCCCTCCTCAAGAGCACCTCTGGGG
GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGC
GTGCACACCTTCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGGCCCTCCAGCAGCTTGGGGAC
CCAGACCTACATCTGCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAATCTC
ACACATGCCCCACCGTGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATG
ATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCCTCACCGTCTCTGC
ACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
GCGAAAGGGGCAACCTGTCACCGTGTGGAGTCTGGGGGAGGCTGGTACAGCCCTCCGGGATGAGCTGACCAAGACAGTCTCCTGTG
CCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
CCGTGCTGGACTCCGACGGTCTCTTCTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAAAGCTTCTTCTCA
TGCTCCGTGATGATGAGGCTCTGCAACAACCACTACACGAGAGAGCCTCTCCCTGTCTCCGGTGGCGGTGGAGGGTCCGGCGG
TGCTGGATGCTGATCACTTACGACGCAACTGGGGGAAAGGCCGCTTACCATCTCCAGAGACAAATCCAAGAACACGCTGTATCT
GCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTTTCGTTGACTACGCCATGGACCTCT
GGGGCAGGGAACCTGTCACCGTGTGCGAGCGGTGGAGGCGGATCGGCGGAGGTGGTTCGGCGCGTGGCGGCTCCGCTGGAGGC
GGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCAACCATCACTTGCCAGGCCAGTCA
GAGCATTAGTTCCTCACTTAACTGGTATCAGCAGAAACAGGGAAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCAT
CTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGAAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGA
ACTTATTACTGCCAACAGGTTATAGTTGGGTAATGTTGATAATGTTTTCGGCGGAGGACCAAGGTGGAGATCAAAGCGCGTGG
AGGGTCCGGCGGTGGTGGCTCCGGACGGTGCCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCT
GTACTGCCTCTGGATTACCATCAGTAGCTACCATGCACTGAGTGGTCCGCCAGGCTCCAGGGAAGGGGTGGAGTACATCGGAACC
ATTAGTAGTGGTGAATGTATACTACGCAAGCTCCGCTAGAGGCGAGTACCATCTCCAGACCCCTCGTCCAAGAACACGGTGA
TCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTACTGTGCGAGAGACTCTGGTTATAGTGATCTCTATGTGGGGC
AGGGAACCCCTGGTCAACGCTCTTTCAGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCA
GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCAACCATCACTGTGAGGCCAGTCAAGACAT
TAGGACTTACTTATCTGTTATCAGCAGAAACAGGGAAAGCCCTAAGCTCCTGATCTATGCTGCAGCAATCTGGCATCTGGGG
TCCCATCAAGGTTCAAGCGGAGTGGATCTGGGACAGATTTCATCTCACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACTTAC
TATTGTGCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAATGA

>Sequence ID 111: SI-77H5 light chain amino acid sequence

ENVLTQSPASLSASPERVITITCSASSSVYMHVYQKPKQAPKLWIYDTSKLASGVPSRFSGSGSGNDHLTLTISSMEPEDFATYY
CFQGSVYPFTFGQGTQKVTVLGGGSGGGGSGGGGSGGGGQVTLKESGPGLVQPGQTLTLTCAFSGFSLSSTGMGVGWIROPFGK
LEWLAHIWDDDKRNPALKSRLTISKDTSKNQVYLQMSLDAEDTAVYYCARMELWSYFDYWGQGTLVTVSSGGGSGGGGSDI
LLTQSPVILSVSPGERVFSFSCRASQSIGTNIHWYQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLINSVESEDIADYYC
QQNNWPTTFGCGTKLELKRITVAAPSVFIFFPSDEQLKSGTASVTVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSY
LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGGSGGGGSGGGGQSALTQPASVSGSPGQSITISCTGTSDDVGG
YNFVSWYQQHPGKAPKLMIYDVSDRPSGVSDRFSKSGNTASLIISGLQADDEADYYCSYGSSTHVIFFGGGTQKVTVLGGGSG
GGGSGGGGSGGGGQVQLQESGGGLVKPGGSLSLSCAASGFTFFSYWMSWVRQAPGKGLEWVANINRDSASYYVDSVKGRFTISR
DDAKNSLYLQMNLSLAEDTAVYYCARDRGVGYFDLWGRGTLVTVSS

>Sequence ID 112: SI-77H5 light chain nucleotide sequence

GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCACTGGTTCGGCTCAGGCAACGATCACACCTTACGATTTCCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTTCACTTTCGGGACAGGGACAAAAGTGACCGTCTTAGGCGGTGGCGGTAGTGGGGAGGCGG
TTCTGGCGGCGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTCAGCCAGGACAGACCC
TTAGCTCAGCTGTGCCTTCACTGGTCTTCTCTTAGCACTAGCGGTATGGGGGTGCGGTGGATTGCGGACGCAAGGT
CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAAATCAAGTGACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCTCGGATGGAATCTGGT
TTGCTGACTCAGTCTCCAGTCATCTGTCTGTGAGTCCAGGAGAAAGAGTCAAGTTTCTCTGACGGCCAGTCAGAGTATTGGCAC
AAACATACACTGGTATCAGCAAAGAACAATGGTTCTCCAAGGCTTCTCATAAAGTATGCTTCTGAGTCTATCTCTGGGATTCTT
CCAGGTTTAGTGGCAGTGGATCAGGGACAGATTTACTCTTAGCATCAACAGTGTGGAGTCTGAAGATATTGACAGATTACTGT
CAACAAAATAATACTGGCCAACACGTTCTGGTTGTGGGACCAAGCTGGAGCTGAAACGTACGGTGGCTGACCATCTGTCTCAT
CTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCTGCTGTGTGCTGCTGAATACTTCTATCCAGAGAGGCGCAAG

TACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
CTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCCTGAGCTC
GCCCGTACAAAGAGCTTCAACAGGGGAGAGTGTGGCGGTGGCGGTAGCGGTGGCGGCGGAAGTGGTGGCGGAGGATCCAGTCTG
CCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACACAGCAGTGACGTTGGTGGT
TATAACTTTGTCTCCTGGTACCAACACACCCAGGCAAGCCCCAACTCATGATCTATGATGTCAGTGATCGGCCCTCAGGGGT
GTCTGATCGCTTCTCGGCTCCAAGTCTGGCAACACGGCCCTCCCTGATCATCTCTGGCTCCAGGCTGACGACAGGGCTGATTATT
ACTGCAGCTCATATGGGAGCAGCAGCACTCATGTATTTTCGGCGGAGGGACCAAGGTGACCGTCTTAGTGGAGCGGTTCAAGC
GGAGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGCGGCTCTCAGGTGCAATTGCAGGAGTCCGGGGGAGGCGCTGGTCAAGCCTGG
AGGGTCCCTGAGTCTCTCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGG
GGCTGGAGTGGGTGGCAACATAAACCGCGATGGAAGTGCAGGTTACTATGTGGACTCTGTGAAGGGCCGATTACCATCTCCAGA
GACGACGCCAAGAACTCAGTGATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGTGG
GGTGGGCTACTTCGATCTCTGGGCGCTGGCACCTGGTCACCGTCTCTAGCTGA

>Sequence ID 113: SI-55H11 heavy chain amino acid sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNWPPTFTGPGTKLTVLGGGSGGGGSGGGGSGGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGLVIWGGNTDYNTPFTSRFTITKDN SKNQVYFKLR SVRADDTAIYYCARALTYDYEFAYWQGT LVT VSSGGGSGGGGSGG
GGSGGGGSEVQLVSEGGGLVQPGGSLRLSCAASGFTISTNAMS WVEAPGKCLEWIGVITGRDITYASWAKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCARDGSSAITSNNIWGGT LVT VSSAGTAKGSPVFP LAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSG
ALTSVHTFPFVQLSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPCPAPEAAGAPSVFLFPKP
KDTLMI SRTP EVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMEALHNHYTQKSLSLSPGGGSGGGGSGGGGSEVQLLES GGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWI
ACIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMD LWGQGT LVT VSSGGGSGGGGSGG
SGGGGSDIQMTQSPSTLSASVGRVTITCQASQSISSLN WYQQKPKAPKLLIYKASTLASGVP SRFGSGSGTEFTLTISLQ
PDDFATYYCQGGYSWGNVDNVFGGGTKVEIKGGGSGGGGSGRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKGL
EYIGTISGGNVYYASARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARD SGYS DPMWQGT LVT VSSGGGSGGGGSGGGG
GGGSDVVMTPSPSSVSASVGRVTITCQASQNI RTYLSWYQQKPKAPKLLIYAAANLASGVP SRFGSGSGTDFTLTISDLEPG
DAATYYCQSTYLGTDYVGAFAFGGKVEIK

>Sequence ID 114: SI-55H11 heavy chain nucleotide sequence

GAAATCGTCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAAGCGCGACTTTCTCTTGCAAGGCAAGTCAATCCAT
AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAAGTATGCAAGTGAGTCTATTTCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
TACTGCCAACAGAAATAAATACTGGCCGACTACCTTCGGACCCAGTACAAAGCTGACCGTTTATAGCGGTGGCGGTATGGGGAGG
CGGTCTTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
CGCTTAGTATAACGTGTACTGTTT CAGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGCGAGGCACCCGGCAAAGGTTTG
GAATGGCTGGGTGTTATTTGGTCAGGTGGAATAACAGACTATAACACCCCTTTACAAGTCGGTTCACAATTACGAAAGATAATTC
CAAAATCAAGTTTATTTCAAGTTGAGATCCGTCGCGCGGAGCAGCACTGCGATCTACTATTGTGCGAGGCGGTATGCTGACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAACAGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTCCGGCGGT
GGCGGCTCCGGTGGAGGCGGCTCTGAGGTGCAGTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGCTCCCTGAGACTCTC
CTGTGCAGCCTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCCGCGAGGCTCCAGGGAAGTGTCTGGAGTGGATCGGAG
TCATTACTGGTTCGTGATATCACATACTACCGAGCTGGCGGAGGAGCAGATTACCATCTCCAGAGACAAATCCAAGAACACGTG
TATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAA
CAACATTTGGGGCCAGGGAACCTGGTCACCGTGTCTCAGCTAGCACCAAGGGCCATCGGTCTTCCCTGGCACCTCTCTCCA
AGAGCACCTCTGGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGAACTCAGGC
GCCCTGACCAGCGGCTGCACACCTTCCGGCTGTCTGACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTC
CAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCAAAT
CTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCTTCCCCCAAACCC
AAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAA
CTGGTACGTGGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCCTGTGTGCTCAGCG
TCCTCACCGTCTTGCAACAGGACTGGTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG
AAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAGAGGTACACCTTGCCCCCATCCCGGGATGAGCTGACCAAGAACCA
GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACCACT
ACAAGACCACGCCTCCGCTCTGGACTCCGACGGCTCCTTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAGACCTCTCCCTGTCTCCGGGTGGCGG
TGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGCTCCCTGAGACTCT
CCTGTGCAGCCTCTGGATTCTCTTACGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGATC
GCATGCATTGCTGCTGGTAGTGTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTCACCATCTCCAGAGACAAATCCAA
GAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGCGGTTTTCTGTCGACT
ACGCCATGGACCTCTGGGGCCAGGGAACCCCTGGTCACCGTGTGAGCGGTGGAGCGGATCTGGCGGAGGTGGTTCGGCGGTGGC
GGCTCCGGTGGAGGGGCTGACATCCAGATGACCAAGTCTCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTACCATCAC
TTGCCAGGCCAGTCAGAGCAATTAGTTCCTTAACTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCCTGATCTATAAGG

CATCCACTCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAG
CCTGATGATTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGA
GATCAAGGGCGGTGGAGGGTCCGGCGGTGGTGGCTCCGGACGGTCCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGT
CCCTGAGACTCTCCTGTACTGCCTCTGGATTACCATCAGTAGCTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGTG
GAGTACATCGGAACCATTAGTAGTGGTGGTAATGTATACTACGCAAGCTCCGCTAGAGGCAGATTACCATCTCCAGACCTCGTC
CAAGAACACGGTGGATCTTCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTG
ATCCTATGTGGGGCCAGGGAACCTGGTCACCGTCTCTTACGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGCGGAGGGTCC
GGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTACCATCACCCTGTCA
GGCCAGTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGCTGCAGCCA
ATCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCGACCTGGAGCCTGGC
GATGCTGCAACTTACTATTGTCTAGTCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGACCAAGTGGAGAT
CAAATGA

>Sequence ID 115: SI-55H11 light chain amino acid sequence

ENVLTQSPASLSASGERVTITCSASSSVSYMHVYQKPKQAPKLIYDTSKLAGVPSRFSGSGSGNDHTLTITSSMEPEDFATYY
CFQGSVYPFTFGQGTQKVTVLGGGGSGGGSGGGSGGGSGVTLKESGPGVLVQPGQTLSTLCAFSGFLSTSGMGVGVIRQPPGKG
LEWLAIHWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGQGLVTVSSGGGGSGGGSDV
VMTQSPSTLSASVGRVTINQASESISWLAHYQKPKGAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYC
QGYFYFISRTYVNSFGCGTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGSALTQPASVSGSPGQSITISCTGTS
SDVGGYNFVSWYQQHPGKAPKLMYDVSDFPSGVDFRFSKSGNTASLIISGLQADDEADYYCSSYGSSTHVIFFGGGTQKVTVLG
GGGGSGGGSGGGSGGGSGVQLQESGGGLVKGSSLSLSCAASGFTFFSYWMSWVRQAPGKGLEWVANINRDSASYYVDSVKGR
FTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSS

>Sequence ID 116: SI-55H11 light chain nucleotide sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGATCCCAATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCTTAGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCC
TTAGCTCAGCTGTCTTCCCTTCAGTGGTCTTCTCTTAGCAGTACGCGGTATGGGGGTTCGGCTGGATTTCGGCAGCCTCCCGGCAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAAATCAAGTGTACTTGCAAAATGAATAGCCTTGACGCGGAGGATACGGCTGTATATTATGCGCTCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTTGGGGGACGGGACTCTCGTCACGGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
GTAGCTCAGCTGTCTTCCCTTCAGTGGTCTTCTCTTAGCAGTACGCGGTATGGGGGTTCGGCTGGATTTCGGCAGCCTCCCGGCAAGGT
TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGGTCCCAT
CAAGGTTACGGCGGAGTGGATCTGGGACAGAATTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGC
CAAGGCTATTTTATTTTATAGTCTGACTTATGTAAATCTTTTCGGCTGTGGGACCAAGGTGGAGATCAACGTACCGTGGCTGC
ACCATCTGCTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTCCTGCTGAATAACTTCTATC
CCAGAGAGGGCCAAAGTACAGTGAAGGTGGATAACGCGCTCCAAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGCGGTGGCGGTAGCGGTGGCGGGGAAGTGGTGGCG
TAGGATCAGCTGCCCTGACTCAGCCTGCCTCCGTGCTCCTGGACAGTTCGATCACCATCTCAGTACCATCTCAGTACCATCTCAGT
AGTGACGTTGGTGGTTATACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCAACTCATGATCTATGATGTCACTGA
TCGGCCCTCAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCTCCAGGCTGACG
ACGAGGCTGATTATTACTGCAGCTCATATGGGAGCAGCAGCATCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTTAGGT
GGAGCGGGTTCAGGCGGAGGTGGTTCGGCGGCTGGCGGCTCCGGTGGAGGCGGCTCTCAGGTGCAATTGCAGGAGTGGGGGGAGG
CCTGGTCAAGCCTGGAGGGTCCCTGAGTCTCTCCTGTGACGCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCC
AGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAACATAAACCAGGATGGAAGTGCAGTTACTATGTGGACTCTGTGAAGGGCCGA
TTCACCATCTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTG
TGCAGAGAGATCGTGGGGTGGGCTACTTTCGATCTCTGGGGCGGCTGGCACCCCTGGTACCCGCTCTCTAGCTGA

>Sequence ID 117: SI-77H4 heavy chain amino acid sequence

EIVMTQSPSTLSASVGRVTITCQASESISWLAHYQKPKGAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
YCQGYFYFISRTYVNSFGQGTKLTVLGGGGSGGGSGGGSGGGSGEVQLVESGGGLVQPGGSLRLSCAASGFTITSTNAMSWSVRQA
PGKLEWVGVTIGRDIYYASWAKGRFTISRDTSKNTVYLMQNSLRAEDTAVYYCARDGSSAITSNNIWQGLTVTVSSGGGGSG
GGGSQVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKCLEWLGVIWSSGNTDYNTPFTSRFTITKDNSKNQVYFKL
RSVRADDTAIYYCARLTYDYEFAYWGQTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTCPCPPAPEAAGAPSVFLFPKPKDITLM
ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLLVQPGGSLRLSCAASGFTFSYGYDMCWVRQAPGKLEWIIACIAA
GSAGITYDANWAKGRFTISRDN SKNTLYLMQNSLRAEDTAVYYCARSAFSDYAMDWLWQGLTVTVSSGGGGSGGGSGGGSGGGG

>Sequence ID 118: SI-77H4 heavy chain nucleotide sequence

>Sequence ID 119: SI-77H4 light chain amino acid sequence

>Sequence ID 120: SI-77H4 light chain nucleotide sequence

>Sequence ID 122: SI-68P7 heavy chain nucleotide sequence

GAAATCGTTATGACACACTGCCCCATCCACTCTTAGCGCTTCTGTAGGGGATCGAGTGATTATCACATGCCGGGCCCTCCCAATCCAT
AGGAACAACCAATACACTGGTATCAACAAAAACAGGCCAGGCAAGCGCAAAACCTGCTTATCTACTACGCTCCGAGATGTTATCTGGAA
TCCCGAGTCGTTCTCAGGTTCTGGAAAGCGCGCTGAGTTTACCTCACAATTTCTTCACTCCAACCGGATGACTTCGCTACATAT
TACTGCCAACAAAACAATAATTGGCCGACGACCTTTGGCCAGGGCACGAACTTACGGTACTTGGCGGTGGCGGTAGTGGGGGAGG
CGTTCTTGGCGGGCGAGGGTCCGGCGGTGGAGGATCAGAAGTACAGCTTGTTCGAGTCCGGTGGGGGGCTTGTTCAGCCAGGGGGT
CCTTGAGGCTTTCTCTCGCTCGCTCTGGGTTTACGTTAGCGAATTACGGCTTCACTGGGTTAGACAAGCAGCGGAAGGGCTG
GAATGGGTCGTTGATATGTCGCGGGGTAATACGGATTACAATACACCTTTCAGTCACGCTTACGATTAGCGGGACAGTC
AAAAAATACAGTCTACTTTCAGATGAATCTCTTAGGGCGGAAGATACGTGCACTTTATTACTGCGCAAGGGTCTTGACATACTACG
ATTATGAATTGTCATATGGGGCCAGGGGACTTTGGTCACGGTCTTCGAGCGGCGGTGGAGGTCGCGGCGGTGGTGGATCAAGA
CAGTTGCAAGAAAGGTGGTGGTAGACTGTTTACGCTGGTGAACCTTGTCACTGACGTGTAAGAACAGCGGCAATGATCTGTCTC
TAACGCCATCGGATGGTCCGACAGGCCAGGAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACG
CAAGTCTGGGCAAAAAGGCGAATTTACGATACACGGAGCACCTCTACAGTTTATTTGAAATGAACCTCCCTCGGTCGGAGGATACC
GCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGCAGGGTACACTGGTTACAGTTTCACTCCGCTAGCACCA
GGGCCCATCGTCTTCCCCCTGGCACCTCTCTCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGA
CTCACTCTCCCTCAGCGCTGGTGACCGTGGCCCTCGACAGCTTGGGCAACCGACACCTACATCTGCAACGTGAATCAAGACCGCCG
CAACACCAAGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAATCACACATGCCACCGTGCCACGCTCAAGCGCCGG
GGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGAACCGTGAGGTACATGCGTGGTGGT

GACGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
GGAGCATATACACAGACAGTACCGTGTGGTCAGCGTCTCACCGTCTGCACACGAGGATGGCTGAATGGCAAGGAGTACAAGTGGC
CGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAAGAAACACTCTCCAAAGCCAAAGGGCAGCCCGAGAACACAGGTGTATACC
TGCCTCCCATCCCGGATGAGTGAACCAAGAACAGTGCAGCTGTCTGCGCGCTCAAAAGGCTTCTATCCCGAGCATCGCGT
GGAGTGGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACCACGCTCTCCGTGCTGGAATCCGACGGCTCCTTCTTCTCTGTC
GCAAGCTCACGCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGTGCTCCGTGATGATGAGGCTGTGCACAAACCATAC
ACGCGAAGAGAGCTCTCCCTGTCTCCGGTGGCGGCGGCGTTCAGGTGGTGGGGATCCCGAGAGGGCCCCGAGCTGTCTCTCTA
TGACCCAGCAGGCTCTTGAACTTGGCGAGGTATGTCGTCAACTGTGGCTCAGAATGTTCTGCTCATTTGATGACCACTCT
CTTGGTATAGTGACCCCGGTCTGGCCGGGGTGAGTCTGACCGGCGGGCTCTCTTATAAAGAGGATATAAGGAACTGGTCGTAGCA
AAAGCGGGCGTTTATTACGTTTTTTTTTCAGTGGAGCTCAGCGCGTGGTGGCGGGCGAGGCGAGTGGCTCTGTGCTCTGGCCCT
GCACTTACAGGCTTTGAGAAGCGCTCAGGTGCTGCCGACTGGCTTTAACTGTTGACCTCCTCCGCGCTCTTCTGAAGTGAAG
ACAGCGCTTTGGCTTTCAAGGGCGCTGCTGCACCTTGAGCGAGGCCAGCGCTTAGGTGTGCACTTATACAGAGGCCAGGGCC
CGACACGCTTGGCAGCTCACACAGGGTGCCACGGTCTCGGACTTTTCCGCGTTACTCCCGAGATCCCCGCTGGCTCGGAAGTAC
TGGTCTCGGTTCTAAACCCGTTCCGCGCAAGGTAGTACTAAAGACGAGAAGGGCCAGAGTTAAGTCCAGTAGACCTGCTGGGCT
TTTTGGACCTCGCGCAGGCACTTTCGCTCAACTGTGGCTCAGAACGCTGCTGATCGATGGCCCCCTGAGTTGGTACAGCGAT
CCCGGCTGGCAGGCGTGTCACTTACAGGGGCGCTCTTTACAAGGAAGACACCAAGAGTTAGTGGTGCCTAAGGCTGGCGTGT
TTACGTTGTTCTTCCAACGGAGCTGAGAAGGTTGTGGCAGGAGAGGAGTGGCGCAGCGTGTCTTTAGCGCTTCACTTGCAGCCCC
TGAGGTCTGCTGTCAGGTGACAGCGCTCTCGCGCTCAGCGTGATCTCCCCCGAGCTCATCTGAAGCTGGAACAGTCACTTGGC
TTTACGGAGACGCTTGCTGCACTTCTCGCTGGACAGAGGCTGGGCGTGACACTTACACAGAGGCCGCTGCCAGGCATGCATGGCA
GCTCACTCAGGGGGCAACAGTGGCTGGTCTCTTCCGCGTGACTCCTGAAATACAGCTGGACTTGGCGGTGGAGGCAGCGCGGAG
GAGGATCTCGTAGGGGGCCAGAATGTGCCCCGATGACCCAGCGGAGTGTGATCTCAGACAGGGCATGTTCTGCTCAGCTTGT
GCCAAAAATGCTCTCTGATTGACGGCCCTTTGAGCTGGTATAGTGATCCCCGCTTGGCGGGGGTATCTCTGACCCGGAGGCGCTCT
CTACAAGGAAGACACAAAGAGCTGGTGGTGGCAAAAGCGGGGGTGATTATGTGTTCTTTCAGCTCGAGCTCGGAGAGTTGTGG
CCGGGAAGGGTCTGGGAGCGTATCTCTTGCACTTCACTGACGCGCTTGGCAGCGCGCTGGAGCCGCGCGCTTGTCTTACT
GTGGATCTGCTCTCTGCTTCTCAGAAGCAGCAACAGCGCTTCCGCTTTCAGGAGCTCTCTGCACTTGTCTCGCAGGACAGAG
GTGCGGCTCCATTTACACACTGAGGCAGGGCAGCGCAGCTTGGCAGCTTACCCAGGGAGCCACCGTGTGGGACTCTTTAGAG
GTACCCCGAGATCCCCGCTGGCTTGTGA

>Sequence ID 123: SI-68P7 light chain amino acid sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKLASGVPSRFSGSGSGNDHTLTITSSMEPEDFATYY
CFQGSVYPTFTFGQGTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPQGTLSLTCAFSGFLSTS GMGVGWIRQPPGKG
LEWLAIHWDDDKRYNPALKSRITISKDTSKNQVYLMQNSLDAEDTAVVYCMELMSYFFDYWGQGTLVTVSSSGGGGGGGSDP
QLTSPHSLSATVYQGRVTRINQSSQSVAKNNLAWFGQKPGPKLLIYSASTLAAGVPSRFSGSGSGTQFTLTITRVQSDSFATY
YCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKKHVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPCPAPEAAGGPSVFLFPPKPKDTLMTSRTPEVTC
VVVDVSHEDPEVKFNQYVVDGVEVHNKATPKREEQYNSYTRVYGVSLTVLHQDWLNGKEYKAVCNSSKDALPAPIEKTIKAKGQPREPQ
VYTLTPSRDELTKNQVSLWCLVWKFPSPDIAVEWESNGQPENNYKTTPLVDSGSEFLYSLKTVKDSRWQQGNVFSVSMHEALH
NRFTQKSLSLSPGGGGGGGGGGSDIQMTQSPSTLSASVGDRTVITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFS
GSGSGTEFTLTITSSLPQDDFATYYCQQGYSGWNVNDVFGGGTKVTVLGGGSGGGGSGGGGSGGGGSEVQLLES GGLVLPGGSL
LSCAASGFSFGSGYDMCVWRQAPGKGLEWIIACIAGSAGITVDANWAKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARSAFSF
DYAMDNLWGOGTLVTVSS

>Sequence ID 124: SI-68P7 light chain nucleotide sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGTCTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACATAGCAGCAAGCTGGCTTCGCGCGTACTCATCCCGCTTCAGTGTTCCGGCTCAGGCACAGCATCACCCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCACTATTATTTGTTTTCCAGGGAGCGTGTACCCATTCACTTTCTGGGACAGGGGACAAAAGTACCCTCTAGGCCGTTCAGGCCGTGGCGGTAGTGGGGAGAGCGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTACGCCAGGACAGACCCTTAGCCTCACTGTGCCCTTCACTGGTTTTCTTCTTAGCATACGCGGTATGGGGGTTCGGCTGGATTTCGCGAGCCTCCCGGCAAGGCTTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACCAACCGTATAATCTTCCCTTGAAGAGTCGGCTGACCATTAGTAAGGATACCTCAAAAAATCAAGTGTACTTTGCAATGAATAGCCTTTGACGCCAGGATACGGCTGTATATTATTTGCGCGCGGATGGAACCTTGGTCTTACTACTTTGATTATTGGGGGACGGGACTCTCGTCACGGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCGCAGAGGGTAAACAATCAATTGCCAGTCAAGCCAGTCGCTAGCGGAAATAATAATTTGGCATGGTTTCAACAAAAACCGGGTAAACCTCCTAACTCTTACTACTGAGCTTCAACCTTCCCGCGGGTGTCCGACCGCGGTCTCAGGCTCAGGTTCCGGGACTCAATTTACATTCACATCTACGCGTCCAAAGTGGAGGATTTTGCAACCTACTATTGTTCTGCACGGGATTCGGGAACATACAGTCCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGCACCATGTGCTTCATCTCCCGGCATCTGATGAGCAGTGTGAATCTGGAACCTGCCTCTGTTGTGTGCCCTGCTGTAATACTCTTATCCGAGAGGCCAAAGTACAGTGAAGGTGGATACAGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTCAAGCAGGACGAGCAGGACAGGACAGACCTACAGCCTCAGCAGCACCTCAGCGTGAGCAAAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGGAGGGCAGAAAACTCACACATGCCACCGTGCCAGCACCTGAAGCGCGGGGGGAGCTGATCTTCTCTTCCCCCAAAACCAAGGACCTCATGATCTCCCGGACCCCTGAGGTGCACATGCGGTGGTGGTGAGCTGAGCCACGGAAGACCTCAGGCTCAGGTTCAAGTTCAACTGGTACGCTGGACGGCGTGGAGGTGCCATATGCCAAGACGAGGCCGGGGAGGAGCAGTACAACAGCAGCTACGGTGTGGTTCAGCGTCTCAGCGTCCCTGACAGGACTGGCTGAATGGCAAGGAG

>Sequence ID 126: SI-79P1 heavy chain nucleotide sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACCGCGCACTTCTCTTGCAGGGCAAGTCAATCCAT
AGGGACTAATATACATCTGGTATCAACAAAGGCGAGTAAACCCAGGCTTTTGATTAAGTATGCAAGTAGAGCTTATTTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGCAAGTGGCACAGAGTTACACCTACCATATCTAGTGTGCAATCAGAGACTTCGCCGTGTAT
TACTGCCAACAGAATAAATACTGGCCGACTACCTTCGGACCCGGTACAAAGTTGGAATCGAAAGGCGGTGGCGGTAGTGGGGGAGG
CGGTTCTGGCGGCGAGGGGTCCGGCGGTGGAGGATACAAAGTACAGTTGCAGCAATCCGGTCCGGTCTCTGTCACAAACCGATGAG
CGCTTAGTATAACGTTGACTGTTTCAGGCTTTAGCCTTACGAACATAGGATTTACTGGAATTCGGCAGGCAACCCGCAAGGTTTG
GAATGGCTGGGTGTTTATTTGGTCAGGTGGAATAACAGACTATAACACCCCTTTTACAAGTCGGTTTACAATTACGAAAGATAATTC
CAAAAATCAAGTTTATTTCAAGTTGAGATCGCTCCGCGCGAGCACACCTGCGATCTACTATTTGTGCGAGGGCAGTACCTACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGAACAGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATACAAGTG
CAGTTGCAAGAAAGTGGTGGTAGACTGGTTGAGCCTGGTGAAACCTTGTCACTGACGTGTAAACACAGCGGCATTGATCTGTCTC
TAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACG
CAAGCTGGGGCAAAAGGGCGATTTACATATACAGGAGCACCTCTACAGTTTATTTGAAATGAATCCCTCCGGTCCGAGGATAACC
GCGATATATTACTGTGCCAGAGGGGGGTACTCCTCTGATATCTGGGGCAGGGTACACTGGTTACAGTTTCACTCCGTAGCACCAA
GGGCCATCGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTTGGTCAGGACTACT
TCCCCGAACCGGTGACGGTGTCTGTGGAACCTGAGCGGCCCTGACCTAGCGGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGA
TCTACTCTCCCTCAGCAGCGCTGGTGACCTGCCCTCCAGACCTTGGGCACCCAGACCTACATCTGCAACGTGAATACAGCGCCAG
CAACCAACAAGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACATGCCCCCGTGGCCAGACCTGAAGCCGCGG
GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTG
GACGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGACCGCGGTGGAGGTGCAATAATGCCAAGACAAAGCCGCGGA
GGAGCAGTACACACAGCAGTACCGTGTGGTCAAGTCTCCTCAGGCTCTGCCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGGC
CGGTCTCCAACAAAGCCCTCCAGGCCCTCATCGAAGAAACCATCTCAAAGCCAAAGGGCAGCCCGGAGAACCAAGGTGTATACC
CTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGTCTGCGCCGTCAAAGGCTTCTATCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACCAACTACAAGCACACGCCCTCCCGTGTGGAATCCGACGGCTCCTTCTTCTCTGTA
CGAAGCTCAGCGCTGGACAAGAGCAGTGGCAGCAGGGGACGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCTAC
ACGCAAGAGGCTCTTCTCTGCTCGGGTGGCGGCGCGGTTTCAAGTGGTGGGGGATCCGAGCTTGTGATGACGAGTCTCTAG
TTCAGTATCAGCGTCTGTTGGGGATCGAGTACGATTACATGCCAGCGAGCCAAAATATTAGGACGTATCTGTCTTGGTATCAAC
AAAAGCTGTGAAGGCTCCAAAACCTCTCATTTACGCCGCTGCCAATCTGGCTAGTGGAGTACCTTACCGTTTAGTGGGTCAAGGT
TCTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACACAGGGGACGCTGCCACGTATTATTGCCAGTCCACCTCACTCGGAC
TGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAACTACTGTACTTGGTGGTGGTGGTTTTCAGGCGGGGGGGGTTCCGGCGGAG
GCGGTTCTGGGGGTGGAGGTTCCGAGGTTTCAGTTGGTTGAAAGTGGGGGGGACTCGTTACGCTTGAGGCTCTTTGCGACTTTCT
TGTAACCGCTTCTGGGTTCACTATAAGTTTCATATCATATGCAATGGGTAAGACAGGCGCTTGTGAAGGACTTGAATACATAGGAAC
ATAAGCTCTGGTGGTAAGCTCTATTACGCTCATCCGCGGGGGGAGGTTTACAATTTTACAGGCTTCTAGCAAAAAACAGGTAAC

>Sequence ID 129: SI-68P13 heavy chain amino acid sequence
EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKGPPRLIIKYASESISGIPDRFSGSGSGTEFTLTISVSQSEDAFVY
YCQQNNNWPTTFPGPGTKLTVLGGGSGGGGSGGGGSGGGGSGVQLQQSGPLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGVIWSSGGNTDYNTPTSFRTITKDNSKNQVYFKLRSVRADDTAIYCARALTYDYEFAYWGQTLTVLTSKSSGGGSGGGSGVE
QLVESGGGLVPGGSLRLSCAASGFTITSNAMSVVRQAPKGLEWIGVITGRDITYYASWAKGRFTISRDNSTKNTLYLQMNSLRAE
DTAVYYCARDGGSSAITSNNIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVKDRVEPKSCDKTHTCPCPAPEAGGSPSVLFPPPKPKDTLMI SRTF
EVTCTVYVDVSHEDPEVKFNWYVDGVEVHNATKPREEQSYSTYRVVSLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISAKKGQ
PEPVYITLPPSRDELTKNFVSLCAVGGFKYPTSDIAEVESNGQPENNYKTTPEVLDSGGSFFLVSKLTVDKSPQGNVFSVCSVMH
EALHHNYTKQSLSLSPGGGGSGGGGSDVMTPQSPSSVSASVGDRTVITCQASNI RTYLSWYQQKPKGAPKLLIYAAANLASGVP

GAAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGTCTATACATGCGATTGGTATGACACAAAAGCCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTACTACCGCGTTTCAGTGGTTCCGGCTCAGGCACAGATCACACCTTACGATTTCAGTATGGAACCCGAAGATTTGCAACTATTATTGTTTTCCAGGGGAGCGTGTAACCATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCTTAGCGCGTGGCGGTAGTGGGGAGAGCGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTACGCCAGGACAGACCTTAGCCTCACTCTGCTCCTCAGTGGTTTTTCTTAGCATACGCGTATGGCGGCTCGGCTGATTTCGCGACGCTTCCGGGCAAAGGCTTGAGTGGTGGTGGCTCACTTTGGTGGGACGACGACAAACGGTAAATCTTGCGCTTGAAAAGTCGGCTGACCTTAGGAAGATATCCAAAGGATCTCAAAAAATCAAGTGACTCTGCAAAATGAATAGCCTTGACGCCAGAGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCGGT

CTTACTACTTTGATTATTGGGGGCGAGGGGACTCTCGTCACGGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
 GTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
 TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGGTCCCAT
 CAAGGTTACGCGGAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGC
 CAAGGCTATTTTTATTTTATAGTCTGACTTATGTAATTTCTTTGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
 ACCATCTGTCTTCTCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATC
 CCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCAAGAGAGGACAGCAGCAAG
 GACAGCACCTCAAGCCTCAGCAGCACCCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCCA
 TCAGGCGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCCTGCCAG
 CACCTGAAGCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC
 ACATGCGTGGTGGTGACCTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA
 GACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCA
 AGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAA
 CCACAGGTGTACACCTGCCCCCAAGCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCC
 CAGCAGATCGCCCGGTGGAGAGCAATGGGAGCGGAGACAACTACAAGACACGCGCTCCCGTCTGAGTCCGACGCTCCGACGGCT
 CTTCTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCAACAACAGATTACGCAAGAGCCTCTCCCTGTCTCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTCAGAT
 GACACAGTCAACGCTACGCTCTCAGCCTCAGTAGGCGATGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTACACC
 TCACTGCTCTTTCGCGCGGCGAGTGGTTTLAGCTTCAGTAGCGGCTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCGT
 TTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACTATTGTGACGA
 GGGTTATAGTTGGGAAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGAGGAAGTGGCGCGCGG
 GAAGCGGAGGTGGTGGCTCCGGCGGGGGTGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGGAAAGC
 CTCTCACTCTCTTTCGCGCGGCGAGTGGTTTLAGCTTCAGTAGCGGCTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCGT
 TGAGTGGATTGCGTGTATCGCGCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTACAATCTCCAGGG
 ACAACTCAAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAGACACCGCAGTCTACTATTGCGCAAGGTACGATTT
 AGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCTGTCACCGTCTCATCTTGA

>Sequence ID 133: SI-68P17 heavy chain amino acid sequence

DVVMTPSPSTLSASVGDRTVINCQASESISWLAHYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
 YCQGYFYFISRTYVNSFGGGTKVEIKGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWSVRQA
 PGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDGSSAITSNNIWQGTLLVTVSSGGGSG
 GGGSQVQLQSGSPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKLEWLVISGGNTDYNTPFTSRFTITKDNSKNQVYFKL
 RSVRADDTAIYYCARALTYDYEFAYWQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTSG
 VHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKRVFEPKSDKTHTCPPCPAPEAAGGPSVFLFPKPKDITLM
 ISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTI SK
 AKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKLSLSLSPGGGGSGGGGSDVMTQSPSSVSASVGDRTVITCQASQNI RTYLSWYQQKPGKAPKLLIYAAANL
 ASGVPSRFSGSGSGTDFLTISDLEFGDAATYYCQSTYLGTDYVGGAFGGGKLTVLGGGGSGGGGSGGGGSEVQLVESGG
 GLVQPGGSLRLSCTASGFTISSYHMQWRQAPGKLEYIGTISGGNVYAS SARGRFTISRPSKNTVDLQMNLSRAEDTAVYYC
 ARDSGYSDPMWQGTLVTVSS

>Sequence ID 134: SI-68P17 heavy chain nucleotide sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
 TAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGG
 TCCCATCAAGGTTACGCGGAGTGGATCTGGGACAGAATTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTAT
 TACTGCCAAGGCTATTTTTATTTTATAGTCTGACTTATGTAATTTCTTTGGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGG
 CGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG
 TCCAGCCTGGGGGCTCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCT
 CCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGATATACATACTACGCGAGCTGGGCGAAAGGCAGATTACCAT
 CTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTACCCTCTCGAGTGGCGGTGGAGGTCCGGC
 GGTGGTGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTC
 AGGCTTTAGCCTTACGAATATGGAGTTCACTGGATTCGGCAGGCACCCGGCAAAGGTTTGGAAATGGCTGGGTGTTATTTGGTCAG
 GTGGAATACAGACTATAACACCCCTTTACAAGTCGGTTACAATTACGAAAGATAATCCAAAAATCAAGTTTATTTCAAGTTG
 AGATCCGTCCGCGCGGACGCACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGATTGGGGGCA
 AGGGACTCTTGTAACAGTCTCCAGTGTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGG
 GCACAGCGGCGCTGGGCTGCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCAC
 CCAGACCTACATCTCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTC
 ACACATGCCACCGTGGCCAGCACCTGAAGCCGCGGGGGGACCCTGAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATG
 ATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGG
 CGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCAGCTCCCTGC
 ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA

GCCAAGGGCAGCCCCGAGAACCACAGGTGTATACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTG
CGCCGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAGACCACGCCCTC
CCGTGCTGGACTCCGACGGCTCCTTCTTCTCGTGAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTCTTCTCA
TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTGGCGGCGCGGTTGAGGTGG
TGGGGGATCCGACGTTGTGATGACGAGTCTCCTAGTTGAGTATCAGCGTCTGTTGGGGATCGAGTCAGATTACATGCCAGGCGA
GCCAAAATATAGGACGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCCTCATTACGCCGCTGCCAACTTG
GCTAGTGGAGTACCTTACGCTTTAGTGGGTGAGGTTCTGGAACAGATTTACGTTGACGATCTCCGATTGGAACACAGGGGACGC
TGCCACGTATATTGCCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTG
GTGGTGGTGGTTGAGCGGGGGGGGTTCCGGCGGAGGCGGTTCTGGGGTGGAGGTTCCGAGGTTGAGTTGGTTGAAAGTGGGGGG
GGACTCGTTGAGCCTGGAGGCTCTTTCGCACTTTCTTGTACCGCTTCTGGGTTCACTATAAGTTTCATATCATATGCAATGGGTAA
ACAGCGCCCTGGTAAGGAGCTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGCTTATTACGCTCATCCGCGGGGGGAGGT
TTACAATTTCCAGGCTTCTAGCAAAAACACGGTAGATCTGCAATGAAGTCTCTTCCGCGTGAAGATACAGCAGTCTACTACTGC
GCCAGGGATTGAGGTATTCTGACCCCATGTGGGGCAGGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 135: SI-68P17 light chain amino acid sequence
ENVLTQSPASLSASPERVTITCSASSSVSYMHVYQKPKQAPKLWIYDTSKLASGVPSRFSGSGSGNDHTLTITSSMEPEDFATYY
CFQGSVYPFTFGQGTKVTVLGGGGSGGGSGGGSGGGSGVTLKESGPGVLVQPGQTLTLTCAFSGFSLSSTSGMGVGVWRQPPGKG
LEWLAIHWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYDYWGQGLTVTVSSGGGGSGGGSGEI
VLTPSPSTLVSPTGERATFCRASQSIGTNIHWYQKPKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSGDFAVYYC
QQNNNWPTTFPGTKLTVLRTVAAPSVEIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS
LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEGGDKHTHTPCPPAPAEAAAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDVLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNR
TQKLSLSLPGGGGGSGGGGSDIQMTQSPSTLSASVGRVITITCQASQSISSHLNWIYQKPKGKAPKLLIYKASTLASGVPSRFSGSG
SGTEFTLTISLQPDFFATYYCQQGYSWGNVDNVFGGGTGKVTVLGGGGSGGGSGGGSGGGSGGGSEVQLLESGLVQPGGSLSLSC
AASGFSFSSGYDMCWVRQAPGKGLEWIAIAAGSAGITYDANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSAFSDYA
MDLWQGGTLTVTVSS

>Sequence ID 136: SI-68P17 light chain nucleotide sequence
GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCACTGGTTCGGGCTCAGGCAACGATCACACCCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCACTTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTCACCTTTCGGGCGAGGGACAAAAGTGACCGTCTTAGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGTCGGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTGAGCCAGGACAGACCC
TTAGCCTCACCTGTGCTTCACTGGTCTTCTCTTAGCATTAGCGGTATGGGGGTGCGGTGGATTTCGGCAGCCTCCCGCAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCGGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTTGGGGGCGAGGGGACTCTCGTCACGGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAAATC
TGCTTACCAATCTCCTGACACACTGAGTGTGAGCCCGGCGAACGCGCGACTTCTCTTGCAAGGGCAAGTCAATCCATAGGGAC
TAATATACATTGGTATCAACAAAAGCCAGGTAACACCCAGGCTTTTGATTAAAGTATGCAAGTGAAGTCTATTTCCGGTATCCCTG
ACCGTCTCTGAGTACAGGAGTGGCACAGAGTTCACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGGCGTGTATTACTGC
CAACAGAATAAATACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTACGTACGGTGGCTGCACCATCTGTCTTCAT
CTTCCCGCATCTCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCGAAAG
TACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACGCAAGGACAGCACCTACAGC
CTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTGCAGAGTCACCCATCAGGGCCTGAGCTC
GCGGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGG
GGGACCGTCACTCTCTCTTCCCCCAAAACCAAGGACACCGTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGT
GACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
GGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGGC
CGGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
CTGCCCCCAAGCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGCTGGTGGTCAAGGCTCTATCCCAAGGCTCACTCGCGT
GGAGTGGGAGAGCAATGGGCGCCGAGAACACTACAAGACCACGCTCCCGTGTGACTCCGACGGCTCTTCTTCTCTTATA
GCAAGCTCACCGTGTGACAAAGCAGGTGGCAGCAGGGGAACGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACAGATT
ACGCGAAGAGCCTCTCCCTGTCTCCGGTGGCGGTGGAGGTCGGCGGTGGTGGATCCGACATTGATGACACAGTCAAGCTC
TACGCTCTCAGCCTCAGTAGGCGATAGGGTGAATCACTGCGCAAGCCTCCCAATCTATAAGTTCACACCTCACTGGTATCAAC
AGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCTCAGGTGTGCCTAGTCGCTTCTCCGGGAGCGGC
TCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCAACCCGACGACTTCGCCACATACTATTGTGACGAGGTTATAGTTGGGG
AAATGTTGACATATGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGAGGGGAGGAAGTGGCGCGCGGAAGCGGAGGTGGTG
GCTCCGGCGGGGTTGGAAGCGAAGTGCAATTGCTCGAAAGTGCTGGCGGACTTGTGCAACCTGGTGAAGCCTCTCACTCTCTTGC
GCGGCGAGTGGTTTTAGCTTCAGTAGCGGTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCTTGAAGTGGATTGCGTG
TATCGCGCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTCAATCTCAGGGACAACTCAAAAATA
CATTTGACCTTCAGATGAATAGCCTGAGAGCCGAAGACACCGCATCTACTATTGCGCAAGGTGAGCATTAGCTTCGATTATGCA
ATGGATCTTTGGGCGCAGGGGACGCTCGTACCGTCTCATCTTGA

>Sequence ID 137: SI-79C1 HC and SI-79X1 HCl amino acid sequence

QVQLKQSGPGLVQPSQSLSTCTVSGFSLTNYGVHWRQSPGKGLEWLGVIWSGGNTDYNTPFTSRLSINKDNSKQVFFKMNSLQ
SNDTAIYYCARALTYDYEFAYWGQGLTVVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQQGVNFVSCSV
MHEALHNHYTQKSLSLSPG

>Sequence ID 138: SI-79C1 HC and SI-79X1 HCl nucleotide sequence

CAAGTTCAGCTCAAGCAGCTGGCCCTGGCTGGTTCAGCCTTCTCAGAGCCTGAGCATCACCTGTACCGTGTCCGGCTTCTCCCT
GACCAATTACGGCGTGCAGTGGGTTCGACAGAGCCCTGGCAAAGGACTGGAATGGCTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTCACCTCTCGGCTGTCTATCAACAGGACAACCTCCAAGAGCCAGGTGTTCTTCAAGATGAACCTCGCTGCAG
TCCAACGACACCGCATCTACTACTGTGCTCGGGCCCTGACCTACTACGACTACGAGTTTGCTTACTGGGGCCAGGGCACCCCTGGT
CACAGCTTTCGCTGTAGCCACCAAGGGCCCATCGGTCTTCCCTTGGCAGCCCTCCTCCAAGAGCACCTTGGGGGACAGCGGGCC
TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGCTGCTGGAAGTCAAGGCGCCCTGACGAGCGCGTGCACACCTTC
CCGGCTGTCTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCCAC
CTGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTTGGGGGACAGCGGGCC
CCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAAGCTCCTCACCGTCTGACCCAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAAAGG
CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACT
CCGACGGCTCTTCTCTCTATAGCAGGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTTGA

>Sequence ID 139: SI-79C1 LC, SI-79C5 LC, SI-79X1 LC1, and SI-79X5 LC1 amino acid sequence

DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRNGSPRLLIKYASESISGIPSRFSGSGSGDFTLSINSVESEDIADY
YCQQNNWPTTFGATKLELKRVTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 140: SI-79C1 LC, SI-79C5 LC, SI-79X1 LC1, and SI-79X5 LC1 nucleotide sequence

GACATCCTGCTGACCCAGTCTCCAGTGATCCTGTCCGTGTCTCTGGCGAGAGAGTGCTCTCAGCTGCAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGCGGACCAACGGCTCCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCTATCAGCGCA
TCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACCAGCTTACCTGTCCATCAACTCCGTGGAATCCGAGGATATCGCCGACTAC
TACTGCCAGCAGAACAACTGGCCACCACTTGGCGCTGGCACCAGCTGGAATTGAAACGTACGGTGGCTGCACCATCTGT
CTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATACTTCTATCCCAGAGAGG
CCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGTAATCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC
TACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGGCCT
GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

>Sequence ID 141: SI-79C2 HC, SI-79C3 HC, SI-79X2 HCl, SI-79X3 HCl amino acid sequence

QVQLQSGPGLVKPSETLSITCTVSGFSLTNYGVHWRQSPGKGLEWLGVIWSGGNTDYNTPFTSRFTITKDNSKNQVYFKLSVR
ADDTAIYYCARALTYDYEFAYWGQGLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQQGVNFVSCSV
MHEALHNHYTQKSLSLSPG

>Sequence ID 142: SI-79C2 HC, SI-79C3 HC, SI-79X2 HCl, SI-79X3 HCl nucleotide sequence

CAAGTTCAGTTCAGCAGCTGGCCCTGGCTGGTCAAGCCTTCTGAGACACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCT
GACCAATTACGGCGTGCAGTGGATCAGACAGGCCCTGGCAAAGGACTGGAATGGCTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTCACAGCCGGTTCACCATACCAAGGACAACCTCCAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGCGG
GCTGATGACACCGCATCTACTACTGTGCTCGGGCCCTGACCTACTACGACTACGAGTTTGCTTACTGGGGCCAGGGCACCCCTGGT
CACAGTTTCTTCTAGTACCAAGGGCCCATCGGTCTTCCCTGGCACCCCTCCTCCAAGAGCACCTTGGGGGACAGCGGGCC
TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGCTGCTGGAAGTCAAGGCGCCCTGACGAGCGCGTGCACACCTTC
CCGGCTGTCTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCCAC
CTGTGCCAGCACCTGAAGCGCGGGGGCACCGTCAGTCTTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCA

TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG
CTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACT
CCGACGGCTCCTTCTCTCTATAGCAGGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTTGA

>Sequence ID 143: SI-79C2 LC and SI-79X2 LC1 amino acid sequence
EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQKPKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNWPTTFPGPTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 144: SI-79C2 LC and SI-79X2 LC1 nucleotide sequence
GAGATCGTGTGACCCAGTCTCCTTCCACACTGTCTGTCTCCCGGCGAGAGGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCCGCAAGCCTCTCGGCTGCTGATTAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCAGAGTTACCTGACCATCTCCTCCGTGCAGTCCGAGGATTTCGCGGTGTAC
TACTGCCAGCAGAACAACTGGCCACCACTTTGGACCCGGCACCAGCTGGAATTGAAACGTACGGTGGCTGCACCATCTGT
CTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCTCTGTGTGTGCTGAATACTTCTATCCAGAGAGG
CCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC
TACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCCATCAGGGCCT
GAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

>Sequence ID 145: SI-9C21 HC, SI-79X1 HC2, SI-79X2 HC2, SI-79X3 HC2, and SI-79X5 HC2
amino acid sequence
EVQLVESGGGLVQPGGSLRLSCTASGFTISTNAMSWVRQAPGKGLEWGVITGRDITYYASWAKGRFTISRDTSKNTVYLQMNLSR
AEDTAVYYCARDGGSSAITSNNIWQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPCPAPEAAGAPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSRDELTKNQVSLTCLLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFLLYSKLTVDKSRWQQGNVFC
SV MHEALHNHYTQKSLSLSPG

>Sequence ID 146: SI-9C21 HC, SI-79X1 HC2, SI-79X2 HC2, SI-79X3 HC2, and SI-79X5 HC2
nucleotide sequence
GAAGTCCAATTGGTAGAAAGTGGCGGTGGTCTGGTGCAACCTGGTGGATCTCTTCGCCTCTCATGCACGGCTAGTGGCTTTACTAT
TTCAACTAATGCGATGAGCTGGGTTCGCCAGGCCCGCGCAAGGACTTGAGTGGGTTCGGCGTCATCACCGGCAGGGACATTACAT
ACTATGCGAGTTGGGCAAAGGGCAGGTTACGATTAGCCGCGATACTTCAAAGAATACCGTTTACCTTCAAATGAATAGCTTGC
GCGGAAGACACAGCTGTGTATTACTGCGCGCGGGATGGAGGTAGTTCCGCCATAACTTCCAACAACATATGGGGACAAGGCACGCT
GGTTACTGTGTCGTAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCAAGAGCACCTCTGGGGGACAGCGG
CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGCTGCACAC
TTCCCGGTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTA
CATCTGCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTGTGACAAAACCTCACACATGCC
CACCCTGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGG
ACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGCAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAGCGTCTCACCCTCTGCACCAGGACT
GGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG
CAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
AGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTGG
ACTCCGACGGCTCCTTCTGCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTTGA

>Sequence ID 147: SI-9C21 LC, SI-79X1 LC2, SI-79X2 LC2, SI-79X3 LC2, and SI-79X5 LC2
amino acid sequence
EIVMTQSPSTLSASVGDRIITCQASESISWLAHYQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
YCQGYFYFISRTYVNSFGQGTKLTVLRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 148: SI-9C21 LC, SI-79X1 LC2, SI-79X2 LC2, SI-79X3 LC2, and SI-79X5 LC2
nucleotide sequence
GAAATCGTTATGACGACAGATCCCTCCACGCTCTCCGCTAGTGTGCGGGATCGCGTCATTATCAGATGCCAGGCCTCCGAGTCAAT
CAGCAGCTGGCTTGCATGGTATCAACAGAAGCCGGGAAAAGCTCCTAAATTGCTGATCTATGAAGCGTCAAATTTGGCGTCTGGTG
TCCCCTAGGTTCTCCGGCTCTGGGTCTGGTGCAGAAATTTACTTTGACAATCTCCAGTCTTCAACCAGACGATTTTCGTACCTAC
TACTGCCAAGGGTATTTCTATTTTATAAGCCGACATATGTAACCTCCTTCGGCCAAGGAACAAAGTTGACTGTTCTTCTGTACGGT
GGCTGCACCATCTGTCTTCTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATAACT

TCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGT
CACCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

>Sequence ID 149: SI-79C3 LC and SI-79X3 LC1 amino acid sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNNWPTTFGPGTKLTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 150: SI-79C3 LC and SI-79X3 LC1 nucleotide sequence

GAGATCGTGTGACCCAGTCTCCTTCCACACTGTCTGTGTCTCCCGCGAGAGAGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAGCCCGGCAAGCCTCCTCGGCTGCTGATTAAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCAGAGTTACCTGACCATCTCCTCCGTGCAGTCCGAGGATTTCCGCGTGTAC
TACTGCCAGCAGAAACAACACTGGCCACCACTTTGGACCCGGCACCAGCTGACCGTGTGCTACGGTGGCTGCACCATCTGT
CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGG
CCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC
TACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCT
GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

>Sequence ID 151: SI-79C5 HC and SI-79X5 HC1 amino acid sequence

QVQLKQSGPGLVQPQSLSITCTVSGFSLTNYGVHWVRQSPGKLEWLGVIWSGGNTDYNTPFTSRLSINKDNSKQVFFKMNSLQ
SEDTAIYYCARALTYDYEFAYWGQGLTVVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTCPCPPAPEAAGAPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQQGNVFSQSV
HEALHNYHTQKSLSLSPG

>Sequence ID 152: SI-79C5 HC and SI-79X5 HC1 nucleotide sequence

CAAGTTCAGTCAAGCAGTCTGGCCCTGGCCTGGTTCAGCCTTCTCAGAGCCTGAGCATCACCTGTACCGTGTCCGGCTTCTCCCT
GACCAATTACGGCGTGCAGTGGGTTCGACAGAGCCCTGGCAAAGGACTGGAATGGCTGGGAGTGATTTGGAGCGGCGGCAACACCG
ACTACAACACCCCTTTCACCTCTCGGCTGTCTATCAACAAGGACAACCTCCAAGAGCCAGGTGTTCTTCAAGATGAACCTCCCTGCAG
TCCGAGGACACCGCCATCTACTACTGTGCTCGGGCCCTGACCTACTACGACTACGAGTTTGCTTACTGGGGCCAGGGCACCCCTGGT
CACAGTTTCTGCTGTAGCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGGCC
TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTC
CCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCAC
CGTGCCACGACCTGAAGCCGCGGGGACCGTCACTCTTCTTCCCCCAAACCCAAAGGACACCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
TAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCCTCACCGCTCTGCACAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGG
CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACT
CCGACGGCTCCTTCTTCTATAGCAGGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGTTGA

>Sequence ID 153: Consensus-VH

QVQLQSGPGLVKPSESLSLTCTVSGFSLTNYGVHWVRQAPGKLEWLGVIWSGGNTDYNTPFTSRFTISKDNSKNQVYFKMNSLR
AEDTAXYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 154: Consensus-VL

EIVLTQSPSTLSVSPGERVTFSCRASQSIGTNIHWYQQKPKQPRLIKYASESISGIPSRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNNWPTTFGQGTKELEK

REFERENCES

1. Graham J, Muhsin M, Kirkpatrick P. Cetuximab. *Nat Rev Drug Discov* 2004; 3:549–50.
2. Bou-Assaly W, Mukherji S. Cetuximab (Erbix). *Am J Neuroradiol* 2010; 31:626–7.
3. Hanck-Silva G, Fatori Trevizan LN, Petrilli R, de Lima FT, Eloy JO, Chorilli M. A Critical Review of Properties and Analytical/Bioanalytical Methods for Characterization of Cetuximab. *Crit Rev Anal Chem* [Internet] 2020; 50:125–35. Available from: <https://doi.org/10.1080/10408347.2019.1581984>
4. García-Foncillas J, Sunakawa Y, Aderka D, Wainberg Z, Ronga P, Witzler P, Stintzing S. Distinguishing Features of Cetuximab and Panitumumab in Colorectal Cancer and Other Solid Tumors. *Front Oncol* 2019; 9:1–16.
5. Kaplon H, Reichert JM. Antibodies to watch in 2021. *MAbs* [Internet] 2021; 13:1–34. Available from: <https://doi.org/10.1080/19420862.2020.1860476>
6. Hwang WYK, Foote J. Immunogenicity of engineered antibodies. *Methods* 2005; 36:3–10.
7. Park SS, Kim J, Brandts JF, Hong HJ. Stability of murine, chimeric and humanized antibodies against pre-S2 surface antigen of hepatitis B virus. *Biologicals* 2003; 31:295–302.
8. Ayoub D, Jabs W, Resemann A, Evers W, Evans C, Main L, Baessmann C, Wagner-Rousset E, Suckau D, Beck A. Correct primary structure assessment and extensive glyco-profiling of cetuximab by a combination of intact, middle-up, middle-down and bottom-up ESI and MALDI mass spectrometry techniques. *MAbs* 2013; 5:699–710.
9. van de Bovenkamp FS, Hafkenscheid L, Rispens T, Rombouts Y. The Emerging Importance of IgG Fab Glycosylation in Immunity. *J Immunol* 2016; 196:1435–41.
10. Chung CH, Mirakhur B, Chan E, Le Q-T, Berlin J, Morse M, Murphy BA, Satinover SM, Hosen J, Mauro D, et al. Cetuximab-Induced Anaphylaxis and IgE Specific for Galactose- α -1,3-Galactose. *N Engl J Med* 2008; 358:1109–17.
11. Kuriakose A, Chirmule N, Nair P. Immunogenicity of Biotherapeutics: Causes and Association with Posttranslational Modifications. *J Immunol Res* 2016; 2016.
12. Zhang P, Woen S, Wang T, Liao B, Zhao S, Chen C, Yang Y, Song Z, Wormald MR, Yu C, et al. Challenges of glycosylation analysis and control: An integrated approach to producing optimal and consistent therapeutic drugs. *Drug Discov Today* [Internet] 2016; 21:740–65. Available from: <http://dx.doi.org/10.1016/j.drudis.2016.01.006>
13. Borrás L, Gunde T, Tietz J, Bauer U, Hulmann-Cottier V, Grimshaw JPA, Urech DM. Generic approach for the generation of stable humanized single-chain Fv fragments from rabbit monoclonal antibodies. *J Biol Chem* 2010; 285:9054–66.

14. Li S, Schmitz KR, Jeffrey PD, Wiltzius JJW, Kussie P, Ferguson KM. Structural basis for inhibition of the epidermal growth factor receptor by cetuximab. *Cancer Cell* 2005; 7:301–11.
15. Ewert S, Huber T, Honegger A, Plückthun A. Biophysical properties of human antibody variable domains. *J Mol Biol* 2003; 325:531–53.
16. Nieba L, Honegger A, Krebber C, Plückthun A. Disrupting the hydrophobic patches at the antibody variable/constant domain interface: Improved in vivo folding and physical characterization of an engineered scFv fragment. *Protein Eng* 1997; 10:435–44.
17. Gao SH, Huang K, Tu H, Adler AS. Monoclonal antibody humanness score and its applications. *BMC Biotechnol* 2013; 13.
18. Racle J, Michaux J, Rockinger GA, Arnaud M, Bobisse S, Chong C, Guillaume P, Coukos G, Harari A, Jandus C, et al. Robust prediction of HLA class II epitopes by deep motif deconvolution of immunopeptidomes. *Nat Biotechnol* [Internet] 2019; 37:1283–6. Available from: <http://dx.doi.org/10.1038/s41587-019-0289-6>
19. Wang C, Wu Y, Wang L, Hong B, Jin Y, Hu D, Chen G, Kong Y, Huang A, Hua G, et al. Engineered soluble monomeric IgG1 Fc with significantly decreased non-specific binding. *Front Immunol* 2017; 8:1–8.
20. Ulitzka M, Carrara S, Grzeschik J, Kornmann H, Hock B, Kolmar H. Engineering therapeutic antibodies for patient safety: Tackling the immunogenicity problem. *Protein Eng Des Sel* 2020; 33:1–12.
21. Banisadr A, Safdari Y, Kianmehr A, Pourafshar M. Production of a germline-humanized cetuximab scFv and evaluation of its activity in recognizing EGFR- overexpressing cancer cells. *Hum Vaccines Immunother* [Internet] 2018; 14:856–63. Available from: <https://doi.org/10.1080/21645515.2017.1407482>
22. Choi Y, Ndong C, Griswold KE, Bailey-Kellogg C. Computationally driven antibody engineering enables simultaneous humanization and thermostabilization. *Protein Eng Des Sel* 2016; 29:419–26.
23. Giddens JP, Lomino J V., DiLillo DJ, Ravetch J V., Wang LX. Site-selective chemoenzymatic glycoengineering of Fab and Fc glycans of a therapeutic antibody. *Proc Natl Acad Sci U S A* 2018; 115:12023–7.

EGFR BINDING COMPLEX AND METHOD OF MAKING AND USING THEREOF

CLAIMS

WHAT IS CLAIMED IS:

1. A human epithelium growth factor receptor (EGFR) binding peptide having a binding specificity to human EGFR, comprising an amino acid sequence having at least 98%, 95%, or 92% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 57, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83.

2. The EGFR binding peptide of Claim 1, comprising a variable heavy (VH) chain and a variable light (VL) chain,

wherein the VH chains comprises an amino acid sequence having at least 98%, 95%, or 92% sequence identify to SEQ ID NO. 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, or 41; and

wherein the VL chain comprises an amino acid sequence having at least 98%, 95%, or 92% sequence identity to SEQ ID NO. 3, 7, 11, 15, 19, 23, 27, 31, 35, 39, or 43.

3. The EGFR binding peptide of Claim 2, comprising a scFv domain, wherein the scFv domain comprises the VH chain and the VL chain, and wherein the scFv domain comprises an amino acid sequence having at least 98% sequence identify to SEQ ID NO. 57, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, or 83.

4. The EGFR binding peptide of Claim 3, comprising a histidine residue linked to at least one end of the scFv domain, and wherein the EGFR binding peptide comprises an amino acid sequence having at least 98% sequence identity to 57.

5. The EGFR binding peptide of Claim 2, comprising a Fab domain, wherein the Fab domain comprises the VH chain and the VL chain.

6. The EGFR binding peptide of Claim 5, further comprising a Fc domain linked to the Fab domain to provide a Fab-monoFc fusion protein, wherein the Fc domain comprises a sequence having at least 98% sequence identity to an amino acid sequence selected from SEQ ID NO. 45 and 47.

7. An antibody-like protein having a binding specificity to human EGFR, comprising an EGFR binding domain having a variable heavy (VH) chain and a variable light (VL) chain,

wherein the VH chains comprises an amino acid sequence having at least 98% sequence identify to SEQ ID NO. 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, or 41; and

wherein the VL chain comprises an amino acid sequence having at least 98% sequence identity to SEQ ID NO. 3, 7, 11, 15, 19, 23, 27, 31, 35, 39, or 43.

8. The antibody-like protein of Claim 7, comprising a scFv domain having an amino acid sequence having at least 98% sequence identity to SEQ ID NO. 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, or a combination thereof.

9. The antibody-like protein of Claim 7, wherein the antibody-like protein is a monospecific antibody comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO. 137, 139; 141, 143; 141, 149, 151, 139; 145, 147, , or a combination thereof.

10. The antibody-like protein of Claim 7, wherein the antibody-like protein is a bispecific antibody comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO. 137, 145, 139, 147, 141, 145, 143, 147, 141, 145, 149, 147, 151, 145, 139, 147 or a combination thereof.

11. The antibody-like protein of Claim 7, wherein the antibody-like protein is a penta-specific antibody comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO. 85, 87; 89, 91; 93, 95, 97, 99, 101, 103, 105, 107, or a combination thereof.

12. The antibody-like protein of Claim 7, wherein the antibody-like protein is a hexa-specific antibody comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO. 109, 111, 113, 115, 117, 119, or a combination thereof.

13. The antibody-like protein of Claim 7, comprising a heavy chain (HC) and a light chain (LC),

wherein the HC comprises an amino acid sequence having at least 98%, 95%, or 92% of sequence identity to SEQ ID NO. 85, 89, 93, 97, 101, 105, 109, 113, 117, 137, 141, 145, or 151; and

wherein the LC comprises an amino acid sequence having at least 98%, 95%, or 92% of sequence identity to SEQ ID NO. 87, 91, 95, 99, 103, 107, 111, 115, 119, 139, 143, 147, or 149.

14. The antibody-like protein of Claim 7 comprising a heavy chain monomer and a light chain monomer, wherein the heavy chain monomer having a N-terminus and a C-terminus, comprising in tandem from the N-terminal to the C-terminal,

an optional first binding domain (D1) at the N-terminal,

a Fab domain as a second binding domain(D2) comprising a light chain,

a Fc domain,

an optional third binding domain (D3), and

an optional fourth binding domain (D4) at the C-terminal,

wherein the light chain comprises an optional fifth binding domain (D5) covalently attached to the C-terminus, an optional sixth binding domain (D6) covalently attached to the N-terminus, or a combination thereof, and wherein at least one of D1, D2, D3, D4, D5 and D6 comprises the EGFR binding domain.

15. The antibody-like protein of Claim 14, wherein at least one of the D1 or D2 comprises the EGFR binding domain.

16. The antibody-like protein of Claim 14, wherein each of the D3, D4, D5 and D6 comprises the EGFR binding domain.

17. The antibody-like protein of Claim 14, wherein antibody-like protein is a bispecific antibody comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO. 137, 145, 139, 147; 141, 145, 143, 147; 141, 145, 149, 147; 151, 145, 139, or 147.

18. The antibody-like protein of Claim 17, wherein the bispecific antibody is asymmetric with the D2 comprising the EGFR binding domain and the D3 has a binding specificity to CD3.

19. The antibody-like protein of Claim 7 having a N-terminus and a C-terminus, comprising,

a first monomer, comprising, from the N-terminus to the C-terminus, a first binding domain (mD1), a variable heavy (VH) chain, a CH1 domain, a first hinge, a first CH2 domain, a first CH3 domain, and a fourth binding domain (mD4),

a second monomer, comprising, from the N-terminus to the C-terminus, a second binding domain (mD2), a variable light (VL) chain, a CL domain, a second hinge, a second CH2 domain, and a second CH3 domain, and a fifth binding domain (mD5),

wherein the CH chain and CL chain forms a third binding domain (mD3),

wherein the first monomer and the second monomer are covalently paired through at least one disulfide bond between the CH1 domain and the CL domain and at least one disulfide bond between the first hinge and the second hinge, and

wherein the multi-specific antibody-like protein is at least bi-specific.

20. The antibody-like protein of Claim 19, wherein at least one of the mD1, mD2, mD3, mD5, and mD5 comprises the EGFR binding domain.

21. The antibody-like protein of Claim 19, wherein at least one of the mD3 or mD2 domain comprises the EGFR binding domain.

22. The antibody-like protein of Claim 19, wherein the mD2, mD4, mD5 each comprises the EGFR binding domain.

23. The antibody-like protein of Claim 19, comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO 121, 123, 125, 127, 129, 131, 133, 135, or a combination thereof.

24. A heavy chain, comprising an amino acid sequence having at least 98% sequence identity to SEQ ID NO 121, 125, 129, or 133.

25. A light chain, comprising an amino acid sequence having at least 98% sequence identity to 123, 127, 131, or 135.

26. An isolated nucleic acid sequence encoding the antibody-like protein of Claim 7.

27. An expression vector comprising the isolated nucleic acid sequences of Claim 26.

28. A host cell comprising the isolated nucleic acid sequence of Claim 26.

29. A pharmaceutical composition, comprising the antibody-like protein of Claim 7 and a pharmaceutically acceptable carrier.

30. An immunoconjugate comprising the antibody-like protein of Claim 7 and a cytotoxic agent.

31. A pharmaceutical composition, comprising the immunoconjugate of Claim 30 and a pharmaceutically acceptable carrier.

32. A method for treating or preventing a cancer, an autoimmune disease, or an infectious disease in a subject, said method comprising administering to the subject a pharmaceutical composition comprising a purified antibody-like protein of Claim 7.

33. A method for producing the antibody-like protein of Claim 7, comprising culturing a host cell such that the DNA sequence encoding the antibody-like protein of Claim 9 is expressed, and purifying said multi-specific antibody-like protein.

34. A solution comprising an effective concentration of the antibody-like protein of Claim 7, wherein the solution is blood plasma in a subject.