

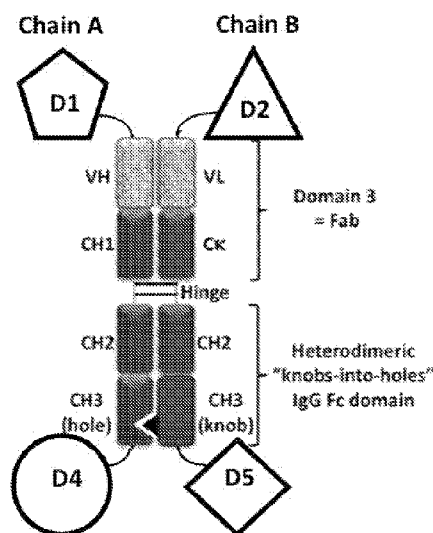
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AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ,(54) Title: MINIATURE GUIDANCE AND NAVIGATION CONTROL (miniGNC) ANTIBODY-LIKE PROTEINS AND
METHODS OF MAKING AND USING THEREOF

Figure 1



(57) **Abstract:** A multi-specific antibody-like protein having a first monomer comprising a first binding monomer, a CH1 domain, a first hinge, a first CH2 domain, and a first CH3 domain, a second monomer comprising a second binding monomer, a CL domain, a second hinge, a second CH2 domain, and a second CH3 domain, wherein the first binding monomer and a second binding monomer are configured to form a dimer, 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, wherein the first monomer and second monomer may comprise optionally a first binding domain (D1) and a second binding domain (D2), and a fourth binding domain (D4) and a fifth binding domain (D5), and wherein the multi-specific antibody-like protein is at least bi-specific.



CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

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MINIATURE GUIDANCE AND NAVIGATION CONTROL (miniGNC) ANTIBODY-LIKE PROTEINS AND METHODS 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. 62/991,042 filed March 17, 2020 under 35 U.S.C. 119(e), the entire disclosures of which are incorporated by reference herein.

TECHNICAL FIELD

The present application generally relates to the technical field of multi-specific antibody for cancer immunotherapy and more particularly relates to making and using miniature Guidance and Navigation Control (miniGNC) antibodies with multiple binding activities against surface molecules of both immune cells and tumor cells.

BACKGROUND

Therapeutic antibodies have become a mainstay in treatment of several diseases, including but not limited to cancer, infection, and autoimmunity. While monoclonal, monospecific antibodies provide a straightforward mechanism to treat disease, e.g., via inhibition or activation of specific signalling pathways, multi-specific antibodies allow more complex therapeutic mechanisms to be explored. By targeting multiple distinct antigens, or multiple epitopes within a single antigen, biological responses such as cell colocalization and activation can be elicited, which enables, for example, the redirection of T cells and other immune cells to the site of specific antigen-expressing tumor cells. In this way, bispecific and multi-specific antibodies have become important platforms in the field of immuno-oncology.

Due to the advantages of multi-specific antibody platforms, many such frameworks have been developed. One such platform is known as Guidance and Navigation Control (GNC). The GNC proteins include the proteins linking multiple functionally independent binding moieties into a single entity that is capable of bringing both effector cells and target cells together (see Applicant's applications, WO/2019/005641, WO2019191120, and PCT/US20/59230, incorporated herein in its entirety). In general, these platforms are restricted to at least two specificities, preventing the exploration of complex therapeutic mechanisms that require binding to more than two antigens. For antibody platforms with more than two specificities, the increased number of binding domains usually necessitates formation of large molecules which often have undesirable physical and biological properties. The increase in molecular weight can reduce developability, as larger and more complex molecules are more likely to have problems with aggregation and solubility. Furthermore, the ability of large macromolecules to penetrate into solid tumors may be hindered compared to proteins of smaller size. Thus, there is a need for multi-specific antibody platforms with more than two specificities that are not significantly larger than monoclonal IgG antibodies.

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 proteins with binding specificities such as multi-specific protein like antibodies including multi-specific antibodies, and the fragments of these binding proteins including without limitation scFv domain, Fab region, Fc domain, VH, VL, light chains, heavy chains, variable regions, and complementary determining region (CDR). The application further provides method of making and using the antibody-like proteins disclosed herein.

In one aspect, the application provides multi-specific antibody-like proteins. In one embodiment, the multi-specific antibody-like protein having a N-terminus and a C-terminus, including, a first monomer, including, from the N-terminus to the C-terminus, a first binding monomer, a CH1 domain, a first hinge, a first CH2 domain, and a first CH3 domain, wherein the first monomer may comprise optionally a first binding domain (D1) linked to the N-terminus, a fourth binding domain (D4) linked to the C-terminus, or both, a second monomer, including, from the N-terminus to the C-terminus, a second binding monomer, a CL domain, a second hinge, a second CH2 domain, and a second CH3 domain, wherein the second monomer may comprise optionally a second binding domain (D2) linked to the N-terminus, a fifth binding domain (D5) linked to the C-terminus, or both, wherein the first binding monomer and a second binding monomer are configured to form a dimer, 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.

In one embodiment, the multi-specific antibody-like protein may be tri-specific, tetra-specific, or penta-specific. In one embodiment, the multi-specific antibody-like protein may be monoclonal antibodies. In one embodiment, the multi-specific antibody-like protein may be purified monoclonal antibody. In one embodiment, the multi-specific antibody-like protein may be humanized antibodies.

In one embodiment, the multi-specific antibody-like protein may further comprise a disulfide bond between the first CH3 domain and a second CH3 domain.

In one embodiment, the multi-specific antibody-like protein may further comprise a second disulfide bond between the first hinge and the second hinge.

In one embodiment, connecting linkers are used between various domains. In one embodiment, the connecting linker may comprise a $(G_xS_y)_n$ linker, wherein n, x, and y each independently is an integer from 1 to 10. In one embodiment, D1, D2, D4 or D5 are linked to N- or C-terminus through a linker. In one embodiment, the linker may comprise a $(G_xS_y)_n$ linker. n, x, and y each independently may be an integer from 1 to 10. In one embodiment, n is 1, 2, 3, 4,

5, 6, 7, 8, 9 and 10. In one embodiment, x is 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10. In one embodiment, y is 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10.

In one embodiment, the first CH3 domain is configured to form a hole structure, wherein the second CH3 domain is configured to form a knob structure, and wherein the first CH2 and CH3 domains and the second CH2 and CH3 domains are configured to heterodimerize to form a complementary Fc domain.

In one embodiment, the first CH3 domain may comprise at least one 'hole' mutation at T366S, L368A or Y407V and the second CH3 domain may comprise a 'knob' mutation at T366W.

In one embodiment, the Fc domain may comprise mutations at H435R/Y436F.

In one embodiment, the Fc domain is engineered to eliminate effector cell functions selected from ADCC, ADCP, or CDC.

In one embodiment, the Fc domain may comprise at least one mutation at L234A, L235A, G237A, K322A (Eu numbering). In one embodiment, the Fc region comprise mutations at L234A/L235A/G237A/K322A. In one embodiment, the Fc region comprise mutations at L234A/L235A/K322A (Eu numbering). In one embodiment, the Fc domain comprise null mutation. In one embodiment, the IgG4 Fc domain comprises the mutation S228P (Eu numbering). In one embodiment, the IgG4 Fc domain comprises the mutations S228P/F234A/L234A (Eu numbering).

In one embodiment, the heavy chain constant sequence may be derived from IgG1 or IgG4.

In one embodiment, the Fc domain may include an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity to SEQ ID NO. 313 or 314.

In one embodiment, the first binding monomer may comprise a VH domain, a second binding monomer may comprise a VL domain, and the VH, CH1, VL, CL domains form a Fab region as a third binding domain (D3). In one embodiment, the Fab region may comprise a disulfide bond between VH-44C and VL 100C.

In one embodiment, the first binding monomer and the second binding monomer form a NKG2D receptor as a third binding domain (D3).

In one embodiment, the D1, D2, D4, and D5 is independently a scFv domain, a VHH domain, a receptor, or a ligand.

In one embodiment, the scFv domain may have a VH domain linked to a VL domain. In one embodiment, the scFv domain have may have VH-VL orientation. In one embodiment, the scFv domain have a VL-VH orientation.

In one embodiment, the scFv domain may comprise a disulphide bond between VL and VH. In one embodiment, the disulfide bond is between VL100 and VH44 of the scFv domain. In one embodiment, the scFv domain may comprise the mutation R19S in the VH.

In one embodiment, the VHH domain may comprise the mutation R19S in the VH or VHH.

In one embodiment, at least one, two, or three of D1, D2, D4, and D5 may be scFv. In one embodiment, all of D1, D2, D4, and D5 may be scFv.

In one embodiment, at least one, two, or three of D1, D2, D4, and D5 may be a VHH domain. In one embodiment, all of D1, D2, D4, and D5 may be VHH domains.

In one embodiment, at least one, two, or three of D1, D2, D4, and D5 may be a receptor. In one embodiment, all of D1, D2, D4, and D5 may be receptors.

In one embodiment, at least one, two, or three of D1, D2, D4, and D5 may be a ligand. In one embodiment, all of D1, D2, D4, and D5 may be ligands.

In one embodiment, the D1, D2, D3, D4, and D5 each independently may have a binding specificity against an antigen selected from a T cell activating receptor, an immune cell binding receptor, an immune checkpoint molecule, a co-stimulation factor, a receptor of a leukocyte, a tumor antigen, a tumor associated antigen (TAA), a receptor of a tissue cell, a receptor of a cancer cell, or a combination thereof.

In one embodiment, the binding domain for T cell activating receptor is adjacent to the binding domain for the tumor associated antigen (TAA).

In one embodiment, T cell activating receptor may comprise CD3.

In one embodiment, an immune checkpoint receptor may comprise PD-L1, PD-1, TIGIT, TIM-3, LAG-3, CTLA4, BTLA, VISTA, PD-L2, CD160, LOX-1, siglec-15, CD47, HVEM SIRP α CSF1R, CD73, Siglec-15, CD47 or a combination thereof.

In one embodiment, a co-stimulating receptor may comprise 4-1BB, CD28, OX40, GITR, CD40L, CD40, ICOS, LIGHT, CD27, CD30, or a combination thereof.

In one embodiment, a tumor associated antigen may comprise EGFR, HER2, HER3, EGFRvIII, CD19, BCMA, CD20, CD33, CD123, CD22, CD30, ROR1, CEA, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypican-3, gpA33, GD2, TROP2, NKG2D ligand, CD39, CLDN18.2, DLL3, HLA-G, FcRH5, GPRC5D, LIV-1, MUC1, CD138, CD70, uPAR, CD38 or a combination thereof.

In one embodiment, the D1, D2, D3, D4, and D5 each independently may have a binding specificity against an antigen selected, EGFR, HER2, HER3, EGFRvIII, ROR1, CD3, CD28, CEA, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypican-3, gpA33, GD2, TROP2, NKG2D, NKG2D ligand, BCMA, CD19, CD20, CD33, CD123, CD22, CD30, PD-L1, PD1, OX40, 4-1BB, GITR, TIGIT, TIM-3, LAG-3, CTLA4, CD40, CD40L, VISTA, ICOS, BTLA, LIGHT, HVEM, CSF1R, CD73, CD39, CLDN18.2, DLL3, HLA-G, FcRH5, GPRC5D, LIV-1, MUC1, CD138, CD70, CD16, uPAR, Siglec-15, CD47, CD38, , NKp46, PD-L2, CD160, LOX-1, SIRP α CD27 and the Fc domain may comprise a human IgG Fc domain.

In one embodiment, D1 may have a binding specificity to CD3, CD20, CEA, HER2, EGFR or NKG2D ligand. In one embodiment, D2 may have a binding specificity to HER3, EGFR, CD3, or CD19. In one embodiment, D3 may have a binding specificity to HER3, EGFR, CD3, or NKG2D ligands. In one embodiment, D4 may have a binding specificity to 4-1BB, or EGFR. In one embodiment, D5 may have a binding specificity to PD-L1 or HER3.

In one embodiment, D1 may have a binding specificity to CD3, D2 may have a binding specificity to HER3, D3 may have a binding specificity to EGFR, D4 may have a binding specificity to 4-1BB, and D5 may have a binding specificity to PD-L1.

In one embodiment, D1 may have a binding specificity to EGFR, D2 may have a binding specificity to HER3, D3 may have a binding specificity to CD3, D4 may have a binding specificity to 4-1BB, and D5 may have a binding specificity to PD-L1.

In one embodiment, D1 may have a binding specificity to EGFR, D2 may have a binding specificity to CD3, D3 may have a binding specificity to HER3, D4 may have a binding specificity to 4-1BB, and D5 may have a binding specificity to PD-L1.

In one embodiment, D1 may have a binding specificity to CD3 or EGFR, D2 may have a binding specificity to CD19, D3 may have a binding specificity to CD3 or EGFR, D4 may have a binding specificity to 4-1BB, and D5 may have a binding specificity to PD-L1.

In one embodiment, D1 and D4 each may have a binding specificity to EGFR, D2 and D5 each may have a binding specificity to HER3, and D3 may have a binding specificity to CD3.

In one embodiment, D1 may have a binding specificity to CD20, D2 may have a binding specificity to CD19, D3 may have a binding specificity to CD3, D4 may have a binding specificity to 4-1BB, and D5 may have a binding specificity to PD-L1.

In one embodiment, D1 may have a binding specificity to NKG2D ligand, D2 may have a binding specificity to CD19, D3 may have a binding specificity to CD3, D4 may have a binding specificity to 4-1BB, and D5 may have a binding specificity to PD-L1.

In one embodiment, D1 may have a binding specificity to CD3, and D3 may comprise a NKG2D receptor. In one embodiment, the protein may further comprise D2 having a binding specificity to CD19. In one embodiment, the protein may further comprise D5 having a binding specificity to PD-L1. In one embodiment, the protein may further comprise D4 having a binding specificity to 4-1BB.

In one embodiment, the multi-specific antibody-like protein is bi-specific. In one embodiment, D2 may have a binding specificity to HER3, D3 may have a binding specificity to CD3. In one embodiment, D1 may have a binding specificity to HER2, D3 may have a binding specificity to CD3. In one embodiment, D1 may have a binding specificity to EGFR, D3 may have a binding specificity to CD3. In one embodiment, D3 may have a binding specificity to CD3, D5 may have a binding specificity to HER3. In one embodiment, D3 may have a binding specificity to CD3, D4 may have a binding specificity to EGFR.

In one embodiment, the bi-specific antibody-like protein may include an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity to SEQ ID NO. 1 and 3; 5 and 7; 9 and 11; 13 and 15; 53 and 55; 57 and 59; 113 and 115; 117 and 119; 121 and 123; 125 and 127; 157 and 159; 297 and 299; or 199 and 201.

In one embodiment, the multi-specific antibody-like protein is tri-specific. In one embodiment, D1 may have a binding specificity to EGFR, D2 may have a binding specificity to

HER3, D3 may have a binding specificity to CD3. In one embodiment, D1 may have a binding specificity to CEA, D2 may have a binding specificity to EGFR, D3 may have a binding specificity to CD3. In one embodiment, D3 may have a binding specificity to CD3, D4 may have a binding specificity to EGFR, D5 may have a binding specificity to HER3. In one embodiment, the antibody is a tri-specific antibody having the binding specificity to EGFR, HER3, and CD3. In one embodiment, the tri-specific antibody-like protein may include an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity to SEQ ID NO. 41 and 43; 45 and 47; 49 and 51; 101 and 103; 105 and 107; 109 and 111; 195 and 197; 137 and 139; or 161 and 163.

In one embodiment, the multi-specific antibody-like protein is tetra-specific. In one embodiment, D1 may have a binding specificity to EGFR, D2 may have a binding specificity to HER3, D3 may have a binding specificity to CD3, D4 may have a binding specificity to 4-1BB. In one embodiment, D1 may have a binding specificity to EGFR, D2 may have a binding specificity to HER3, D3 may have a binding specificity to CD3, D5 may have a binding specificity to PD-L1. the antibody is a tetra-specific antibody having the binding specificity to EGFR, HER3, CD3, and 4-1BB. the antibody is a tetra-specific antibody having the binding specificity to EGFR, HER3, CD3, and PD-L1. In one embodiment, the tetra-specific antibody-like protein may include an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity to SEQ ID NO. 33 and 35; 37 and 39; 141 and 143; 145 and 147; or 165 and 167.

In one embodiment, the antibody is penta-specific. In one embodiment, the antibody-like protein may have the binding specificity to EGFR, HER3, CD3, 4-1BB and PD-L1. In one embodiment, the penta-specific antibody-like protein may include an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity to SEQ ID NO. 17 and 19; 21 and 23; 25 and 27; 29 and 31; 69 and 71; 73 and 75; 77 and 79; 81 and 83; 85 and 87; 89 and 91; 93 and 95; 97 and 99; 129 and 131; 133 and 135; 149 and 151; 169 and 171; 173 and 175; or 177 and 179.

In a second aspect, the application provides novel sequences for complimentary determining regions (CDRs). In one embodiment, the application provides proteins, antibody-like proteins or antibodies comprising the CDRs as disclosed herein.

In one embodiment, the CDRs may have an affinity to CEA. In one embodiment, the CDRs may have an equilibrium dissociation constant (KD) to CEA, wherein the KD is not more than 0.1 nM, 2nM, 5nM, 10 nM, 20nM, 30nM or 50nM. In one embodiment, the CDR may include an amino acid sequence having at least 80% sequence identity to SEQ ID NO. 301, 302, 303, 304, 305, or 306.

In one embodiment, the application provides a protein having an affinity to CEA. In one embodiment, the protein may have a CDR H1 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.301. In one embodiment, the protein may have a CDR H2 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.302. In one

embodiment, the protein may have a CDR H3 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.303. In one embodiment, the protein may have a CDR L1 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.314. In one embodiment, the protein may have a CDR L2 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.305. In one embodiment, the protein may have a CDR L3 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.306. In one embodiment, the protein may include an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NO. 279, 280, 281 or 282. In one embodiment, the protein may include an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NO. 279, 280, 281 or 282.

In one embodiment, the application provides a multi-specific antibody-like protein having a variable region, wherein the variable region may comprise an amino acid sequence selected from SEQ ID NO. 301, 302, 303, 304, 305, or 306.

In one embodiment, the CDRs may have an affinity to CD3. In one embodiment, the CDR may have an equilibrium dissociation constant (KD) to CD3, wherein the KD is not more than 10 nM, 20nM, 30nM or 50nM, 100nM, 200nM, 300nM, 400nM or 500nM. In one embodiment, the CDR may include an amino acid sequence having at least 80% sequence identity to SEQ ID NO. 307, 308, 309, 310, 311 or 312.

In one embodiment, the protein having an affinity to CD3 includes CDR H1 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.307. In one embodiment, the protein having an affinity to CD3 includes CDR H2 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.308. In one embodiment, the protein having an affinity to CD3 includes CDR H3 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.309. In one embodiment, the protein having an affinity to CD3 includes CDR L1 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.310. In one embodiment, the protein having an affinity to CD3 includes CDR L2 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.311. In one embodiment, the protein having an affinity to CD3 includes CDR L3 having an amino acid sequence having at least 80% sequence identity to SEQ ID NO.312.

In one embodiment, the protein may comprise an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NO. 227-230, 231-234, 235-238, 239-242 and 291-294. In one embodiment, the multi-specific antibody-like protein may comprise an amino acid sequence having at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NO. 227-230, 231-234, 235-238, 239-242 and 291-294.

In one embodiment, the multi-specific antibody-like protein may have a variable region wherein the variable region may comprise an amino acid sequence selected from SEQ ID 307, 308, 309, 310, 311 or 312.

In a further aspect, the application provides isolated nucleic acid sequences encoding the multi-specific antibody-like proteins, fragments, domains, regions as disclosed herein.

In a further aspect, the application provides expression vectors including the isolated nucleic acid sequences as disclosed herein.

In a further aspect, the application provides host cells including the isolated nucleic acid sequences as disclosed herein. In one embodiment, the host cell includes the expression vector as disclosed herein. In one embodiment, the host cell may be a prokaryotic cell or a eukaryotic cell.

In a further aspect, the application provides methods for producing the multi-specific antibody like proteins as disclosed herein. In one embodiment, the method includes the steps of culturing a host cell such that the DNA sequence encoding the multi-specific antibody-like protein is expressed, and purifying said multi-specific antibody. In one embodiment, the method includes the steps of culturing a host cell under conditions wherein said multi-specific antibody-like proteins are produced and recovering said antibody-like protein.

In a further aspect, the application provides immunoconjugates. In one embodiment, the immunoconjugate may include the multi-specific antibody-like proteins linked to a cytotoxic agent, an imaging agent, or both.

In a further aspect, the application provides pharmaceutical compositions. In one embodiment, the pharmaceutical composition may include the multi-specific antibody-like protein and a pharmaceutically acceptable carrier. In one embodiment, the pharmaceutical composition may further include radioisotope, radionuclide, a toxin, a therapeutic agent, a chemotherapeutic agent or a combination thereof. In one embodiment, the pharmaceutical composition may include the immunoconjugate as disclosed thereof and a pharmaceutically acceptable carrier.

In a further 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 steps of administering to the subject a pharmaceutical composition including a purified multi-specific antibody-like protein, an immunoconjugate, or a pharmaceutical composition as disclosed herein. In one embodiment, the method may further include co-administering an effective amount of a therapeutic agent. In one embodiment, the therapeutic agent may comprise an antibody, a chemotherapy agent, an enzyme, or a combination thereof.

In one embodiment, the subject is a human. In one embodiment, the subject is a mammal. In one embodiment, the subject is a chimpanzee. In one embodiment, the subject is a pet animal.

In a further aspect, the application provides a solution including an effective concentration of the multi-specific antibody-like protein, immunoconjugate, or pharmaceutical composition as disclosed herein. In one embodiment, the solution is blood plasma in a subject.

BRIEF DESCRIPTION OF THE DRAWINGS

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

Figure 1 depicts the heterodimeric configuration of miniGNC molecules with five binding domains (D1-D5), of which the two monomers are encoded by Chain A (N-D1-D3/VH-CH1-CH2-CH3-D4-C) and Chain B (N-D2-D3/VL-CL-CH2-CH3-D5-C);

Figure 2 shows the dimerization of engineered miniGNC Chain A and Chain B with knockout mutations (KO) on either VH or Fc: **(2A)** by Protein-A purification to fractionate the mixture into the homodimer (a), the desired heterodimer (b), and the Chain B monomer (c); and **(2B)** by SDS-PAGE analysis of Protein-A fractionated homodimer (a), heterodimer (b), Chain B monomer (c), and Chain A monomer (d), at the expected sizes under non-reducing and reducing conditions;

Figure 3 shows the comparative potency of multi-specific miniGNC molecules mediated TDCC on BXP3 tumor cells by using penta-miniGNC (SI-75P6), tetra-miniGNC (SI-75E2), tri-miniGNC (SI-75X3), bi-miniGNC (SI-75X2), and mono-miniGNC (SI-75O2) molecules;

Figure 4 shows the comparative potency of miniGNC molecules mediated TDCC on BXP3 tumor cell line with EC50 values in the range of 0.1 to 5.5 pM;

FIGURE 5 shows the survival curves of TDCC assays measuring comparative potency of **(A)** multi-specific miniGNC molecules with stapled domains, including penta-miniGNC (SI-68P1), tetra-miniGNC (SI-68E2 and SI-68E1), and tri-miniGNC (SI-68x2), for killing pancreatic cancer cells (HPAFII) in TDCC assay, and **(B)** SI-68X1 against MCF-7 breast cancer cells; and

Figure 6 shows the functionality of multi-specific miniGNC molecules possessing a dimeric NKG2D receptor, including tri-specific (SI-49R25), tetra-specific (SI-49P_X), penta-specific (SI-49PM1 and SI-49P8) in killing breast cancer cells (MDA-MB-231) in TDCC assay.

DETAILED DESCRIPTION

In the following detailed description, reference is made to the accompanying drawings, which form a part hereof. In the drawings, similar symbols typically identify similar components, unless context dictates otherwise. The illustrative embodiments described in the detailed description, drawings, and claims are not meant to be limiting. Other embodiments may be utilized, and other changes may be made, without departing from the spirit or scope of the subject matter presented herein. It will be readily understood that the aspects of the present

disclosure, as generally described herein, and illustrated in the Figures, can be arranged, substituted, combined, separated, and designed in a wide variety of different configurations, all of which are explicitly contemplated herein.

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

The present application discloses multi-specific Guidance and Navigation Control (GNC) antibodies in miniature configurations (miniGNC). A miniGNC platform molecule is an assembled heterodimer of two polypeptide chains characterized by the formation of a Fab-Hinge-Fc region core structure with one, two, three, or four additional binding domains (from D1 to D5), as elucidated in **Figure 1**. The two polypeptides may be configured, for Chain A (or Chain 1): N-D1-D3(VH)-CH1-Hinge-CH2-CH3-D4-C; and for Chain B (or chain 2): N-D2-D3(VL)-CL-Hinge-CH2-CH3-D5-C. The Fc domains of the two chains are engineered to contain complementary mutations, also known as “knobs-into-holes”, to enhance the formation of the heterodimer. A miniGNC platform molecule may have variable components. For example, the VH and VL of the Fab region may be replaced by a non-Fab dimer with or without binding specificity. An additional binding domain may be an antibody fragment, such as scFv or VHH, or a non-antibody structure, such as a ligand or a receptor. A miniGNC platform antibody may be bivalent, trivalent, tetravalent, or pentavalent with up to five distinct specificities, and retains the approximate size of a normal bivalent IgG antibody (tri-miniGNC Ab at 150 kD) or slightly larger (tetra-miniGNC Ab at 175 kD, and penta-miniGNC Ab at 200 kD).

The present application relates to methods of making and using miniGNC antibodies, in particular, penta-specific miniGNC antibodies (penta-miniGNC Ab). In general, GNC proteins, such as GNC antibodies, are characterized by comprising two moieties for engaging immune cells, such as activating T cells, while targeting tumor cells. Similar to GNC antibodies, miniGNC antibodies retain multiple antigen binding domains for engaging immune cells, such as anti-CD3 for T cell activation, anti-4-1BB for co-stimulation, and anti-PD-L1 for inhibiting immune checkpoint. To improve the efficacy of antibody therapy for treating cancer, miniGNC antibodies are designed to be structurally stable and compact while retaining the characteristic feature of two moieties in GNC antibodies. This improvement allows an additional binding specificity to a second tumor associated antigen on the same or different tumor cell. As compared to GNC antibodies, miniGNC contains an Fc domain that allows for FcRn-mediated recycling and half-life extension, as well as facile protein A-based purification. The Fc receptor-mediated immunity may be incorporated if desired. An Fc-containing miniGNC antibody is quite compact, which allows for better developability and increased tumor penetration. GNC antibodies are usually larger

than an IgG antibody due to increased number of antigen binding domains (AgBD), which provides spatial flexibility for binding to both a T cell and a tumor cell. On the other hand, miniGNC antibodies retains the same approximate size as human IgG antibodies calculated at approximately 110-130 kD for bi-specific; 120-160 for tri-specific; 130-190 kD for tetra-specific; 140-220 kD for penta-specific; as compared to 150 kD for human IgG. The incorporation of one or two scFvs onto each chain may reduce chain-pairing complications and improve stability while navigating through tumor microenvironment. With these characteristic features, GNC and miniGNC antibodies may be alternative of an efficacious antibody therapy for treating the same cancer, since the moiety for targeting tumor associated antigens remains the same, including but not limited to, EGFR, HER2, HER3, EGFRV8, CD19, BCMA, CD20, CD33, CD123, CD22, CD30, ROR1, CEA, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypican-3, gpA33, GD2, TROP2, NKG2D ligand, CD39, CLDN18.2, DLL3, HLA-G, FcRH5, GPRC5D, LIV-1, MUC1, CD138, CD70, uPAR, CD38.

The term “antibody” is used in the broadest sense and specifically covers single monoclonal antibodies (including agonist and antagonist antibodies), antibody compositions with polyepitopic specificity, as well as antibody fragments (e.g., Fab, F(ab')₂, and Fv), so long as they exhibit the desired biological activity. In some embodiments, the antibody may be monoclonal, polyclonal, chimeric, single chain, bispecific or bi-effective, 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. In some embodiments, antibody may include immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e. molecules that contain a binding site that immunospecifically bind an antigen. The immunoglobulin can be of any type (IgG, IgM, IgD, IgE, IgA and IgY) or class (IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclasses of immunoglobulin molecule. In one embodiment, the antibody may be whole antibodies and any antigen-binding fragment derived from the whole antibodies. A typical antibody refers to heterotetrameric protein comprising typically of two heavy (H) chains and two light (L) chains. Each heavy chain is comprised of a heavy chain variable domain (abbreviated as VH) and a heavy chain constant domain. Each light chain is comprised of a light chain variable domain (abbreviated as VL) and a light chain constant domain. The VH and VL regions can be further subdivided into domains of hypervariable complementarity determining regions (CDR), and more conserved regions called framework regions (FR). Each variable domain (either VH or VL) is typically composed of three CDRs and four FRs, arranged in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4 from amino-terminus to carboxy-terminus. Within the variable regions of the light and heavy chains there are binding regions that interacts with the antigen.

The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be

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

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

Monoclonal antibodies can be produced using various methods including mouse hybridoma or phage display (see Siegel. *Transfus. Clin. Biol.* 9:15-22 (2002) for a review) or from molecular cloning of antibodies directly from primary B cells (see Tiller. *New Biotechnol.* 28:453-7 (2011)). In the present disclosure antibodies were created by methods of immunizing rabbits, mice, or llama in combination with subsequent strategies like hybridoma or display. Rabbits are known to create antibodies of high affinity, diversity and specificity (Weber et al. *Exp. Mol. Med.* 49:e305). Besides immunization of rabbits followed by B cell culture, other common strategies for antibody generation and discovery include immunization of other animals (e.g., mice, llamas) followed by hybridoma and/or display on phage, yeast, or mammalian cells; or display using synthetic variable gene libraries. This general method of antibody discovery is similar to that described in Seeber et al. *PLOS One*. 9:e86184 (2014).

The term “antigen- or epitope-binding portion or fragment” refers to fragments of an antibody that are capable of binding to an antigen. These fragments may be capable of the antigen-binding function and additional functions of the intact antibody. Examples of binding fragments include, but are not limited to a single-chain Fv fragment (scFv) consisting of the VL and VH domains of a single arm of an antibody connected in a single polypeptide chain by a synthetic linker or a Fab fragment which is a monovalent fragment consisting of the VL, constant light (CL), VH and constant heavy 1 (CH1) domains. Antibody fragments can be even smaller 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 fragments” can be derived from an antibody of the present disclosure by a number of art-known techniques. For example, purified monoclonal antibodies can be cleaved with an enzyme, such as pepsin, and subjected to HPLC gel filtration. The appropriate fraction containing Fab fragments can then be collected and concentrated by membrane filtration and the like. For further description of general techniques for the isolation of active fragments of antibodies, see for example, Khaw, B. A. et al. J. Nucl. Med. 23:1011-1019 (1982); Rousseaux et al. Methods Enzymology, 121:663-69, Academic Press, 1986.

Papain digestion of antibodies produces two identical antigen binding fragments, called “Fab” fragments, each with a single antigen binding site, and a residual “Fc” fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

The Fab fragment may contain the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other, chemical couplings of antibody fragments are also known.

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

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

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

epsilon, γ , and μ , respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

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

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

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

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

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

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

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

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

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

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

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: Configuration of penta-specific miniGNC antibodies

The design of miniGNC antibodies relies on the co-expression and assembling of two polypeptide chains of a heterodimer between Chain A and Chain B (**Figure 1**). While Chain A may be a native heavy chain (HC), Chain B is a recombinant fusion peptide between the light chain and the Fc domain of HC. At the core of this antibody structure, there is a Fab region (VH-CH1/VL-CL) followed by the hinge and Fc region (CH2-CH3/CH2-CH3) of human IgG1. “Knobs-into-holes” mutations or other complementary sets of mutations may be introduced into the CH3 domains to destabilize homodimers and favor heterodimer formation (Ridgway JB, Presta LG, Carter P., Protein Eng 1996;9:617–21). The “hole” mutations in the CH3 domain of Chain A consist of

T366S, L368A, and Y470V, while the “knob” mutation in the CH3 domain of Chain B is T366W. The “knob” created by the T366W mutation on Chain B preferentially interacts with the “hole” created by the three mutations on Chain A. This preferential pairing may further stabilize the heterodimer while the non-covalent pairing of the Fab domain components (i.e. between VH-CH1 on Chain A and VL-Ck on Chain B) creates a functional Fab region. In other words, a functional D3 binding domain, such as a functional Fab region or a non-Fab receptor dimer, can only be created in Chain A-Chain B heterodimers. As compared to GNC antibodies, miniGNC antibodies also contain antibody fragments from native IgG (Fab, Fc) and other variable-sequence based structures, such as scFv and VHH, but are engineered to preferentially configure a Fab region-Hinge-Fc region structure after the formation of a heterodimer. The characteristic feature of miniGNC antibodies is the compactness of this engineered structure.

One or more structurally diversified antigen binding domain may be added to the two N-terminals and the two C-terminals of a miniGNC molecule as D1, D2 D4, or D5, thereby creating up to five binding specificities. Each of these added binding domains may be variable-sequence-based structures, such as scFv and VHH, or non-variable sequence-based structures, such as ligand and receptor. As elucidated in **Figure 1**, D1 and D2 refer to the binding domains linked to the N-terminals of Chain A and Chain B, respectively, whereas D4 and D5 refer to the binding domains linked to the C-terminals of Chain A and Chain B, respectively. Thus, the two polypeptides of a penta-specific miniGNC (penta-miniGNC) antibody may be configured as

Chain A: N-D1-D3(VH)-CH1-Hinge-CH2-CH3-D4-C; and

Chain B: N-D2-D3(VL)-CL-Hinge-CH2-CH3-D5-C;

where VL may be either $V\lambda$ or $V\kappa$ and CL may be either $C\lambda$ or $C\kappa$ as shown in **Figure 1**.

Depending on the number of binding domains and their binding specificities, the structural configuration of the penta-miniGNC antibody in **Figure 1** may be simplified by reducing one or more binding domains and becoming tetra-, tri-, and bi-miniGNC. For incidence, **Table 1** depicts the generation and characterization of a family of anti-CD3 miniGNC antibodies for optimizing their efficacy of targeting EGFR and HER3. In this case, each binding domain exerts one binding specificity. When two of its five binding domains target the same epitope of an antigen, i.e. the same binding specificity, the penta-miniGNC antibody becomes a tetra-specific penta-miniGNC antibody.

Example 2: Engineered core structure of miniGNC antibodies

To demonstrate that the configuration of miniGNC may be translated into stable and functional heterodimeric protein, a simplified asymmetric format was designed for evaluating the effect of configuration and mutations to the heterodimer formation of miniGNC molecules. Briefly, a single scFv (D1) is fused to the N-terminus of Chain A, whereas the Chain B does not have any added binding domain. In this way, the proportion of each species of dimerization between Chain A and Chain B may be distinguished by SDS-PAGE and SEC, as the predicted sizes

for a Chain A homodimer (not observed), a Chain B homodimer, and a Chain A and Chain B heterodimer are 100 kDa, 150 kDa, and 125 kDa, respectively) (**Figure 2**).

To engineer a strategy for selectively purifying the heterodimeric miniGNC molecule from a mixture, two amino acid residues in the CH3 domain (H435 and Y436) of the Chain B are substituted. In particular, the histidine (H435) is critical for the Chain B to bind to protein-A resins during the purification of therapeutic antibodies (Tustian et al., 2016), and the substitution of this amino acid or a ProA knockout mutation (ProAKO) terminates the protein-A binding. This strategy may allow separation of the heterodimer via selective elution from a protein-A column. As the protein-A column retains the heterodimer through its parental heavy chain binding site, the Chain B homodimer flows through as the Chain B lacks protein-A binding. The design of a ProAKO on the Chain B minimizes any possible issue of altering immunogenicity by amino acid substitutions of the protein-A binding site with residues taken from the homologous region in the IgG3 subclass. Although most of miniGNC molecules will predominantly incorporate the structure and sequence of IgG1 subtype, IgG3 has an overall similar structure to other IgG subclasses with some specific structural perturbations in binding to protein-A, protein-G and FcRn (neonatal Fc receptor). This difference is based on Fc sequence difference as revealed earlier where the presence of R435 (H435 in other subtypes) in IgG3 ablates its Fc interaction with protein-A. Hence, in representative miniGNC molecules, amino acids critical for protein-A binding on miniGNC Chain B (H435 and F436) have been mutated to the IgG3 counterpart sequences (R435 and Y436).

In the class of multi-specific miniGNC antibodies with an addition of scFv fused to the N terminal of Chain B, the interaction to protein-A binding is still possible if the scFv comes from VH3 family. VH3 encoded antibodies are known to interact with Staphylococcal Protein A (SPA) and residues in FR1, CDR2 and FR3 have been identified to be involved in SPA binding (Roben, et al., 1995), and structural data indicated that the replacement of a single involved region with the corresponding region from the nonbinding immunoglobulin ablates protein-A binding by VH3 encoded antibodies. Substitution of the amino acid R19 in FR1 was identified to be critical in binding to protein-A and was undertaken with the amino acid sequence (S19) from equivalent region in the VH4 family.

Four sets of miniGNC molecules (SEQ ID 1-16) with four different versions of chain B mutations (SEQ ID 3,7,11 and 15) embracing different combinations of ProAKO: H435R/Y436F (Fc) and R19S (VH) were purified and analyzed with analytical size exclusion chromatography. Only protein containing Chain B with both sets of mutations allowed complete removal of Chain B contaminants (**Figure 2A**). This VH3 protein A knockout mutation (R19S) together with Fc ProteinA knockout mutations (H435R, F436Y) on Chain B was incorporated in most of the multi-specific antibody formats and used to produce bi-, tri-, tetra- and penta-miniGNC molecules.

To demonstrate the feasibility of generating functional miniGNC proteins with alternative antibody isotypes, an example miniGNC containing IgG4 constant regions was generated. SI-

75XM9 (SEQ ID 297-300) is analogous to SI-75X5 (SEQ ID 1-4) bispecific miniGNC, except that the IgG1 CH1, hinge, and Fc were replaced with IgG4 CH1, hinge, and Fc. Notably, both proteins have the same binding domains (anti-HER3 domain in D2 and anti-CD3* domain in D3) and contain the same core structure and mutations (Knobs-into-Holes Fc mutation; R19S in anti-HER3 scFv; and H435R/Y436F mutations in Fc). As shown in **Table 8**, SI-75XM9 had comparable titer to SI-77X5, and had a significant 19% increase in the percent protein of interest (85.6% POI vs. 72.2% POI) after protein A purification, as assessed by analytical SEC. The reduction in high molecular weight species could be related to the shorter hinge length of IgG4 (12 amino acids instead of 15), which could reduce the propensity for association of higher-order oligomers. Thus, generation of miniGNC proteins with alternative antibody isotypes is not only possible, but can lead to more favorable properties such as decreased aggregation.

Example 3: Configuration of multi-specific miniGNC antibodies

To generate and characterize the first group of multi-specific miniGNC antibodies, a trio of moiety 1 binding domains, i.e. α CD3, α PD-L1, and α 4-1BB, and two moiety 2 binding domains against EGFR and HER3, respectively, were selected for comparison. As shown in **Table 1**, the group was subdivided into penta-miniGNC, tetra-miniGNC, tri-miniGNC, and bi-miniGNC groups. Of each subgroup, there was at least one miniGNC antibody having the CD3 binding from D3. The penta-miniGNC group includes SI-75P6 (SEQ ID 17, 19, with α EGFR from D3 position), SI-75P4 (SEQ ID 21, 23, with 41BBL, the ligand to 4-1BB receptor, at D4), SI-75P3 (SEQ ID 25, 27), and SI-75P9 (SEQ ID 29, 31, with α HER3 from D3). The tetra-miniGNC group have two antibodies, SI-75E1 (SEQ ID 33, 35) and SI-75E2 (SEQ ID 37, 39) comparing the effect in the presence and absence of either α 4-1BB or α PD-L1 domain. The tri-miniGNC group have three antibodies, SI-75X3 (SEQ ID 41, 43), SI-75X16 (SEQ ID 45, 47), and SI-75X18 (SEQ ID 49, 51) for comparing the two moiety 2 binding domains on either N- or C-terminus of the heterodimer. The bi-miniGNC group have three antibodies, SI-75X1 (SEQ ID 53, 55), SI-75X2 (SEQ ID 57, 59), and SI-75X5 (SEQ ID 1, 3), each of which has one moiety 1 binding domain and one moiety 2 binding domain.

The DNA encoding each member of the first group of miniGNC antibodies were cloned into vector pTT5, which were expressed with acceptable titers using ExpiCHO expression systems for 9 days. The miniGNC antibodies were purified with 5mL MabSelect protein-A columns followed by Size Exclusion using a highload 16/600 200 pg preparative SEC column on either an Akta Avant or Purifier system. SEC aggregates were analyzed using a waters HPLC linked to multi angle light scattering (MALS, Wyatt systems) to identify correct molecular weight by dn/dc calculated methods.

Example 4: Octet analysis of binding affinity

To assess the functionality of miniGNC antibodies, the binding affinity of each domain was determined by using Biolayer Interferometry (Octet 384 system). Octet analysis was used to

ensure that the selected miniGNC antibody retains the binding specificity and affinity to all their cognate antigens. Each miniGNC antibody was loaded onto AHC sensors for 180 seconds at 10 ug/ml, followed by a 60-second baseline step, a 180-second association step with 100 nM of commercially purchased human antigen, and a 360-second dissociation step. Samples for all steps were in Octet buffer (PBS containing 0.1% Tween 20 and 1% BSA). Fits were performed using a 1:1 binding model to extract affinity KD values. As shown in Table 1, the binding affinity for each binding domain, as measured by its KD, varies within an acceptable range. For moiety 1 binding, the KD for α CD3 domain may vary between 17.4 and 36.2 nM, for α PD-L1 between 1 and 2.72 nM, and for α 4-1BB between 7.51 and 37.3 nM; and for moiety 2 binding, the KD for α EGFR varies between 5.56 and 11.1, and for α HER3 between 112.8 and 185 nM.

Example 5: Comparative potency of multi-specific miniGNC antibodies

The first group of multi-specific miniGNC antibodies was subjected to T-cell dependent cellular cytotoxicity (TDCC) assay for measuring the potency for killing cancer cells. With an α CD3 binding domain in all molecules, this group of miniGNC antibodies was equipped to engage T cells, redirect T-cell mediated cytotoxicity, and ultimately kill 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. Luciferised BXPC3 human pancreatic cancer cell lines (ATCC, Manassas, VA) were cultured at 37°C, 5% CO₂ in RPMI (ATCC, Manassas, VA) medium with 10% heat-inactivated fetal bovine serum (Invitrogen, Waltham, MA). Cell viability was monitored with a Vi-CELL automated cell counter (Beckman Coulter, Pasadena, CA). Target cell surface expression was measured by flow cytometry. Human pancreatic cancer cells, BXPC3 cells, were co-cultured with human pan T-cells at an effector-to-target (E:T) ratio of 5:1 and antibodies were added with a 5-fold dilution series (0 – 30 nM). Using a Multidrop bulk liquid dispenser (BIOTEK, Winooski, VT), 500 cells per well of target cells (20 μ L per well) and 25,00 cells per well of T-cells (20 μ L/ well) were plated sequentially into 384-well, white, flat-bottom, polystyrene TC-treated microplates (Corning, Corning, NY). Antibody dilutions were added (10 μ L/well) and plates were incubated for 72 hrs at 37°C, 5% CO₂ before luminescence-based cell viability quantification. 20 μ L of Bright-Glo (Promega) was added to wells, and luminescence corresponding to viability of tumor cells was determined using a CLARIOstar plate reader.

Data were fit to a sigmoidal function to calculate and list EC₅₀ values in Table 1 for comparison. Figure 3 shows the dose-dependent cell viability curves of miniGNC antibodies selected from a penta-miniGNC (SI-75P6), a tetra-miniGNC (SI-75E2), a tri-miniGNC (SI-75X3), a bi-miniGNC (SI-75X2), and a mono-miniGNC (SI-75O2) molecule. While all multi-specific miniGNC antibodies were capable of killing BXPC3 cells completely, both pent- and tetra-miniGNC antibodies steadily displayed high potency in the range of EC₅₀ in pM. In this regard, SI-75X1 was exceptionally potent. The data demonstrate the important roles of moiety 1 binding

domains, in particular, the α PD-L1 domain as an immune checkpoint inhibitor when targeting BXP3C cancer cells.

Example 6: Configuration of CD3 binding domain in miniGNC antibodies

By definition, a miniGNC antibody is capable of interfacing with at least one immune effector cell and one target cancer cell through the binding of its moiety 1 and 2 binding domains, respectively. Using the general scheme of miniGNC antibody configuration (Figure 1), it is possible that assigning two moiety 2 binding domains to D1 and D2 may lead to different efficacy from assigning them to D1 and D4 or D2 and D5 because the relative position of the targets on the cell surface is different, either on the top and bottom or on both sides. In this context, a second group of penta-miniGNC antibodies were configured and listed in Table 2. This group of miniGNC antibodies share the same binding specificities to CD3, CD19, EGFR, 4-1BB, and PD-L1, and the same binding domains at D2, D4, and D5. SI-68P13 (SEQ ID 69, 71) has α CD3 D3 domain, which is comparable to SI-75P3 of the first group except the difference in D2, i.e. α CD19 vs. α HER3, and to SI-68P17 (SEQ ID 73, 75) of the second group except the switch of α CD3 domain to D1. The rest of the second group of miniGNC antibodies share the same binding specificities from D1 (α CD3) and D3 (α EGFR). SI-68P17 (with the binding specificity to CD19, 4-1BB and PD-L1, respectively).

Anti-CD3 antibody plays a central role in T cell activation based immune therapy. Humanized antibody is desirable for the development of a therapeutic antibody. CD3 domain was incorporated into positions D1 and D3 to generate SI-68P17 (SEQ ID 73,75) and SI-68P13 (SEQ ID 69, 71) for testing positional effect. The anti-CD3 sequences in humanized framework 1 (CD3**), 2 (CD3***) 3 (CD****) and 4 (CD*****) were cloned into an expression cassette for producing SI-68P15 (SEQ ID NO. 77, 79), SI-68P18 (SEQ ID 81, 83), SI-68P19 (SEQ ID 85, 87), and SI-68P16 (SEQ ID 89, 91) (**Table 2**). Each expression cassette was transfected into 25 mL of ExpiCHO and expressed for 8 days followed by protein-A affinity chromatography for harvesting and purifying each penta-miniGNC antibody. The antibodies were produced with good titer (Table 2). Octet was used to verify that the penta-miniGNC antibodies containing different CD3 domains, can bind to human CD3, respectively (**Table 2**). Each penta-miniGNC antibody was 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 CD3. The resulting global fit to a 1:1 binding model demonstrated that the penta-GNC antibodies bind to CD3 with affinities in the low nanomolar range (Table 2).

To evaluate the effect of CD3-mediated T cell directed cytotoxicity on cancer cells, BXP3C tumor cell line was used as target. Serial dilutions (0 to 30 nM; 1 to 5 dilution factor) of antibodies were added to a white 384-well plate containing luciferized target cells and activated T cells (plated immediately before drug; effector:target = 5:1) in a total volume of 50 μ l. After an additional 72 hours, 20 μ l of Bright-Glo (Promega) was added to wells, and luminescence

corresponding to viability of luciferized tumor cells was determined using a CLARIOstar plate reader. Data were fit to a sigmoidal function to calculate EC50 values, which were in the range of 0.1 to 5.5 pM as shown by Figure 4 and listed in Table 2. The data demonstrate that there are certain degrees of flexibility in anti-CD3 positioning, configuration, and binding affinity.

Example 7. multi-specific miniGNC antibodies having VHH as binding domains

To multi-specific antibody platforms, such as GNC and miniGNC antibodies that contain multiple scFv domains, a potential issue is related to chain mispairing due to multiple VH and VL domains in the same molecule. Different VH and VL domains have different propensities to interact with each other. If binding domains of different specificity have superior interaction energy, then the wrong pairings may form when the protein assembles. As a result, none of the binding domains will bind their targeted antigens.

VHH refers to “antibodies” with single Ig domains, i.e. “heavy chain only”, also known as a single-domain antibody (sdAb) or a nanobody. The first single-domain antibodies were engineered from heavy-chain antibodies found in camelids, also known as V_HH fragment (VHH). VHH domains have been increasingly incorporated into antibody-based therapeutics due to several favorable properties. VHH domains may have increased stability and solubility compared to more traditionally used scFv domains. Whereas the VH/VL interface of traditional antibody variable regions is hydrophobic, the transient exposure of these surfaces can result in significant aggregation or precipitation. On the other hand, VHH domains have a naturally more hydrophilic surface and therefore can have superior solubility and stability properties. An obvious benefit of VHH domains over Fab or scFv domains is their small size. Where Fab domains are about 50 kDa and scFv domains are about 25 kDa, VHH domains are a very compact 12-15 kDa. The penta-miniGNC antibodies contain five binding domains (**Figure 1**). Incorporation of VHH domains instead of scFv domains may significantly decrease molecular size, and increase tumor penetration.

A third group of multi-specific miniGNC antibodies were created and configured to have VHH binding domains against EGFR and HER3 (Gottlin et al., 2009; Eliseev et al., 2018) (**Table 3**). Penta, Tri, and bi specific single domain variable regions (VHH) –incorporated miniGNC molecules were constructed and purified with reasonable titer. Binding activity of each domain of multi-specific miniGNCs : SI-75P5 (SEQ ID 93, 95), SI-75P8 (SEQ ID 97, 99), SI-75X4 (SEQ ID 101,103), SI-75X17 (SEQ ID 105, 107), SI-75X19 (SEQ ID 109, 111), SI-75X9 (SEQ ID 113-115), SI-75X11 (SEQ ID 117,119), SI-75X15 (SEQ ID 121,123)and SI-75X13 (SEQ ID 125, 127) were verified using Octet. AHC sensors were used to capture the GNC antibody at a concentration of 10 ug/ml for 180 seconds. After a 60-second baseline step, a single concentration of antigen was used for a 180-second association step. Antigens tested include 200 nM human EGFR (purified in-house), 100 nM human CD3 (Acro CDD-H52W1), 20 nM human PD-L1 (Acro PD1-H5229), 400 nM human 4-1BB (purified in-house), 200 nM human HER3 (Acro ER3-H5223). After association, a 420-second

dissociation step was used. The tabulated K_D values were calculated using a one-to-one binding model in ForteBio Data Analysis software version 11. The data demonstrated that all domains retained high affinity in the VHH-incorporated miniGNC platform.

T cell directed cytotoxicity on cancer cells, BXP3 tumor Cell line was used as target. Serial dilutions (0 to 30 nM; 1 to 5 dilution factor) of antibodies were added to a white 384-well plate containing luciferized target cells and activated T cells (plated immediately before drug; effector: target = 5:1) in a total volume of 50 μ l. After an additional 72 hours, 20 μ l of Bright-Glo (Promega) was added to wells, and luminescence corresponding to viability of luciferized tumor cells was determined using a CLARIOstar plate reader. EC50 values are tabulated in **Table 3**.

Example 8. Engineered Fab (D3) domain for improved expression and protein quality.

A disulphide staple was optionally introduced in the VH-VL interface of the fab region (**Figure 5**). The purpose of this engineering was improving heterodimer pairing and stabilize the overall structure by the formation of a covalent disulphide bond (Weatherill et al., 2012) at the core-fab interface. Cysteines pair was optionally introduced to form disulphide bond at V_LA100 on Chain B and its corresponding V_HA44 on Chain A fab region.

A pair of penta-miniGNC antibodies (SI-38P11 and SI-76PM1) (**SEQ ID NO. 129 and 131; 133 and 135**) with identical binding specificities were created for analysing the effect of stapled variable region in the Fab. The Chain A of the two antibodies comprises α CD20 scFv at D1, α CD3 VH at D3 (VH Fab-CH1-Fc), and α 4-1BB at D4, whereas Chain B comprises α CD19 at D2, α CD3V_L at D3 (VKappa Fab CL-Fc) and α PD-L1 scFv at D5 (**Table 4**) according to the naming system in **Figure 1**. SI-76PM1 was constructed with an additional disulphide in the D3 (VH/VL Fab-CH1/CL-Fc) and SI-38P11 was constructed without any additional disulphide pairing in the VH/VL fab.

Penta-miniGNC antibody constructs with and without the disulphide staple at position D3 were expressed in ExpiCHO system. Construct with stapled D3 (SI-76PM1) was produced with significantly higher titer than SI-38P11. Both proteins were purified with 5mL MabSelect protein A columns followed by Size Exclusion using a hiload 16/600 200 pg preparative SEC column on either an Akta Avant or Akta Pure Purifier system. SEC aggregates were analyzed using a waters HPLC linked to multi angle light scattering (MALS, Wyatt systems) to identify correct molecular weight by dn/dc calculated methods. With all of the analyses conducted as shown in **Table 4**, the disulfide bonded, i.e. "D3 stapled Fab", penta-miniGNC antibodies displayed 5% higher protein of interest production. Both molecules exhibited comparable antigen binding kinetics (**Table 4**).

Example 9. Multi-specific miniGNC antibodies with stapled scFv binding domains

The core structure of multi-specific miniGNC molecules were engineered to acquire several features in order to stabilize the heterodimer, including the covalently linked hinge and non-covalent and preferential interaction of "knobs-into-holes" by the CH3 domains in Fc region. While the stability and compactness are desirable, it remains unclear whether the closer

proximity of D1 and D2 or D3 and D4 may affect their stability and independent function. To maintain the stability and independence of each added binding domains, one option is to introduce a disulfide bond at V_L100 and V_H44 in each scFv domain, i.e. to staple each scFv domain. A disulfide bond between V_L and V_H may be used for all scFv domains to stabilize the overall structure. Alternatively, a disulphide bond may be introduced into at least one selected scFv domain at any position.

Four miniGNC antibodies have their D1 and D2 targeting EGFR and HER3 were grouped for measuring comparative potency of TDCC to the pancreatic cancer cells (HPAF-II), including tri-miniGNC (SI-68X2, SEQ ID NO. 137,139), tetra-miniGNC (SI-68E1, SEQ ID NO. 141, 143, and SI-68E2, SEQ ID NO. 145, 147), and penta-miniGNC (SI-68P1, SEQ ID NO. 149, 151) molecules. The moiety 1 binding specificities to 4-1BB and PD-L1 were the variable, whereas CD3 was the constant as D3 in the group interms of multispecificity. The expression construct encoding each of these four miniGNC antibodies was modified such that all scFv domains carrying a disulfide bond. The constructs were expressed individually in ExpiCHO system and each antibody was purified with reasonable titer. The binding kinetics to respective antigens were verified using Octet. AHC sensors were used to capture the miniGNC antibody at a concentration of 10 ug/ml for 180 seconds. After a 60-second baseline step, a single concentration of antigen was used for a 180-second association step. Antigens tested included 200 nM human EGFR (purified in-house), 100 nM human CD3 (Acro CDD-H52W1), 20 nM human PD-L1 (Acro PD1-H5229), 400 nM human 4-1BB (purified in-house), 200 nM human HER3 (Acro ER3-H5223). After association, a 420-second dissociation step was used. The tabulated K_D values were calculated using a one-to-one binding model in ForteBio Data Analysis software version 11. Analysed K_D values for each miniGNC molecule with all stapled scFv domains, as shown in **Table 5**, were compared with K_Ds of monoclonal antibody controls for respective antigens as shown in **Table 6**. The binding kinetics data shows comparable binding affinity of each stapled scFv domain with its respective mAb or Fc-scFv control SI-1C3 (SEQ ID 181, 183) SI-1C7 (SEQ ID 185), SI-9C21 (SEQ ID 187, 189), SI-35SF11 (SEQ ID 191), SI-3SF11 (SEQ ID 193), SI-20C14 (SEQ ID 287 and 289) (**Table6**), suggesting that stapling one or more scFv domains seems to have little effect to the binding affinity.

To evaluate the effect of stapled scFv domains to the potency of the miniGNC antibody, T cell directed cytotoxicity (TDCC) assay was used and the target cells were HPAF -II, human a human pancreatic cancer cell line (ATCC, Manassas, VA). The surface expression of the target cells was validated by flow cytometry. Serial dilutions (0 to 30 nM; 1 to 5 dilution factor) of antibodies were added to a white 384-well plate containing target cells and activated T cells (plated immediately before drug; effector: target = 5:1) in a total volume of 50 ul. After an additional 72 hours, 20 ul of Bright-Glo (Promega) was added to wells, and luminescence corresponding to viability of luciferised tumor cells was determined using a CLARIOstar plate reader. Data were fit to a sigmoidal function to calculate EC₅₀ values. As shown in **Figure 6 and Table 5**, the survival curves revealed that the potency of all four miniGNC antibodies was be

within the dose range of pM and with a tendency of the penta-miniGNC antibody exerting higher TDCC potency than that of tetra-miniGNC and tri-miniGNC antibodies. This observation again shows little effect by using stapled scFv domains.

Example 10. miniGNC having NKG2D receptor dimer as a binding domain

An increased number of binding specificities allows the GNC antibodies to bind not only T cells but also subsets of T cells, natural killer cells, and other types of immune cells, collectively known as moiety 1 binding domains/specificities (see Applicant's applications, WO/2019/005641 and WO2019191120, incorporated herein in its entirety). Some of moiety 1 binding specificities may replace the cellular response to or recognition of targeted cells. For example, NKG2D is a major recognition receptor for the detection and elimination of transformed and infected cells, as its ligands are induced during cellular stress, either as a result of viral infection or genomic stress, such as in cancer. In humans, NKG2D is expressed by NK cells, cells, and CD8+ T cells. The addition of NKG2D as a binding domain/specificity to the class of miniGNC antibodies may improve the cytotoxicity and efficacy of the antibody as a single multi-functional therapeutic agent.

In NK cells, NKG2D serves as an activating receptor, which itself can trigger cytotoxicity, whereas on CD8⁺ T cells the function of NKG2D is to send co-stimulatory signals to activate them. NKG2D forms a homodimer whose ectodomains serve for ligand binding. This feature qualifies NKG2D as a non-variable-sequence-based binding domain in a miniGNC format and other binding domains can be added to create a class of multi-specific NKG2D-miniGNC protein. In one miniGNC format, individual NKG2D monomer was incorporated in the D3 position on chain A and chain B which formed a dimeric NKG2D receptor on Fc dimerization. Thus, NKG2D can act as a receptor for the multi-specific miniGNC molecule to bind its ligand. In other miniGNC format, a NKG2D tandem repeat was designed by adding a (GxSy)_n spacer/linker between individual NKG2D monomers which homodimerizes and forms a functional dimeric receptor. This NKG2D tandem dimeric structure can be positioned in D1, D2, D4 or D5.

As listed in **Table 7**, this class includes mono-NKG2D-miniGNC (SI-49R26, SEQ ID NO. 153, 155), bi-miniGNC (SI-49R27, SEQ ID NO. 157, 159), tri-miniGNC (SI-49R25, SEQ ID NO. 161, 163), tetra-miniGNC (SI-49P_X, SEQ ID NO. 165, 167), and penta-mini-GNC molecules (SI49P8, SI-49P9, SEQ ID. NO. 169, 171, 177, and 179). A control penta-miniGNC, SI-49PM1 (SEQ ID NO. 173, 175), was created by switching the positions of D1 (α CD3) and D3 of SI-49P8, and the Octet binding affinity for either NKG2D or CD3 was not affected by this switch. While the binding affinity of other moiety 1 binding domains remained stable in this class of NKG2D-miniGNC molecules, the binding affinity of NKG2D was within 2-fold. Thus, the penta-miniGNC molecule possesses the binding function of NKG2D receptor for binding to NKG2D ligand.

To assess and compare the potency of TDCC of NKG2D-miniGNC molecules, tri-, tetra-, and penta-miniGNC molecules, SI-49R25, SI-49P_X, and SI-49P8 and SI-49PM1 were used to target MDA-MB-231 breast cancer cell line. Serial dilutions (0 to 30 nM; 1 to 5 dilution factor) of the miniGNC protein were added to a white 384-well plate containing luciferised MDA-MB-231 cells 24 hours prior and grown at 37 °C. Activated T cells were plated immediately before miniGNC molecules (effector: target = 15:1) in a total volume of 50 ul. After incubated for additional 72 hours, 20 ul of Bright-Glo (Promega) was added to wells, and the luminescence corresponding to viability of luciferised tumor cells was determined using a CLARIOstar plate reader. Data were fit to a sigmoidal function to calculate EC50 values (**Figure 7**). Based on the dose-viability curves, there were two groups, the tetra- and penta-miniGNC molecules were more potent than the tri-miniGNC molecule, SI-49R25. As listed in Table 7, the difference might result from the addition of α PD-L1. However, the EC50 value (59.3nM) of SI-49R25 should be considered as relatively potent. To the breast cancer cell line MDA-MB-231, CD19, which is a pan-B cell marker, is a non-participating tumor antigen. In this regard, SI-49R25 may be viewed as having two binding specificities to CD3 and NKG2D ligand. Thus, the data indicates that the incorporation of NKG2D receptor to different miniGNC antibody format contributes to the potency of TDCC. In a broader sense, the miniGNC antibody molecules can accommodate multiple binding specificities to modulate, cooperate, and direct an optimized immune response to targeted cells, such as cancer.

TABLES

Table 1. The configuration, production, binding affinity, and potency of multi-specific minGNC molecules when targeting EGFR and/or HER3-expressing pancreatic cancer cells (BXPC3).

Protein ID	D1 /KD (nM)	D2 /KD (nM)	D3 /KD (nM)	D4 /KD (nM)	D5 /KD (nM)	Titer (μg/ml)	EC50 (pM)
Penta-miniGNC							
SI-75P6	αCD3	αHER3	αEGFR	α4-1BB	αPDL-1	96.5	0.011
	36.2	138	5.56	37.3	1.45		
SI-75P4	αEGFR	αHER3	αCD3	α4-1BBL	αPDL-1	48.4	0.102
	10.4	150	22.7	115	2.72		
SI-75P3	αEGFR	αHER3	αCD3	α4-1BB	αPDL-1	39.4	1.300
	8.91	158	17.4	7.51	1		
SI-75P9	αEGFR	αCD3	αHER3	α4-1BB	αPDL-1	30	0.160
	11.1	20.1	140	21.2	2.7		
Tetra-miniGNC							
SI-75E1	αEGFR	αHER3	αCD3	α 4-1BB	--	30.2	5.800
	8.9	185	20.3	17.8	--		
SI-75E2	αEGFR	αHER3	αCD3	--	αPDL-1	172.3	0.085
	8.24	114	22.1	--	1.36		
Tri-miniGNC							
SI-75X3	αEGFR	αHER3	αCD3			193.5	5417
	8.47	146	18.2	--	--		
SI-75X16	αEGFR	αHER3	αCD3*			183.5	95540
	6.8	112.8	33.4	--	--		
SI-75X18			αCD3*	αEGFR	αHER3	38.2	6090
			47.3	2.72	93.75		
Bi-miniGNC							
SI-75X1	αEGFR		αCD3			246.1	0.71
	8.11		24	--	--		
SI-75X2		αHER3	αCD3			237.7	433.8
		162	27.8	--	--		
SI-75X5		αHER3	αCD3*			192.9	9,095
		139.2	44.4	--	--		

Table 2. The effect of the position and binding affinity of the CD3 binding domain on the potency of penta-minGNC molecules when targeting EGFR-expressing pancreatic cancer cells (BXPC3).

Protein ID	D1 /KD (nM)	D2 /KD (nM)	D3 /KD (nM)	D4 /KD (nM)	D5 /KD (nM)	Titer (μ g/ml)	EC50 (pM)
SI-68P13	α EGFR	α CD19	α CD3	α 4-1BB	α PD-L1	35.1	0.09
	5.64	4.33	25.9	14.8	1.04		
SI-68P17	α CD3	α CD19	α EGFR	α 4-1BB	α PD-L1	40	0.6
	15.82	5.05	5.38	26.8	2.72		
SI-68P15	α CD3**	α CD19	α EGFR	α 4-1BB	α PD-L1	58.1	0.16
	22.4	2.85	2.42	17.1	0.4		
SI-68P18	α CD3***	α CD19	α EGFR	α 4-1BB	α PD-L1	26	0.19
	14.46	1.35	8.18	7.51	1.00		
SI-68P19	α CD3****	α CD19	α EGFR	α 4-1BB	α PD-L1	28	0.12
	16.74	3.44	4.43	21.2	0.7		
SI-68P16	α CD3*****	α CD19	α EGFR	α 4-1BB	α PD-L1	72	5.5
	60.6	2.55	2.41	23.3	0.5		

Table 3. The effect of VHH single binding domain(s) on the potency of multi-specific minGNC molecules when targeting BXP3 tumor cells

Protein ID	D1 /KD (nM)	D2 /KD (nM)	D3 /KD (nM)	D4 /KD (nM)	D5 /KD (nM)	Titer (μ g/ml)	EC50 (pM)
SI-75P5	α EGFR VHH	α HER3 VHH	α CD3	α 4-1BB	α PD-L1	200.5	443
	23.5	4.68	26.1	23.3	3.25		
SI-75P8	α EGFR VHH	α HER3 VHH	α CD3*	α EGFR	α HER3	295	967468000
	6.22	0.786	44.1	6.22	0.786		
SI-75X4	α EGFR VHH	α HER3 VHH	α CD3	--	--	65.8	5766
	51.5	7.68	26.3	--	--		
SI-75X17	α EGFR VHH	α HER3 VHH	α CD3*	--	--	330	No killing
	14.8	4.58	68	--	--		
SI-75X19	--	--	α CD3*	α EGFR VHH	α HER3 VHH	223.4	1873
			64.4	20.6	10.52		
SI-75X9	--	α HER3 VHH	α CD3*	--	--	234	2584
	--	3.86	84.2	--	--		
SI-75X11	α EGFR VHH	--	α CD3*	--	--	214	564
	21.6	--	65.7	--	--		
SI-75X15	--	--	α CD3*	--	α HER3 VHH	161.3	27400
	--		38.08	--	13.7		
SI-75X13	--	--	α CD3*	α EGFR VHH	--	165.6	4858
		--	56	34--	--		

Table 4. The effect of “stapled” CD3 binding domain at D3 position on the production of multi-specific miniGNC molecules.

Protein ID	D1 /KD (nM)	D2 /KD (nM)	D3 (Stapled) /KD (nM)	D4 /KD (nM)	D5 /KD (nM)	Titer (μ g/ml)	%POI
	α CD20	α CD19	α CD3	α 4-1BB	α PD-L1		
SI-38P11	7.33	1.89	5.23 (No)	14.8	1.1	80	69
SI-76PM1	6.09	3.30	3.22 (Yes)	22.43	1.47	129	75

Table 5. Comparative potency of multi-specific miniGNC molecules with “stapled” scFv at all positions when targeting tumor cells.

Protein ID	D1 (Stapled) /KD (nM)	D2 (Stapled) /KD (nM)	D3 /KD (nM)	D4 (Stapled) /KD (nM)	D5 (Stapled) /KD (nM)	Titer (μg/ml)	EC50 (pM)
	αEGFR*	αHER3	αCD3	α4-1BB	αPD-L1		HPAF-II
SI-68X2	<0.001	114.4	24.3	--	--	88.9	6.6
SI-68E1	<0.001	138.8	26.2	12.7	--	114.8	3.6
SI-68E2	<0.001	120	28.4	--	0.4	67	1.3
SI-68P1	<0.001	93.4	24.3	9.8	0.6	87.1	1.02
	αCEA	αEGFR*	αCD3				MCF-7
SI-68X1	<0.001	<0.001	14.3	--	--	69	4.2
	αHER2	--	αCD3				
SI-68X3	NA		NA			57	NA

Table 6. Characterization of the unstapled versions of each domain (D1-D5) in mAb or scFv format to respective antigens.

Protein ID	Unstapled Controls	Domain Structure	Titer (μg/ml)	KD (nM)
SI-1C3	D1 = αEGFR*	mAb	44.9	<0.001
SI-1C7	D2= αHER3	Fc-scFv	290.7	136.5
SI-9C21	D3 = αCD3	mAb	252.1	26.3
SI-35FS11	D4 = α4-1BB	Fc-ScFv	7.67	14.9
SI-3FS11	D5 = αPD-L1	Fc-ScFv	18	0.94
SI-20C14	D1= αCEA	mAb	NA	<0.001

Table 7. The characterization of multi-specific minGNC molecules with NKG2D receptor dimer incorporated in miniGNC format and potency of tri, tetra and penta molecules in killing MDA-MB-231 tumor cells

Protein ID	D1 /KD (nM)	D2 /KD (nM)	D3 /KD (nM)	D4 /KD (nM)	D5 /KD (nM)	Titer (μg/ml)	EC50 (pM)
SI-49R26	--	--	NKG2D	--	--	28	n.a.
	--	--	17.7-	--	--		
SI-49R27	αCD3	--	NKG2D	--	--	38.6	n.a.
	32.2	--	16	--	--		
SI-49R25	αCD3	αCD19	NKG2D	--	--	50	59330
	34.50	7.62	12.80	--	--		
SI-49P_X	αCD3	αCD19	NKG2D	--	αPD-L1	8.8	119.5
	30.45	1.31	10.4	--	0.2		
SI-49P8	αCD3	αCD19	NKG2D	α4-1BB	αPD-L1	62.3	570.3
	36.3	2.98	24.3	7.71	1.08		
SI-49PM1	NKG2D	αCD19	αCD3	α4-1BB	αPD-L1	30.3	946.5
	24.49	5.5	30.2	2.74	2.23		
SI-49P9	αCD3	αCD19	NKG2D	41BBL	αPD-L1	28.9	n.a.
	29.80	6.4	27.2	112	2.01		

Table 8. The characterization of bispecific miniGNC molecules with different IgG subtypes in the Fc domain.

Protein	IgG subtype	D1	D2	D3	D4	D5	Titer (μg/ml)	%POI
SI-75X5	IgG1	-	αHER3	αCD3*	-	-	192.9	72.2
SI-75XM9	IgG4	-	αHER3	αCD3*	-	-	150.5	85.6

Table 9. Annotation of binding domains for their binding specificity, domain structure, origin, and sequence identification number (SEQ ID).

Target	Binding Domain	Structure in miniGNC	Origin	SEQ ID NO.
CD20	Ritu	scFv	Rituximab	259-262
EGFR	EGFR	scFv and Fab	α EGFR H7	203-206
EGFR	EGFR*	scFv	Panitumumab	207-210
HER3	MM-111	scFv and Fab	MM-111	255-258
CD3	α CD3	scFv and Fab	284A10	219-222
CD3	α CD3*	scFv and Fab	283E3BSM	227-230
CD3	α CD3**	scFv	284A10 FR 1	231-234
CD3	α CD3***	scFv	284A10 FR 2	235-238
CD3	α CD3****	scFv	284A10 FR 3	239-242
CD3	α CD3*****	scFv	283E3FRS	291-294
PD-L1	α PD-L1	scFv	PL221G5	243-246
4-1BB	α 4-1BB	scFv	466F6	247-250
NKG2D Ligand	NKG2D	Receptor		253-254
4-1BB	41BBL	Ligand		251-252
EGFR	α EGFR VHH	VHH	VHH-122	263-264
HER3	α HER3 VHH	VHH	VHH BCD090-M2	265-266
CD19	huBU12	scFv	SI-huBU12 -H4,	215-218
CEA	α CEA-H1	scFv	CEA-656E11	279-282
HER2	Tras	scFv	Trastuzumab	284-285
		Human IgG1 heavy chain		313
		Human IgG4 light chain		314

SEQUENCE LISTING

Sample ID	Chain	SEQ ID NO.		Fc ProA KO (H435R/Y436F)	VH3 ProA KO (R19S)
		Protein	DNA		
SI-75X5	A	1	2	+	+
	B	3	4		
SI-75X6	A	5	6	+	-
	B	7	8		
SI-75X7	A	9	10	-	+
	B	11	12		
SI-75X8	A	13	14	-	-
	B	15	16		
SI-75P6	A	17	18	+	+
	B	19	20		
SI-75P4	A	21	22	+	+
	B	23	24		
SI-75P3	A	25	26	+	+
	B	27	28		
SI-75P9	A	29	30	+	+
	B	31	32		
SI-75E1	A	33	34	+	+
	B	35	36		
SI-75E2	A	37	38	+	+
	B	39	40		
SI-75X3	A	41	42	+	+
	B	43	44		
SI-75X16	A	45	46	+	+
	B	47	48		
SI-75X18	A	49	50	+	+
	B	51	52		
SI-75X1	A	53	54	+	NA
	B	55	56		
SI-75X2	A	57	58	+	+
	B	59	60		
SI-75O2	A	61	62	+	NA
	B	63	64		
SI-75O7	A	65	66	+	NA
	B	67	68		
SI-68P13	A	69	70	+	+
	B	71	72		
SI-68P17	A	73	74	+	+
	B	75	76		
SI-68P15	A	77	78	+	+
	B	79	80		
SI-68P18	A	81	82	+	+

	B	83	84		
SI-68P19	A	85	86	+	+
	B	87	88		
SI-68P16	A	89	90	+	+
	B	91	92		
SI-75P5	A	93	94	+	+
	B	95	96		
SI-75P8	A	97	98	+	+
	B	99	100		
SI-75X4	A	101	102	+	NA
	B	103	104		
SI-75X17	A	105	106	+	NA
	B	107	108		
SI-75X19	A	109	110	+	NA
	B	111	112		
SI-75X9	A	113	114	+	NA
	B	115	116		
SI-75X11	A	117	118	+	NA
	B	119	120		
SI-75X15	A	121	122	+	NA
	B	123	124		
SI-75X13	A	125	126	+	NA
	B	127	128		
SI-38P11	A	129	130	+	+
	B	131	132		
SI-76PM1	A	133	134	+	+
	B	135	136		
SI-68X1	A	195	196	-	-
	B	197	198		
SI-68X3	A	199	200	-	-
	B	201	202		
SI-68X2	A	137	138	-	-
	B	139	140		
SI-68E1	A	141	142	-	-
	B	143	144		
SI-68E2	A	145	146	-	-
	B	147	148		
SI-68P1	A	149	150	-	-
	B	151	152		
SI-49R26	A	153	154	+	NA
	B	155	156		

SI-49R27	A	157	158	+	NA
	B	159	160		
SI-49R25	A	161	162	-	-
	B	163	164		
SI-49P_X	A	165	166	-	-
	B	167	168		
SI-49P8	A	169	170	-	-
	B	171	172		
SI-49PM1	A	173	174	+	+
	B	175	176		
SI-49P9	A	177	178	-	-
	B	179	180		
SI-75XM9	A	297	298	+	+
	B	299	300		

Protein ID	Format	SEQ ID NO.	
		Protein	Protein
SI-1C3 HC	α EGFR mAb	181	182
SI-1C3 LC	α EGFR mAb	183	184
SI-1C7	α HER3 Fc-scFv	185	186
SI-9C21 HC	α CD3 mAb	187	188
SI-9C21 LC	α CD3 mAb	189	190
SI-35FS11	α 4-1BB Fc-scFv	191	192
SI-3FS11	α PD-L1 Fc-SCFv	193	194
SI-20C14 HC	α CEA mAb 656E11	287	288
SI-20C14 LC	α CEA mAb 656E11	289	290

Domains	Variable Chains	SEQ ID	
		Protein	DNA
α EGFR	VH	203	204
	VL	205	206
α EGFR *	VH	207	208
	VL	209	210
α EGFR * Stapled	VH	211	212
	VL	213	214
α CD19	VH	215	216
	VL	217	218
α CD3	VH	219	220
	VL	221	222
α CD3 Stapled	VH	223	224

	VL	225	226
α CD3 *	VH	227	228
	VL	229	230
α CD3 **	VH	231	232
	VL	233	234
α CD3 ***	VH	235	236
	VL	237	238
α CD3 ****	VH	239	240
	VL	241	242
α PDL1	VH	243	244
	VL	245	246
α 41BB	VH	247	248
	VL	249	250
41BBL	NA	251	252
NKG2D dimer	NA	253	254
α HER3	VH	255	256
	VL	257	258
α CD20	VH	259	260
	VL	261	262
EGFR VHH	VHH	263	264
HER3 VHH	VHH	265	266
α PDL1 Stapled	VH	267	268
	VL	269	270
α 41BB stapled	VH	271	272
	VL	273	274
α HER3 stapled	VH	275	276
	VL	277	278
α CEA	VH	279	280
	VL	281	282
α HER2 stapled	VH	283	284
	VL	285	286
α CD3 *****	VH	291	292
	VL	293	294
NKG2D monomer	NA	295	296

Antibody	Kabat CDR	AA SEQ ID
α CEA 656E11	CDR-H1	301
	CDR-H2	302
	CDR-H3	303
	CDR-L1	304

αCD3 283E3 (BSM/FRS)	CDR-L2	305
	CDR-L3	306
	CDR-H1	307
	CDR-H2	308
	CDR-H3	309
	CDR-L1	310
	CDR-L2	311
	CDR-L3	312

>Sequence ID 1: SI-75X5 Chain A Amino Acid Sequence

QVQLQESGGRLVQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSE
DTAIYYCARGGYSSDIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFCSCVMHEALHN
HYTQKSLSLSPG

>Sequence ID 2: SI-75X5 Chain A Nucleotide Sequence

CAAGTGCAAGTTCAGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTTGTCAGTGTACAGTGTAAACAAGCGGCATTGATCT
GTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGGCGATTTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGGTACTCCTCTGATATCTGGGGGCGAGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAGAGGCCCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGG
ACTACTTCCCAGAGCCTGTGACTGTGTCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGC
TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAA
GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCCCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGG
CTGCTGGAGGCCCTCTGTGTTCTCTTCCCTCCAAGCCCAAGGACACCCCTGATGATCTCCAGGACCCAGAAAGTCACTGTGTG
GTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCC
CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTC
TACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACAT
TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCTGTCATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 3: SI-75X5 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYCYSSYSSSTHVIFFGGTKVTVLGGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYWMSWVRQAP
GKGLEWVANINRDGSASYVDVSVKGRFTISRDDAKNSLYLQMNLSRAEDTAVYYCARDRGVGYFDLWGRGLTVTVSSGGGGSGGGG
SDPQLTQSPSSLSATVGRVTINQSSQSVAKNNNLAWFQKPKPKPKLLIYASASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDF
ATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS
KDSYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE
VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHE
ALHNRFTQKSLSLSPG

>Sequence ID 4: SI-75X5 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTGCATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCAAACTCATGATCTATGATGTGAGTGTGCGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTAGGCGGTGGCGG
TAGTGGGGGAGGCGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCTTGTC
AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCCAAATAAACCGCGATGGAAGTGCGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG

ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGATCCTCAATTGACCCAGTCCCTTAGTAGCCTTTCTGCAACCGTGGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGTAGCGAAGAATAATAATTTGGCATGGTTCACACAAAAACCGGTAACCTCCTAAACTCCTTATCTACTCAGCTTCAACCCCTGCGCGGGTGTGCCAGCCGGTTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTGCAACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGCCCCCTCTGTGTTTCATCTTCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCTACCCAGAGAAGCCAAGGTGCAGTGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGTATGCCTGTGAGGTGACCCACCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCCAGCCCCAGAAGCTGCTGGAGGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAATCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGAAGTGCACAAATGCAGAACAGCCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTACCCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTCTGTGCATGCATGAGGCCCTGCACAACCGCTTCAACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 5: SI-75X6 Chain A Amino Acid Sequence

QVQLQESGGRVLPGEPLSLTCKTSGIDLSSNAIGWVRQAPGKLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSEDTAIYYCARGGYSSDIWQGTILTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKPKDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLVSKLTVDKSRWQQGNVVFSCSVMHLEAHNHYTQKSLSLSPG

>Sequence ID 6: SI-75X6 Chain A Nucleotide Sequence

CAAGTGCAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTGTCACTGACGTGTAAACAAGCGGCATTGATCTGTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACGCAAGCTGGGCAAAAGGGCGATTTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAGGATACCCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGAGGGTACACTGGTTACAGTTTCATCCGCTAGCACCAAAGGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGGACTACTTCCCAGAGCCTGTGACTGTGCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGCTCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCAAGGCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGGCTGCTGGAGGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAAGTCACTGTGTGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAAATGCCAAGACCAAGCCAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAGGCTTCTACCCCAGTGACATGTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTTGCTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTCTGTGCATGCATGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 7: SI-75X6 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEADYYCSSYSSSTHVFVGGGKTVTLVGGGSGGGGSGGGGSGGGGSGVQLQESGGGLVKPGGSLRLSCAASGFTFSSYWMWVRQAPGKLEWVANINRDGSASYYVDSVKGRFTISRDDAKNSLYLQMNLSRAEDTAVYYCARDRGVGYFDLWGRGTLTVSSGGGSGGGGSDPQLTQSPSSLSATVGRVTINQSSQSVAKNNNLAWFQQKPKPKLLIYASSTLAAGVPSRFSGSGSGTQFTLTITRVQSEDFATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVVFSCSVMHLEAHNRFTQKSLSLSPG

>Sequence ID 8: SI-75X6 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACAGCAGTGACGTGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCAAACTCATGATCTATGATGTGAGTGATCGGCCCTCAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCTGATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCCGGCGAGGGACCAAGGTGACCGTCTAGCGGGTGGCGGTAGTGGGGGAGGCGGTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCGGTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGTGGCCAACATAAACCGCGATGGAAGTGGGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT

CTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGA
 TCAGATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTC
 CGTAGCGAAGAATAATAATTGGCATGGTTCCAACAAAAACGGGTAAACCTCCTAAACTCCTTATCTACTCAGCTTCAACCCCTTG
 CCGCGGGTGTGCCCAGCGGGTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGGTCCAAAGTGAGGATTTT
 GCAACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCCTTTGGGGTGGAACTCGGGTGGAGATAAAACGTACGGTGGC
 TGCCCCCTCTGTGTTCTCTCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCT
 ACCCCAGAGAAGCCAAGGTGCAGTGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGC
 AAGGACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGAGGTGAC
 CCACCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCC
 CAGCCCCAGAAGCTGTGGAGGCCCCCTCTGTGTTCTCTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAA
 GTCACTGTGTGTCGAGTGTGTCAGGATGAAGACCCAGAGTCAAGTTCAACTGGTATGTGGATGGAGTGAAGTGACCAATGC
 CAAGACCAAGCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATG
 GGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGCCCAAGGGCCAGCCCAGA
 GAGCCCCAGGTGTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAAGGCTTCTA
 CCCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTGATG
 GCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGCATGAG
 GCCCTGCACAACCGCTTCAACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 9: SI-75X7 Chain A Amino Acid Sequence

QVQLQESGGRVLPGEPLSLTCKTSGIDLSSNAIGWVRQAPGKLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSE
 DTAIYYCARGGYSSDIWQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSNSGALTSGVHTFPAVLQS
 SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQV
 YTLPPSRDELTKNQVSLVSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLVSKLTVDKSRWQQGNVFSCSVMEALHN
 HYTKLSLSLSPG

>Sequence ID 10: SI-75X7 Chain A Nucleotide Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTTGTCACTGACGTGTAAAAACAAGCGGCATTGATCT
 GTCCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACAT
 ACTACGCAAGCTGGGCAAAAGGCGATTACGATATCAGGAGACCTCTACAGTTTATTTGAAATGAATCACTCCCTCCGTCAGG
 GATACCGGATATATTACTGTGTCAGAGGGGGTACTCCTCTGATATCTGGGGGACGGGTACACTGGTTACAGTTTCTATCCGCTAG
 CACCAAAGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGG
 ACTACTTCCCAGAGCCTGTGACTGTGTCCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGC
 TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAA
 GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGG
 CTGCTGGAGGCCCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAAGTCACTGTGTG
 GTGGTGGATGTGCCATGAAGACCCAGAAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGACAATGCCAAGACCAAGCC
 CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
 AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTC
 TACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACAT
 TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGAGTCTGATGGCTCCTTCTTCC
 TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGCATGAGGCCCTGCACAAC
 CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 11: SI-75X7 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGSSDVGGYNFVSWYQQHPGKAPKLMYIDVSDRPSGVSDRFSKSGNTASLIISGLQADDEA
 DYICSSYGSSSTHVFIFGGGKVTVLGGGGSGGGGSGGGGSGGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYWMSWVRQAP
 GKLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNLSRAEDTAVYYCARDRGVGYFDLWGRGLTVTVSSGGGGSGGGG
 SDPQLTQSPSSLSATVGQRVTINCQSSQSVAKNNNLAWFQQKPKPKLLIYASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDF
 ATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
 KDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE
 VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPR
 EPQVYTLPPSRDELTKNQVSLVCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLVSKLTVDKSRWQQGNVFSCSVME
 ALHNHYTKLSLSLSPG

>Sequence ID 12: SI-75X7 Chain B Amino Acid Sequence

CAGTCTGCCCTGACTCAGCCTGCCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
 TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCAAACCTCATGATCTATGATGTGAGTGTGCGCCCT
 CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACAGGCT
 GATTATTACTGCAGCTCATATGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTAGGCGGTGGCGG
 TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCCTGGTCA
 AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA

GGGAAGGGGCTGGAGTGGGTGGCCAACATAAACCGCGATGGAAGTGCAGGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGA
TCAGATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTC
CGTAGCGAAGAATAATAATTTGGCATGGTTCCAACAAAAACCGGTAAACCTCCTAACTCCTTATCTACTCAGCTTCAACCCTTG
CCGCGGGTGTGCCAGCCGGTTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTT
GCAACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCCTTTGGGGTGGAACTCGGGTGGAGATAAAACGTACGGTGGC
TGCCCCCTCTGTGTTCTATCTTCCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCT
ACCCAGAGAAGCCAAGGTGCAGTGGAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGTATGCCTGTGAGGTGAC
CCACAGGGGCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCC
CAGCCCCAAGAGTGTGTGGAGGCCCTCTGTGTTCTCTTCCCTGCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAA
GTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGCACAATGC
CAAGACCAAGCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATG
GGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAA
GAGCCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTA
CCCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACACTACAAGACCACCCCTCCTGTGCTGGACTCTGATG
GCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGCATGAG
GCCCTGCACAACCACTACACCCAGAAGACCTGAGCCTGAGCCCTGGA

>Sequence ID 13: SI-75X8 Chain A Amino Acid Sequence

QVQLQESGGRLVQPGEPISLTCTKTSIDLSSNAIGWVRQAPGKLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSE
DTAIYYCARGGYSSDIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVKDRVEPKSCKDTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFSVMHEALHN
HYTQKSLSLSPG

>Sequence ID 14: SI-75X8 Chain A Nucleotide Acid Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTTGCTACTGACGTGTAAACAAGCGGCATTGATCT
GTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGGCGATTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGCGAGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAGAGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGG
ACTACTTCCCAGAGCCTGTGACTGTGCTCCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGC
TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCAACCCAGACCTACATCTGCAATGTGAACCACAA
GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCCAAGTCCTGTGACAAGACCCACACCTGCCCTCCTCCAGCCCCAGAGG
CTGCTGGAGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAAGTCACTGTGTG
GTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCC
CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTC
TACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACAT
TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACACTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGCATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 15: SI-75X8 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQHPGKAPKLMYIDVSDRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYCYSSYSSSTHVIFGGGKVTVLGGGGSGGGGSGGGGSGGGGQVQLQESGGGLVKPGGSLRLSCAASGFTFSYWMWVRQAP
GKLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNLSLAEDTAVYYCARDRGVGYFDLWGRGLTVTVSSGGGGSGGGG
SDPQLTQSPSSLSATVGRVTINQSSQSVAKNNNLAWFQQKPGKPKLLIYASTLAAGVPSRFSGSGSGTQFTLTITRVSQSEDF
ATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
KDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPE
VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHE
ALHNHYTQKSLSLSPG

>Sequence ID 16: SI-75X8 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCAAACCTCATGATCTATGATGTGATGATCGGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCTCCAGGCTGACGACGAGGCT

GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCCTAGGCGGTGGCGG
TAGTGGGGGAGGCGGTCTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCGGGGGGAGGCGTGGTCA
AGCCTGGAGGGTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCCAACATAAACCCGATGGAAGTGCGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACCAAGGTCAGTGTATCTGCAATGAACAGCTGAGAGCTGAGGACACGGAGTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGG
TCAGATCCTCAATTGACCCAGTCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTC
CGTAGCGAAGAATAATAATTTGGCATGGTTCCAACAAAAACCGGTAAACCTCCTAAACTCCTTATCTACTCAGCTTCAACCCCTG
CCGCGGGTGTGCCAGCCGGTCTCAGGCTCAGGTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTT
GCAACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCCTTTGGGGGTGGAACTCGGGTGGAGATAAAACGTACGGTGGC
TGCCCCCTCTGTGTTCTCTCCACCCAGTGTGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCT
ACCCAGAGAGAAGCAAGGTGCAAGTGGCAATGCCCTGACAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGTATGCCTGTGAGGTGAC
CCACCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCC
CAGCCCCAGAAGTGTGAGGAGCCCTCTGTGTTCTTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCAGAA
GTCACCTGTGTGGTGGTGGATGTGTCCTATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGAAGTGCACAATGC
CAAGACCAAGCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATG
GGAAGGAGTACAAGTGTGCTGTGTCACCAAGGCCCTGCCCTGCCCATTTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCGAGA
GAGCCCCAGGTCTACACCTGCCCTCCCTCCAGAGATGAGCTGACCAAGAACAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTA
CCCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAATAAGACACCCCTCCTGTGCTGGACTCTGATG
GCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCATGCATGAG
GCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 17: SI-75P6 Chain A Amino Acid Sequence

DVVMTQSPSTLSASVGDRTVINQASESISWLAHYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
YCQGYFYFISRTYVNSFGGGTKVEIKGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSVMRQA
PGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGGSSAITSNINWQGTLLTVSSGGGSG
GGGQVQLQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPKGLEWLVISGGNTDYNTPFTSRFTITKDNSKNQVYFKL
RSVRADDTAIYYCARALTYDYEFAYWQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLM
ISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLLVSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKLSLSLSPGGGGSGGGSDVVMTQSPSSVSASVGDRTVITCQASQNIIRTYLSWYQQKPGKAPKLLIYAAANL
ASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTLDYVGAFGGGTCLTVLGGGGSGGGSGGGSGGGSEVQLVESGG
GLVQPGGSLRLSCASGFTISSYHMQWVRQAPKGLEIYIGTISGGNVYYASSARGFTISRPSKNTVDLQMNSLRAEDTAVYYC
ARDSGYSDPMWQGTLTVSS

>Sequence ID 18: SI-75P6 Chain A Nucleotide Sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
TAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGG
TCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCTTAT
TACTGCCAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGG
CGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG
TCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCT
CCAGGCAAGGGGCTGGAGTGGATCGGAGTCATTACTGCTGATCAGATACATACACTACGCGAGCTGGCGAAGGAGCATTCACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG
ACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGC
GGTGGTGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTC
AGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGGCAGGCACCCGGCAAAGGTTTGAATGGCTGGGTGTTATTTGGTCAG
GTGGAATACAGACTATAACACCCCTTTACAAGTCGGTTTACAATACGAAAGATAATTCCAAAAATCAAGTTTATTTCAAGTTG
AGATCCGTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGATTGGGGGCA
AGGGACTCTTGTAACAGTCTCCAGTGCTAGCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGG
GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGGC
GTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTC
ACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCCCTCATG
ATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCAATATGCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTATACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGTCTG
CGCGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAAACACTACAAGACCACGCCTC
CGGTGCTGGACTCCGACGGCTCCTTCTTCTCTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCTGTCTCCGGTGGCGGCGGCGGTTCAGGTGG

TGGGGGATCCGACGTTGTGATGACGCAGTCTCCTAGTTTCACTATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCGA
GCCAAAATATTAGGACGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCCTCATTACGCCGCTGCCAACTTG
GCTAGTGGAGTACCTTCACGCTTTAGTGGGTCAAGTTCTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACAGGGGACGC
TGCCACGTATTATTGCCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTG
GTGGTGGTGGTTCAGGCGGGGGGGTTCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCACTTGGTTGAAAGTGGGGG
GGACTCGTTTACGCTGGAGGCTCTTTCGCACTTTCTTGTACCGCTTCTGGGTTCACTATAAGTTTATATCATATGCAATGGGTAAG
ACAGGCGCCTGGTAAGGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGTCATTACGCCCTCATCCGCGCGGGGGAGGT
TTACAATTTCCAGGCCTTCTAGCAAAAACACGGTAGATCTGCAATGAAGTCTCTTCGCGCTGAAGATACAGCAGTCTACTACTGC
GCCAGGGATTACAGGTATTCTGACCCCATGTGGGGGACGGGCACATTGGTTACCGTGTCTCT

>Sequence ID 19: SI-75P6 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYCYSSYSSSTHVFVGGGKTVTLVGGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYMSWVRQAP
GKLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNLSRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSSGGGGSGGGG
SEIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASEISGIPDRFSGSGSGTEFTLTISVQSEDFAV
YYCQNNNNWPTTFGPGTKLTVLRTVAAPSVFI FPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALH
NRFTQKSLSLSPGGGGSGGGGSDIQTQSPSTLSASVGRVTITCQASQSISSHLNHWYQQKPKAPKLLIYKASTLASGVPSRFS
GSGSGTEFTLTISLQPDFFATYYCQQGYSGWNVNDFVGGGKTVTLVGGGGSGGGSGGGSGGGSGEVQLLESGLVQPGGSL
LSAASGFSFSSGYDMCWVRQAPGKLEWIAICIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARSAFSD
DYAMD LWGQGLTVTVSS

>Sequence ID 20: SI-75P6 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCCAAGCCCCAACTCATGATCTATGATGTGAGTGTGCGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTAGCGGCTGGCGG
TAGTGGGGAGGCGGTTCTGGCGGGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCGGGGGAGGCGCTGGTCA
AGCTTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCTCTGGAATTCACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCGCAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCCAAACATAAACCCGCGATGGAAGTGCGAGTTACTATGTGGAAGTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAAGTCACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGG
TCAGAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACCGCGCACTTCTCTTGCAGGGCAAGTCAATC
CATAGGGACTAATATACATTTGGTATCAACAAAAGCCAGGTAACCCAGGCTTTTATTAAGTATGCAAGTGAGTCTATTTCCG
GTATCCCTGACCGCTTCTCTGGATCAGGCGAGTGGCACAGATTCACACTCACCATACTAGTGTGCAATCAGAGGACTTCGCCGTG
TATTACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTACGTACGGTGGCTGCACCATC
TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAAATTCTATCCCAGAG
AGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC
ACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCAACCATCAGGG
CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGCACGACCTG
AAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGC
GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGT
ACAAGTGCAGCGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAG
GTGTACACCCCTGCCCAAGCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCCTTCT
TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC
AACAGATTACGCAGAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTACAGATGACACA
GTCACCGTCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGAATACCTGCCAAGCCTCCCAATCTATAAGTTACACCTCAACT
GGTATCAACAGAAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCTCAGGTGTGCCTAGTCGCTTCTCC
GGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCAACCCGACGACTTCGCCACATACTATTGTGACGAGGGTTA
TAGTTGGGGAAATGTTGACAATGTGTTTGGAGGGGAACGAAAGTGAAGTGTGTTGGAGGGGGAGGAGTGGCGGCGCGGAAGCG
GAGGTGGTGGCTCCGGCGGGGGTGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGGAAAGCCTCTCA
CTCTCTTCCGCGGCGAGTGGTTTTAGCTTCACTAGCGGCTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCCTTGAGTG
GATTGCTGTATCGCCGCCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTCACAATCTCCAGGGACAAC
CAAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTTAGCTTC
GATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTACCGTCTCATCTTGA

>Sequence ID 21: SI-75P4 Chain A Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDAFVY
 YCQQNNNWPTTFPGTKLTVLGGGSGGGGSGGGGSGGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
 EWLGVWISGGNTDYNTPFTSRFTITKDNSKNQVYFKLRSVRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSGGGSGGGGSEV
 QLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAE
 DTAVYYCARDGSSAITSNNIWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPP
 AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPCPAPEAAAGGPSVFLFPPKPKDTLMI SRT
 EVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIKAKGQP
 REPQVYTLPPSRDELTKNQVSLSCAVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSVMH
 EALHNHYTQKSLSLSPGGGGSGGGGSGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGPLSWYSDPGLAGVSLTGGLSYKED
 TKELVVAAGVYVFFQLELRVAVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNASAFGFQGRLLHLSAGQRLGVH
 LHTEARARHAWQLTQGATVLGLFRVTPPEIPAGLGSTGSGSKPGSGEGSTKGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDG
 PLWYSDPGLAGVSLTGGLSYKEDTKELVVAAGVYVFFQLELRVAVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSE
 ARNASAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPPEIPAGLGSGGGSGGGGSGREGPELSPDDPAGLLDLRQ
 GMFAQLVAQNVLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKELVVAAGVYVFFQLELRVAVAGEGSGSVSLALHLQPLRSAAG
 AAALALTVDLPPASSEARNASAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPPEIPAGL

>Sequence ID 22: SI-75P4 Chain A Nucleotide Sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAAGCGCGACTTTCTCTTGACAGGGCAAGTCAATCCAT
 AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAGTATGCAAGTGAGTCTATTTCGGGTA
 TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTTCACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
 TACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAGCTGACCGTTTTAGGCGGTGGCGGTAGTGGGGGAGG
 CGGTTCTGGCGGGGAGGGTCCGGCGGTGGAGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
 CGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCTTACGAATATGGAGTTCACTGGATTCCGGCAGGCACCCGGCAAAGGTTTG
 GAATGGCTGGGTGTTATTTGGTCAGGTGGAATACAGACTATAACACCCCTTTACAAGTCGGTTCACAATTACGAAGATAATTC
 CAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCTGCACACTTACG
 ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAACAGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
 CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
 CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGATATCACATACTACG
 CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATTCCAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
 GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTCAC
 CGTGTCTCAGCTAGCACCAAGGGCCATCGGTCTTCCCTTGGCACCTCTCCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCTTGGTCAAGGACTACTTCCCGAACCCTGACGGTGTCTGTGGAAGTCAAGCGCCCTGACCGAGGGCTGCACACTTCCCG
 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
 CAACGTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGT
 GCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCT
 GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
 TGCCAAGACAAAGCCGCGGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTCTGCACCCAGGAGTGGCTGA
 ATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAGCCCTCCGAGCCCTCAGAGAAACCATCTCCAAGGACCAAGGAGCGCC
 CGAGAACCACAGGTGTATACCTTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTT
 CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGTGGACTCCG
 ACGGCTCCTTCTTCTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
 GAGGCTCTGCACAACTACACGAGAGAGCTCTCCCTGTCTCCGGGTGGCGGCGCGGTTCAGGTGGTGGGGGATCCCGAGA
 GGGCCCCGAGCTGTCTCTGATGACCCAGCAGGCTCTTGAGCTTGCGGCAGGGTATGTTTCGCTCAACTTGTGGCTCAGAATGTT
 TGCTCATTGATGGACACTCTCTTGGTATAGTGACCCCGGTCTGGCCGGGTGAGTCTGACCGGCGGGCTCTCTTATAAAGAGGAT
 ACTAAGGAACCTGGTCGTAGCAAAAAGCGGGCTTTATTACGTTTTTTTTCAGCTGGAGCTCAGGCGCGTGGTGCCCGGCGAGGGCAG
 TGGCTCTGTGTCCCTGGCCCTGCACTTACAGCCCTTGAGAAGCGCTGCAGGTGCTGCCGCACTGGCTTTAACTGTTGACCTCCCTC
 CGGCCTCTTCTGAAGCTAGAAACAGCGCTTTTCGGCTTCAAGGGCGCTGCTGCACCTGAGCGCAGGCCAGCGCTTAGGTGTGCAC
 CTTTCATACAGAGGCCAGGGCCGACAGCTTGGCAGCTCACACAGGCTGCCACGGTCTCGGACTTTTCCGCGTTACTCCCGAGAT
 CCCCCTGGCCTCGGAAGTACTGGTCTGGGTCTAAACCCGCTTCCGGCGAAGGTAGTACTAAAGGACGAGAAGGGCCAGAGTTAA
 GTCCAGATGACCTGCTGGGCTTTTGGACCTGCGGCAGGGCATGTTTCGCTCAACTGGTGGCTCAGAACGTGCTGCTGATCGATGGC
 CCCCTGAGTTGGTACAGCATCCCGGGCTGGCAGCGGTGCTACTTACAGGGGGCTCTCTTACAAGGAAGACACCAAGGAGTTAGT
 GGTGCTAAGGCTGGCGTGTATTACGTGTTCTTCCAAGTGGAGCTGAGAAGGGTTGTGGCAGGAGAGGTTAGCGGCAGCGTGTCTT
 TAGCCCTTCACTTGCAGCCCTGAGGTCTGCTGCAGGTGCAGCGCTCTCGCGCTCACCGTGGATCTCCCCCAGCCTCATCTGAA
 GCTAGGAACAGTGCATTTGGCTTTAGGGACGCTTGTGTCACCTCTCCGCTGGACAGAGGCTGGGCGTGCACCTTACACAGAGGC
 CCGTGCCAGGCATGCATGGCAGCTCACTCAGGGGGCAACAGTGTGGGTCTCTTCCGCGTGAATCTGAAATACCAGCTGGACTTG
 GCGGTGGAGGCAGCGCGGAGGAGATCTCGTGAGGGGCCAGAACTGTCCCCGATGACCCAGCCGGACTGCTCGATCTCAGACAG
 GGCATGTTTCGCTCAGCTTGTAGCCCAAATGTCTCTGATTGACGGCCCTTTGAGCTGGTATAGTGATCCCGGCTTGGCCGGGT
 ATCTGTGACCGGAGGCTCTCTTACAAGGAAGACACAAAGAGCTGGTGGCAGGAGGTTGATGTTGTTCTTTTTCAGC
 TCGAGCTGCGGAGAGTTGTGGCCGGGAAGGCTGGGAGCGTATCTCTTGCACCTTCACTGACGCCCCGCGCAGCGCGCTGGA
 GCCGCGGCCCTTGTCTTACTGTGGATCTGCCTCTGCTTCTCAGAAGCACGCAACAGCGCCTTCGGCTTTCAAGGACGTCTCT
 GCACTTGTCCGCGAGACAGAGGTTGGGCGTCCATTACACACTGAGGCACGGGCACGCACGCTTGGCAGCTTACCAGGGAGCCA
 CCGTGTGGGACTCTTTAGAGTGACACCCGAGATCCCCGCTGGCTTGTGA

>Sequence ID 23: SI-75P4 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMIIYDVS DRPSGVSDRFS GSKSGNTASLIISGLQADDEA
 DYYCSSYSSSSTHVIFGGGT KVTVLGGGGSGGGSGGGSGGGSSQVQLQESGGGLVKP GGSLSLSLSCAASGFTFSSYWSWVRQAP
 GKGLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSSGGGGSGGGG
 SDVMTQSPSTLSASVGDRTINCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFAT
 YYCQGYFYFISRTYVNSFGGGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
 DSKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRT
 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVM
 HEALHNRFTQKSLSLSPGGGGSGGGGSDIQMTQSPSTLSASVGDRTITCQASQSISSHLNWIYQQKPGKAPKLLIYKASTLASGV
 PSRFSGSGSGTEFTLTISLQPDFFATYYCQGYSWGNVDNVFGGGT KVTVLGGGGSGGGSGGGSGGGSGGGSEVQLLES GGGLVQP
 GGSLSLSLSCAASGFSFSSGYDMCWVRQAPGKLEWIIACIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR
 SAFSFDYAMD LWGQGLTVTVSS

>Sequence ID 24: SI-75P4 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
 TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCAAACCTCATGATCTATGATGTGATGATCGGCCCT
 CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
 GATTATTACTGCAGCTCATATGGGAGCAGCAGCAGCTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCCTAGGCGGTGGCGG
 TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCCTGGTCA
 AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
 GGAAGGGGCTGGAGTGGGTGGCAACATAAACCCGATGGAAGTGGGAGTTACTATGTGGACTCTGTGAAGGGCCGATTCACCAT
 CTCCAGAGACGACGCCAAGAATCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAACGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGA
 TCAGACGTCGTGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAG
 CATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTG
 GGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCT
 TATTACTGCCAAGGCTATTTTTATTATTATTAGTCTGACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
 GGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATA
 ACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAG
 GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCAG
 AGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAACTCACACATGCCAC
 CGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCA
 TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACACAGCAGCTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGC
 TGAATGGCAAGGAGTACAAGTGC CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
 CCCCAGAACCAAGGTGTACACCCTGCCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGG
 CTCTCTATCCCAGGACATCGCGGTGGAGTGGGAGAGCAATGGGACGCCGGAACAACTACAAGACACGCTCCGCTCCGCTGGACT
 CCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACAGATTACGCGAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGA
 CATTGAGATGACACAGTCAACGCTCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAA
 GTTACACCTCAACTGGTATCAACAGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCTCAGGTGTG
 CCTAGTCGCTTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACTA
 TTGTGAGCAGGGTTATAGTTGGGAAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGAAGTGTGTTGGGAGGGGGAGGAAGTG
 GCGCGGCGGAAGCGGAGGTGGTGGCTCCGGCGGGGTGGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCT
 GGTGGAAGCCTCTCACTCTCTTGC CGCGGAGTGGTTTTAGCTTCACTAGCGGCTACGATATGTGCTGGGTAAAGACAGGCTCCTGG
 TAAAGGCCTTGAGTGGATTGCGTGTATCGCCGCCGGGTCTGCTGGTATAACATACGATGCAAAGTGGGCGAAAGGGCGCTTCACAA
 TCTCCAGGGACAACCTCAAAAAATACATTGTACCTCCAGATGAATAGCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGG
 TCAGCATTTAGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 25: SI-75P3 Chain A Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
 YCQQNNNWPTTFPGTKLTVLGGGGSGGGSGGGSGGGSSQVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
 EWLGVIIWGGNTDYNTPTFSRTITKDN SKNQVYFKLRSVRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSGGGGSGGGGSEV
 QLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKLEWIGVITGRDITYASWAKGRFTISRDN SKNTLYLQMNSLRAE
 DTAIVYYCARDGSSAITSNNIWGGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSVGHVTFP
 AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE
 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
 REPQVYTLPPSRDELTKNQVSLCAVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFS CSVMH
 EALHNHYTQKSLSLSPGGGGSGGGGSDVMTQSPSSVSASVGDRTITCQASQNI RTYLSWYQQKPGKAPKLLIYAAANLASGV
 PSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGT DYVGGAFGGGT KLTVLGGGGSGGGSGGGSGGGSGGGSEVQLVESGGGLVQP

GGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISSGNVYYASSARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARD SG
YSDPMWGQGLTVTVSS

>Sequence ID 26: SI-75P3 Chain A Nucleotide Sequence

GAAATCGTCCCTACACAATCTCTAGCACACTGAGTGTGAGCCCCGGCGAACGCGGACTTTCTCTTGCAAGGCAAGTCAATCCAT
AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGTATTAAGTATGCAAGTGAGTCTATTTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTTCACTACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
TACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTAGGCGGTGGCGGTAGTGGGGGAGG
CGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
CGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCTTACGAATATGGAGTTCACTGGATTCCGGCAGGCACCCGGCAAAGGTTTG
GAATGGCTGGGTGTTATTTGGTCAGGTGGAAATACAGACTATAACACCCCCCTTTACAAGTCGGTTCACAATTACGAAAGATAATTC
CAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAACAGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGATATCACATACTACG
CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATCCAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTCAC
CGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCGTGGCACCCTCCTCCAAGAGCACCTCTGGGGCCAGGCGGCCCTGG
GCTGCCTGGTCAAGGACTACTTCCCGAACCCTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCG
GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGT
GCCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCT
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
TGCCAAGACAAAGCCGCGGGGAGGAGCAGTACAACAGCAGTACCCTGGTGGTCAAGCTCTCACCCTCTGCACCAAGGACTGGCTGA
ATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCC
CGAGAACCACAGGTGTATACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTT
CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGTGGACTCCG
ACGGCTCCTTCTTCTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGCTCTGCACAACTACACGCAGAAAGAGCTCTCCCTGTCTCCGGGTGGCGCGCGCGGTTCAGGTGGTGGGGGATCCGACGT
TGTGATGACGCAGTCTCCTAGTTCACTATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCGAGCCAAATATTAGGA
CGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAACTCCTCATTACGCCGTGCCAATTGGCTAGTGGAGTACCT
TCACGCTTTAGTGGGTGAGTTCTGGAACAGATTTACGTTGACGATCTCCGATTGGAACACAGGGGACGCTGCCACGTATTATTG
CCAGTCCACCTACCTCGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTGGTGGTGGTGGTTCAG
GCGGGGGGGGTTCCGGCGGAGGCGGTCTGGGGGTGGAGGTTCCGAGGTTCACTTGGTTGAAAGTGGGGGGGACTCGTTAGCCT
GGAGGCTCTTTGCGACTTTCTGTACCGCTTCTGGGTTCACTATAAGTTTCATATCATATGCAATGGTAAGACAGGCGCTGGTAA
GGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGTCTATTACGCCTCATCCGCGCGGGGGAGGTTTACAATTTCCAGGC
CTTCTAGCAAAAACACGGTAGATCTGCAATGAATCTCTTCGCGCTGAAGATACAGCAGTCTACTACTGCGCCAGGGATTACGGG
TATTCTGACCCCATGTGGGGGCAGGGCACATTGGTTACCGTGTCTCT

>Sequence ID 27: SI-75P3 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMIYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYCYSSYSSSTHVIFFGGTKVTVLGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYMSWVRQAP
GKGLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGLTVTVSSGGGGSGGGG
SDVMTQSPSTLSASVGRDVTINCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFAT
YYCQYFYFI SRTYVNSFGGTVKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
DSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDITLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV
HEALHNRFTQKLSLSLSPGGGGSGGGGSDIQTQSPSTLSASVGRDVTITCQASQSISSHLNWIYQQKPGKAPKLLIYKASTLASGV
PSRFSGSGSGTEFTLTISLQPDFFATYYCQYQGYSGWNVNDNVFGGKTQVTVLGGGSGGGSGGGSGGGSGGGSEVQLLESGGGLVQP
GGSLSLSCAASGFSFSSGYDMCWVRQAPGKLEWIAACIAAGSAGITYDANWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR
SAFSFDYAMDLDWGQGLTVTVSS

>Sequence ID 28: SI-75P3 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCAAACCTCATGATCTATGATGTGAGTATCGGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCTCCCTGATCATCTCTGGCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTAGGCGGTGGCGG
TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCTGGTCA
AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCAACATAAACCGCGATGGAAGTCCGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAATCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGA

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACGCGCGACTTTCTCTTGCAAGGGCAAGTCAATCCAT
AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAGTATGCAAGTGAGTCTATTTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCCGTGTAT
TACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTATAGCGCGGTGGCGGTAGTGGGGGAGC
CGGTTCTGGCGCGGAGGTCCTGGCGGTGGAGGATCAACAAGTACAGTTGACGCAATCCGGTCCCGGTCTCGTCAAAACGGTGTGAG
CGCTTAGTATAACGTGAGTCTGTTTCAAGCTTTAGCCTTTACGAACATATGGAGTTCACTGGATTCCGCAAGGCACCCGGCAAGGTTTG
GAATGGCTGGGTGTTATTTGGTCAGGTGGAAATACAGACTATAACACCCCTTTTACAAGTCGGTTTACAATTACGAAAGATAATTC
CAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGGCACTGACCTACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAACAGTCTCGAGCGCGCGGTGGAGGGTCCGCGCGGTGGTGGATCAAGGTG
CAGCTGCAGGAGAGTGGAGGAGGCCCTGGTGAAGCCCTGGAGCGAGCCTGGGGTGTCTCTGTGCTGCCCTTGGCTTCACTTCTCTC
CTACTGGATGAGTGGGTGCGCGAGGCCCTCAGGCAAGGGCCTGGAGTGGGTGGCCAACTCAACAGAGATGGCTTGCCCTCCTACT
ATGTGGACTCTGTGAAAGGCCGCTTCACCATCTCCAGAGATGATGCCAAGAAGCAGCCTGTACCTGCAGATGAACAGCCTGAGAGCT
GAGGACACAGCTGTGTACTACTGTGCCAGAGACCGAGGTGTGGGCTACTTTGACCTGTGGGGCAGAGGCACCCTGGTGAAGTGTGTC
CTCTGCTAGACCAAGGGGCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACTCTGGGGGCAAGCGGCCCTGGGCTGCC
TGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTGACACACCTTCCCCGGCTGTG
CTACAGTCTCAGGACTACTCCTCAGCAGCTGTGTTGACCTGCCCTCGCAGCTTGGGCACCCAGACCTACATCTGCAACGT
GAATCAAGGCCAGCAACCAAGGTGACAAGAGAGTTGAGGCCAAATCTTGTGACAAAACCTCACATGCCACCCTGCCAG
CACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTG
ACATGCGTGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA
GACAAGCGCGCGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAGCGTCTCACCGTCTCAAGCCAGCAGGACTGGCTGAATGGCA
AGGAGTACAAGTGGCGGCTTCCAACAAAGCCCTCCGACCCCTCAGAAACCACTCCTCAAGCCAAAGGGCAGCCCGAGAA
CCACAGGTGTATACCCTGCCCTCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCTGTCTCGCCGTCAAAGGCTTCTATCC

CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT
 CCTTCTTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGCGCGGTTTCAAGTGGTGGGGGATCCGACGTTGTGAT
 GACGCAGTCTCCTAGTTTCACTATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCGAGCCAAAATATTAGGACGTATC
 TGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCTCATTTACGCCGCTGCCAACTTGGCTAGTGGAGTACCTTCACGC
 TTTAGTGGGTCAAGTTCTGGAACAGATTTTACGTTGACGATCTCCGATTTTGAACACAGGGGACGCTGCCACGTATTATTGCCAGTC
 CACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTGGTGGTGGTGGTTCAGGCGGGG
 GGGGTTCCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCACTTGGTTGAAAGTGGGGGGGACTCGTTCAAGCTGGAGGC
 TCTTTGCGACTTCTTGTACCGCTTCTGGGTTCACTATAAGTTCATATCATATGCAATGGGTAAGACAGGCGCCTGGTAAGGGACT
 TGAATACATAGGAACAATAAGCTCTGGTGGTAACGTCTATTACGCCCTCATCCGCGCGGGGGAGGTTTACAATTTCCAGGCTTCTA
 GCAAAAACACGGTAGATCTGCAATGAACTCTCTTCGCGCTGAAGATACAGCAGTCTACTACTGCCACAGGGATTCAAGGTATTCT
 GACCCCATGTGGGGCAGGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 31: SI-75P9 Chain B Amino Acid Sequence

DVVMTQSPSTLSASVGDVRTINQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
 YCQGYFYFISRTYVNSFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSVMRQA
 PGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGGSSAITSNNIWQGTLLTVSSGGGGSG
 GGGQSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPKAPKLLIYDVS DRPSGVSDRFSGSKSGNTASLIISGLQA
 DDEADYYCSSLSSSTHVI FGGGTVLRLTPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTK
 PSKQSNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSGGDKTHTCPFCPEAAGGPSVFLFPPKPKDLMISR
 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAG
 QPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCSSV
 MHEALHNRFTQKSLSLSPGGGGSGGGGSDIQMTQSPSTLSASVGDVRTITCQASQSISSHLNWIYQQKPGKAPKLLIYKASTLASG
 VPSRFSGSGSGTEFTLTISLQPDFFATYCYCQGYSGWNVNDVFGGGTKVTVLGGGSGGGGSGGGGSGGGGSEVQLLES GGGGLVQ
 PGGSLSLSCAASGFSFSSGYDMCWVRQAPGKLEWIIACIAAGSAGITYDANWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCA
 RSAFSFDYAMDWLWGQGLTVTVSS

>Sequence ID 32: SI-75P9 Chain B Nucleotide Sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
 TAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGG
 TCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTCAACTTAT
 TACTGCCAAGGCTATTTTATTTTATTAGTCGTACTTATGTAATTTCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGG
 CGGTAGTGGGGGAGGCGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG
 TCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCT
 CCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGTATATCACATACTACGCGAGCTGGGCGAAAGGCAGATTCAACCAT
 CTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTCACCGTGTCTCAGGCGGTGGAGGGTCCGGC
 GGTGGTGGATCACAGAGTGCCCTGACCCAGCCAGCCTCTGTCTCTGGCAGCCAGGCCAGTCCATCACCATCTCCTGCACAGGCAC
 CTCCAGTGATGTGGGAGGCTACAACCTTTGTGTCTGGTACCAGCAGCACCCAGGCAAGGCCCCCAAGCTCATGATCTATGATGTGT
 CTGACAGACCCTCTGGAGTCTCTGACAGATTCTCTGGCTCCAAGAGTGGCAACACAGCCTCCCTCATCATCTCTGGCCTGCAGGCT
 GATGATGAAGCTGACTACTACTGCTCCTCTATGGCTCCTCCTCACCCTATGTCATCTTTGGAGGAGGCACCAAGGTCACTGTGCT
 GCGTACGCCCAAGGCCAACCCACCGTGACCCTGTTCCCCCAAGCAGCGAGGAAGTGCAGGCCAACAAAGGCCACCCCTCGTGTGCC
 TGATCAGCGACTTCTACCTTGGCGCGGTGACCTGGCTGGAGTGGAGTGGATCTCCCGTGAAGGCCGGCGTGGAAACCAACAG
 CCGAGCAGCAGAGCAACAACAAATACGCCCGCAGCTCTCACTGAGCCTGACCCCGAGCAGTCCCACCGTCTCTACAG
 CTGCCAGGTACACACGAAGGCAGCACCGTGGAAAAGACAGTGGCCCCACCGAGTGCAGCGGAGGCGACAAAACCTCACACATGCC
 CACCGTGGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAGGACACCCCTCATGATCTCCCGG
 ACCCTGAGGTGCATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGT
 GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACAGGACT
 GGCTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGG
 CAGCCCCGAGAACCACAGGTGACACCCTGCCCCAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCTGTGGTGGCTTGGTCAAG
 AGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGGCAATGGGCAGCCGAGAGCAAACTACAAGACCACGCCTCCCGTGTGG
 ACTCCGACGGCTCCTTCTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
 ATGCATGAGGCTCTGCACAACAGATTACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATC
 CGACATTCAAGTACACAGTACCGTCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGAATATCACCTGCCAAGCCTCCCAATCTA
 TAAGTTACACCTCAACTGGTATCAACAGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCCTCAGGT
 GTGCCTAGTCGCTTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCAACCCGACGACTTCGCCACATA
 CTATTGTCAAGAGGTTATAGTTGGGGAATGTTGACAATGTGTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGGAGGAA
 GTGGCGGCGGCGGAAGCGGAGGTGGTGGCTCCGGCGGGGGTGGAAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAA
 CCTGGTGGAAAGCCTCTCACTCTCTTGGCGGCGAGTGGTTTTAGCTTCAGTAGCGGCTACGATATGTGCTGGGTAAGACAGGCTCC
 TGGTAAAGGCTTGTAGTGGATTGCGTGTATCGCCGCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGCGCCTTCA
 CAATCTCCAGGGACAACCAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCA
 AAGTCAGCATTTAGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCT

>Sequence ID 33: SI-75E1 Chain A Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKGKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDAVY
 YCQNNNNWPTTFGPGLTLVLGGGGSGGGSGGGSGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
 EWLGVIWSGGNTDYNTPFTSRFTITKDNSKNQVYFKLRVSRADDTAIYYCARALTYDYEFAYWGQGLVTVSSGGGGSGGGGSEV
 QLVESSGGGLVQPGGSLRLSCAASGFTISTNAMSWSVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAE
 DTAVYYCARDGSSAITSNNIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPP
 AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTF
 EVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKISKAKGQP
 REPQVYTLPPSRDELTKNQVSLCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFSVMH
 EALHNHYTQKSLSLSPGGGGSGGGSGGGSGGGSGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
 SRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTIDYVGGAFGGGKTLTVLGGGGSGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPG
 GGSRLSCTASGFTISSYHMQWVRQAPGKGLYIGTISGGNVYASSARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARDSG
 YSDPMWQGGLTVTVSS

>Sequence ID 34: SI-75E1 Chain A Nucleotide Sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGCAACGCGCGACTTTCTCTTGCAGGGCAAGTCAATCCAT
 AGGGACTAATATACATTGGTATCAACAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAGTATGCAAGTGAGTCTATTCCGGTA
 TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
 TACTGCCAACAGAATAATACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTAGGCGGTGGCGGTAGTGGGGGAGG
 CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
 CGCTTAGTATAACGTGTACTGTTTACGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGGCAGGCACCCGGCAAGGTTTG
 GAATGGCTGGGTGTTATTTGGTCAGGTGGAAATACAGACTATAACACCCCCCTTTACAAGTCGGTTCACAATTACGAAAGATAATTC
 CAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
 ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAACAGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
 CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGACGCTCTGGATTACCATCAGTAC
 CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACATACTACG
 CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
 GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTCAC
 CGTGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
 GCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
 CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACATGCCCCACCGT
 GCCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCT
 GAGGTACATCGCTGGTGGTGGACGTGAGCCAGGACCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGCGTGGAGGTGCATAA
 TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACGCTCCTCACCGTCTGCACAGGAGTGGCTGA
 ATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCC
 CGAGAACCACAGGTGTATACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTT
 CTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGACAACACTACAAGACCACGCTCCCGTGTGGACTCCG
 ACGGCTCCTTCTCTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
 GAGGCTCTGCAACAACCACTACACGAGAAGAGCCTCTCCTGTCTCCGGGTGGCGGCGGCGGTTGAGTGGTGGGGGATCCGACGT
 TGTGATGACGCGAGTCTCCTAGTTCAGTATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCGAGCCAAATATTAGGA
 CGTATCTGTCTTGGTATCAACAAAGCCTGGTAAGGCTCCAAAACCTCTCATTTACGCCGCTGCCAATTGGCTAGTGGAGTACCT
 TCACGCTTTAGTGGGTGAGTTCTGGAACAGATTTACGTTGACGATCTCCGATTTGGAACCAGGGGACGCTGCCACGTATTATTG
 CCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTGGTGGTGGTGGTTCAG
 GCGGGGGGGGTTCCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTGAGTTGGTTGAAAGTGGGGGGGACTCGTTACGCT
 GGAGGCTCTTTGCGACTTTCTGTACCGCTTCTGGGTTCACTATAAGTTTCATATCATATGCAATGGGTAAGACAGGCGCCTGGTAA
 GGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGCTCTATTACGCTCATCCGCGCGGGGGAGGTTTACAATTTCCAGGC
 CTTCTAGCAAAAACACGGTAGATCTGCAATGAACCTCTTTCGCGCTGAAGATACAGCAGTCTACTACTGCGCCAGGGATTACAGG
 TATTCTGACCCCATGTGGGGGCGAGGACATTTGGTTACCGTGTCTCTTGA

>Sequence ID 35: SI-75E1 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGSSDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
 DYYCSSYSSSTHVFIFGGGKTVTVLGGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYWMSWVRQAP
 GKGLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGLTVTVSSGGGGSGGGG
 SDVMTQSPSTLSASVGRVTINQASESISWLAWYQQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFAT
 YYCQGYFYFISRTYVNSFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQ
 DSKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRT

PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV
HEALHNRFTQKSLSLSPG

>Sequence ID 36: SI-75E1 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCAACTCATGATCTATGATGTGAGTGATCGGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTTAGCGGTGGCGG
TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCGGTGGTCA
AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCCAACATAAACCAGGATGGAAGTGCAGGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAATCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAACGCTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGA
TCAGACGTCTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAG
CATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTG
GGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACT
TATTACTGCCAAGGCTATTTTTATTATTATTAGTCTACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
GGTGGCTGCCCCCTCTGTGTTCTATCTTCCACCAGTGTATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACA
ACTTCTACCCAGAGAAGCCAAGGTGCAGTGGAAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGA
GGTGACCCAGGCGCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTC
CCTGCCAGCCCCAGAAGCTGTGGAGGCCCCCTGTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACC
CCAGAAGTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTCAACTGGTATGTGGATGGAGTGGAAAGTGCA
CAATGCCAAGACCAAGCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGC
TGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAG
CCCAGAGAGCCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGG
CTTCTACCCAGTGCATTTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAATAAGACCAACCCCTCCTGTGCTGGACT
CTGATGGCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGACCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCTATG
CATGAGGCCCTGCACAACCGCTTCAACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 37: SI-75E2 Chain A Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQKPKGKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNNWPTTFPGTKLTVLGGGSGGGSGGGSGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGVIWGGNTDYNTPFTSRFTITKDNSKNQVYFKLSVRADDTAIYYCARALTYDYEFAYWGQGLVTVSSGGGSGGGGSEV
QLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAE
DTAVYYCARDGGSSAITSNNIWGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKPSCKDTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTP
EVTCTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSV
HEALHNYHTQKSLSLSPG

>Sequence ID 38: SI-75E2 Chain A Nucleotide Sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACGCGGACTTTCTCTTGCAAGGCAAGTCAATCCAT
AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAGTATGCAAGTGAAGTCTATTTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACTACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
TACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTAGGCGGTGGCGGTAGTGGGGGAGG
CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
CGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGCGAGGCACCCGGCAAAGGTTTG
GAATGGCTGGGTGTATTTGGTCAGGTGGAATACAGACTATAACACCCCTTTTACAAGTCCGGTTCACAATTACGAAAGATAATTC
CAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGGCACTGACCTACTACG
ATTACGAATTTGGTATTTGGGGCAAGGGACTCTGTAAACAGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
CAGCTGCGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACATACTACG
CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTCAC
CGTGTCTCAGCTAGCACCAAAGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGG
GCTGCTGTGTAAGGACTACTTCCAGAGCCTGTGACTGTGTCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCT

GCTGTGCTGCAGAGCTCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTG
CAATGTGAACCACAAGCCCTCCACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGCCACACCTGCCCTCCCT
GCCCAGCCCCAGAGGCTGCTGGAGGCCCCCTCTGTGTTCTCTCCCTCCCAAGCCCAAGGACACCCGTGATGATCTCCAGGACCCCCA
GAAGTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCACTGGTATGTGGATGGAGTGGAGGTGCACAA
TGCCAAGACCAAGCCCAGAGAAGAGCAGTACAACCTACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACACAGGACTGGCTGA
ATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCC
AGAGAGCCCCAGGTCTACACCCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTT
CTACCCCAAGTACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACACTACAAGACCACCCCTCCTGTGCTGGACTCTG
ATGGCTCCTTCTCTCTGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTCTGCTGTGCATGCAT
GAGGCCCTGCACAACCACTACACCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 39: SI-75E2 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYCYSSYSSSTHVFIFGGGTKVTVLGGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYMSWVRQAP
GKLEWVANINRDGSASYYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSSGGGGSGGGG
SDVVMTQSPSTLSASVGDRTINCQASESISWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDDEFAT
YYCQGYFYFISRTYVNSFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYFPREAKVQWKVDNALQSGNSQESVTEQ
DSKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPFVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQ
PREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM
HEALHNRFTQKSLSLSPGGGGSGGGGSDIQMTQSPSTLSASVGDRTITCQASQSISSHLNWIYQQKPGKAPKLLIYKASTLASGV
PSRFSGSGSGTEFTLTISLQPDDEFATYYCQGYSWGNVDNFGGGTKVTVLGGGGSGGGSGGGSGGGSGGGSEVQLLESGLLVQF
GGSLSLSLSCAASGFSFSSGYDMCWVRQAPGKLEWIIACIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR
SAFSFDYAMDLDWGQTLVTVSS

>Sequence ID 40: SI-75E2 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCCTCCGTGTCTGGGTCTCCTGGACAGTGCATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCCAAGCCCCCAAACCTCATGATCTATGATGTGAGTGCAGGCCCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTAGCGGGTGGCGG
TAGTGGGGGAGCGGTCTTGGCGGGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCGGTGCTCA
AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCTCTGGAATTCACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCGAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCCAAACATAAACCCGCGATGGAAGTGCGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGG
TCAGACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCAACATCAATTGCCAAGCCAGTGAGAG
CATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACAGGGAAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTG
GGTCCCATCAAGGTTCAAGCGGAGTGGATCTGGGACAGAATTCACCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACT
TATTACTGCCAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAATTTCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
GGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATA
ACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAAGTCCCAGGAGAGTGTACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGA
AGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCAC
CGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGGTGGAGGTGCA
TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAAGCTCCTACCGTCTGCACAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCAGGCTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCCTGCCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGG
CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACT
CCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACAGATTACGCAGAAAGACCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGA
CATTGAGATGACACAGTCAACGCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAA
GTTACACCTCAACTGGTATCAACAGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCTCAGGTGTG
CCTAGTCGCTTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTCCCTCCAACCCGACGACTTCGCCACATACTA
TTGTGACAGGGTTATAGTTGGGAAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTACTGTGTTGGGAGGGGGAGGAAGTG
GCGGCGGCGGAAGCGGAGGTGGTGGCTCCGGCGGGGGTGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCT
GGTGAAGCCTCTCACTCTCTTGCAGCGGAGTGGTTTTAGCTTCAGTAGCGGCTACGATATGTCTGGGTAAAGACAGGCTCCTGG
TAAAGGCCTTGAGTGGATTGCGTGTATCGCCGCGGGTCTGCTGTGATAACATACGATGCAAACTGGGCGAAAGGGCGCTTACAA
TCTCCAGGGACAACCTCAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGG
TCAGCATTTAGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 41: SI-75x3 Chain A Amino Acid Sequence

GGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGAATTCCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACT
TATTACTGCCAAGGCTATTTTTATTTTATTAGTCTACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
GGTGGCTGCCCCCTCTGTGTTCATCTTCCCACCCAGTGTATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACA
ACTTCTACCCACAGAGAAGCCAAGGTGCAGTGGAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTGTCTCCACCCCTGACCCCTGCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGA
GGTGACCCACCCAGGCGCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTC
CCTGCCCAGCCCCAGAAGCTGCTGGAGGCCCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACC
CCAGAAGTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTCAACTGGTATGTGGATGGAGTGAAGTGC
CAATGCCAAGACCAAGCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGC
TGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAG
CCCAGAGAGCCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGG
CTTCTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACACCCCTCCTGTGCTGGACT
CTGATGGCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCATG
CATGAGGCCCTGCACAACCGCTTCACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 45: SI-75X16 Chain A Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPPRLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDAVY
YCQQNNNWPTTFPGTKLTVLGGGSGGGSGGGSGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGVIWGGNTDYNTPTFSRFTITKDNSKNQVYFKLRSVRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSGGGSGGGGSGV
QLQESGGRLVQPEPLSLTCKTSGIDLSSNAIGWVRQAPGKLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSRSED
AIYYCARGGYSSDIWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSG
LYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYT
LPSPRDELTKNQVSLSCAVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFCSSVMHEALHNHY
TQKLSLSLSPG

>Sequence ID 46: SI-75X16 Chain A Nucleotide Sequence

GAGATCGTGCTGACCCAGTCTCCTTCCACACTGTCTGTGTCTCCCGCGGAGAGAGCCACCTTCAGCTGTAGAGCCTCTCAGTCCAT
CGGCACCAACATCCACTGGTATCAGCAGAAGCCCGGCAAGCCTCCTCGGCTGCTGATTAAGTACGCCTCCGAGTCCATCAGCGGCA
TCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCAGAGTTTACCCTGACCATCTCCTCCGTGCAGTCCGAGGATTTCCGGCTGTAC
TACTGCCAGCAGAAACAACACTGGCCACCACCTTTGGACCCGGCACCAGCTGACAGTTCTTGGCGGCGGAGGATCTGGCGGAGG
TGGAAGCGGAGGCGGAGGAAGCGGTGGCGGCGGATCTCAAGTTCAGTTGCAGCAGTCTGGCCCTGGCCTGGTCAAGCCTTCTGAGA
CACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCAGTGGATCAGACAGGCCCCCTGGCAAAGGACTG
GAATGGCTGGGAGTGATTTGGAGCGGCGGCAACACCGACTACAACACCCCTTTACCAGCCGGTTCACCATCACCAGGACAACTC
CAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGCGGGCTGATGACACCGCCATCTACTACTGTGCTCGGGCCCTGACCTACTACG
ACTACGAGTTTGTCTACTGGGGCCAGGGCACCCCTGGTCACAGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAGTG
CAGTTGCAAGAAAGTGGTGGTAGACTGGTTACGCTGGTGAACCTTGTCACTGACGTGTAAAACAAGCGGCATTGATCTGTCTCTC
TAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACG
CAAGCTGGGCAAAAGGGCGATTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAGGATACG
GGCATATATTACTGTCCAGAGGGGGGTACTCCTGTGATATCTGGGGCAGGGTACACTGGTTACAGTTTCATCGCTAGCACCAA
AGGCCCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGGCTGGTGAAGGACTACT
TCCCAGAGCCTGTGACTGTGTCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGCTCTGGC
CTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAAGCCCTC
CAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGGCTGCTG
GAGGCCCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCCAAGTCACTGTGTGGTGGT
GATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCCAGAGA
AGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTGTG
CTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTCTACACC
CTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACATTGCTGT
GGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGGTCT
CCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCATGCATGAGGCCCTGCACAACCACTAC
ACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 47: SI-75X16 Chain B Amino Acid Sequence

AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTC
TACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCCAAGTGACAT
TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACACTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCAATGCATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCTGAGCCTGAGCCCTGGAGGAGGAGGAGGCTCTGGAGGAGGAGGATCCCAAGTTCAAGTTCAGTGCAGAGTC
TGCCCTTGGCCTGGTCAAGCCTTCTGAGACACTGTCCACTCTACCTGTACCGTGTCCGGCTTCTCCTGACCAATTACGGCGTGCAC
GGATCAGACAGGCCCTGGCAAAGGACTGGAATGGCTGGGAGTGATTTGGAGCGGCGGCAACACCCGACTACAACACCCCTTTACC
AGCCGGTTCACCATCACCAAGGACAACCTCCAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGCGGGCTGATGACACCGCCATCTA
CTACTGTGCTCGGGCCCTGACCTACTACGACTACGAGTTTGCTTACTGGGGCCAGGGCACCCTGGTCACAGTTTCTTCTGGTGGTG
GTGGTTCAGGCGGGGGGGGTTCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGATCGTGCTGACCCAGTCTCCTTCCACACTG
TCTGTGTCTCCCGGCGAGAGAGCCACCTTCAGCTGTAGAGCCTCTCAGTCCATCGGCACCAACATCCACTGGTATCAGCAGAAGCC
CGGCAAGCCTCCTCGGCTGCTGATTAAAGTAGCCTCCGAGTCCATCAGCGGCATCCCTGACAGATTCTCCGGCTCTGGCTCTGGCA
CCGAGTTTACCTCTGACCATCTCCTTCGTACGACTCCGAGGATTTGCGCGTGTA

>Sequence ID 51: SI-75X18 Chain B Amino Acid Sequence

DPQLTQSPSSLSATVGQRTVINCQSSQSVAKNNNLAWFQQKPGKPKPLLIYSASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDFATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTCPPCPAPEAAGGPSVFLFPPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISAKAGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFNFSVMHEALHNRFTQKSLSLSPGGGGGSGGGGSQVQLQESGGGLVKPGGSLSLSCAASGFTFSSYWMWVRQAPGKGLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGTLTVTVSSGGGGSGGGSGGGGSQSALTQPASVSGSPGQSITISCTGTSDDVGGYNFVSWYQQHPGKAPKLMIYDVSDRPSGVSDRFSGSKSGNTASLIISGLQADDEADYYCASYGSSSTHVFGGGTKVTVL

>Sequence ID 52: SI-75X18 Chain B Nucleotide Sequence

GATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGT
AGCGAAGAATAATAATTTGGCATGTTTCCAACAAAAACCGGGTAAACCTCCTAAACTCCTTATCTACTCAGCTTCAACCCCTTGCCG
CGGGTGTGCCCAGCCGGTTCCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCA
ACCTACTATTGTTCTGCACGGGATTCGGGAACATACAGTCTTTGGGGGTGGAACTCGGGTGGAGATAAAACGTACGGTGGCTGC
CCCCCTGTGTTTCATCTCCCAACCATGATGAGCAGCTGAAGAGTGGCAGAGCCTCTGTGGTGTGCTTGCTCAACAACCTTCTACC
CCAGAGAAGCCCAAGGTGCACTGGAAAGGTGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGAGGTGACCCA
CCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAG
CCCCAGAAGCTGCTGGAGGCCCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCAGAAGTC
ACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGCACAAATGCCAA
GACCAAGCCCCAGAGAAGAGCAGTACAACAGCACCTACCGATGGTGTCTGTGCTGACTGTGCTGCACCCAGGACTGGCTGAATGGGA
AGGAGTACAAGTGTGCTGTCTTCCAACAAGGCCCTGCCCTGCCCAATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAG
CCCCAGGTCTACACCTGCCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAAGGCTTCTACCC
CAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACATAAAGACCACCCCTCCTGTGCTGGACTCTGATGGCT
CCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCTATGCATGAGGCC
CTGCACAACCCTTACCCAGAAGAGCCTGAGCCTGAGCCCTGGAGGAGGAGGAGGCTCTGGAGGAGGAGGATCCAGGTGCAGCT
GCAGGAGTCGGGGGGAGGCCCTGGTCAAGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATT
GGATGAGCTGGGTCCGCGAGCCTCAGGAGAGGGGCTGGATGGGTGGCCAAACATAAACCAGCATGGAAGTGCAGTTACTATTGTG
GACTCTGTGAAGGGCCGATTCAACATCTCAGAGACGACGCCAAGAACTCACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGA
CACGGCTGTGATTACTGTGCGAGAGATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTACCCTGTCTAGCG
GTGGAGGCGGTTCAGGCGGAGGTGGTTCGGCGGTGGCGGCTCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCT
GGACAGTGCATCACCATCTCCTGCACTGAACACAGCAGTGACGTTGGTGGTTATAACTTTGTCTCCTGGTACCAACACACCCAGG
CAAAGCCCCCAAACCTCATGATCTATGATGTCACTGATCGGCTCAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACA
CGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACACGAGGCTGATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTG
ATTTTCGGCGGAGGGACCAAGGTGACCGTCTCTATAA

>Sequence ID 53: SI-75X1 Chain A Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLLIKYASESISGIPDRFSGSGSGTEFTLTISVVSQSEDAVY
 YCQQNNNWPTTFPGTKLTVLGGGSGGGGSGGGGSGGGGSGVQLVQSGSPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
 EWLGVIEWSGNTDYNTPFTSRFTITKDNSKNQVYFKLSVRADDTAIYCARALTYDYEFAYWGQGTLTVTSSGGGSGGGGSEV
 QLVESSGGGLVQPGGSLRLSCAASGFTLTSTNAMSWVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAE
 DTAIVYICARDGGSSALTSNNIWGGQTLTVTSSASTKGPSVFLEPASPSTSGGTAALGKLVKDYFPEPVTVSWNSGALTSGVHTFP
 AVLQSSGLYSLSVVTVPSSSLGTQYICNVNHKPSNTKVDKRVKPSCKDTHCTCPPEAPEAAGSGSVFLFPPKPKDITLMI SRT

EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPG

>Sequence ID 54: SI-75X1 Chain A Nucleotide Sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAAGCGCGGACTTTCTCTTGCAGGGCAAGTCAATCCAT
AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAAGTATGCAAGTGAAGTCTATTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTTACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
TACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTAGGCGGTGGCGGTAGTGGGGGAGG
CGGTTCTGGCGGGGAGGGTCCGGCGGTGGAGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
CGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGGCAGGCACCCGGCAAGGTTTG
GAATGGCTGGGTGTTATTTGGTCAGGTGGAAATACAGACTATAACACCCCTTTTACAAGTCGGTTTACAATTACGAAAGATAATTC
CAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTGTAAACAGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACATACTACG
CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATCCAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTCAC
CGTGTCTCAGCTAGCACCAAGGCCCTCTGTGTTCCCTCTGGCCCCCTCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGG
GCTGCCCTGGTGAAGGACTACTTCCAGAGCCTGTGACTGTGTCTGGAACCTCTGGAGCCTGACCTCTGGAGTGCACACCTTCCCT
GCTGTGCTGCAGAGCTCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCTCCAGCCTGGGCACCCAGACCTACATCTG
CAATGTGAACCACAAGCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCCT
GCCAGCCCCAGAGGCTGCTGGAGGCCCTCTGTGTTCCCTCTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCCA
GAAGTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAA
TGCCAAGACCAAGCCAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGA
ATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCC
AGAGAGCCCCAGGTCTACACCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTT
CTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACATAAAGACCACCCCTCCTGTGCTGGACTCTG
ATGGCTCCTTCTTCTGCTGTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCATGCAT
GAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 55: SI-75X1 Chain B Amino Acid Sequence

DVVMTQSPSTLSASVGDRTINCQASESISSWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDDEFATY
YCQGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRT
EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMH
EALHNRFTQKSLSLSPG

>Sequence ID 56: SI-75X1 Chain B Nucleotide Sequence

GACGTGGTCATGACACAGAGCCCTTCCACACTGTCTGCCTCCGTGGGCGATAGAGTGACCATCAACTGTCAGGCCTCCGAGTCCAT
CTCCTCTTGGCTGGCTTGGTATCAGCAGAAGCCTGGCAAGGCCCTTAAGCTGCTGATCTACGAGGCTTCCAAGCTGGCCTCTGGCG
TGCCCTCTAGATTTCCGGCTCTGGCTCTGGCACCGAGTTTACCCTGACAATCTCCAGCCTGCAGCCTGACGACTTCGCCACCTAC
TACTGCCAAGGCTACTTCTACTTCATCTCCCGACCTACGTGAACCTCTCGGCGGAGGCACCAAGGTGGAGATCAAGCGTACGGT
GGCTGCCCCCTCTGTGTTTCATCTTCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAAC
TCTACCCAGAGAAGCCAAGGTGCAGTGGAAAGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTGTCTCCACCTGACCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGAGGT
GACCCACAGGGCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCT
GCCAGCCCCAGAAGCTGCTGGAGGCCCTCTGTGTTCCCTCTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCCA
GAAGTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGCACAA
TGCCAAGACCAAGCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGA
ATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCC
AGAGAGCCCCAGGTCTACACCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTT
CTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACATAAAGACCACCCCTCCTGTGCTGGACTCTG
ATGGCTCCTTCTTCTGCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCATGCAT
GAGGCCCTGCACAACCGCTTACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 57: SI-75X2 Chain A Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNSLR
AEDTAVYYCARDGGSSAITSNNIWQGGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVKDRVEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDITLMI SR
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPG

>Sequence ID 58: SI-75X2 Chain A Nucleotide Sequence

GAGGTGCAGCTGGTTGAATCTGGCGGAGGATTGGTTACGCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCTTCTGGCTTACCAT
CTCCACCAACGCCATGTCCTGGGTCGACAGGCTCTGGCAAAGGCCTGGAATGGATCGGCGTGATCACCAGCAGAGATATTACCT
ACTACGCCTCCTGGGCAAGGGCAGATTACCATCAGCGGGACAACTCCAAGAACCCTGTACCTGCAGATGAATCCTGAGA
GCCGAGGACACCGCGTGTACTACTGTGCTAGAGATGGCGGCAGCAGCGCCATCACCTCCAACAATATTTGGGGCCAGGGCACCCT
GGTCACTGTGTCCTCTGCTAGCACCAAAGGCCCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTG
CCTGGGCTGCCTGGTGAAGGACTACTTCCCAGAGCCTGTGACTGTGCTCCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACC
TTCCCTGCTGTGCTGCAGAGCTCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTA
CATCTGCAATGTGAACCACAAGCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCC
CTCCCTGCCAGCCCCAGAGGCTGTGGAGGCCCTCTGTGTTCCCTCTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGG
ACCCCAAGAAGTCACTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGT
GCACAATGCCAAGACCAAGCCAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACT
GGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGC
CAGCCCAGAGAGCCCCAGGTCTACACCCTGCCTCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAA
AGGCTTCTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGG
ACTCTGATGGCTCCTTCTCTCTGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTGTGCT
ATGCATGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 59: SI-75X2 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMYDVSDRPSGVSDRFGSGSKSGNTASLIISGLQADDEA
DYCYSSYSSSTHVIFFGGTKVTVLGGGSGGGGSGGGGSGGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYWSWVRQAP
GKGLEWVANINRDGSASYVDSVKGRTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSSGGGSGGGG
SDVVMTQSPSTLSASVGDRTINCQASESISWLAWYQQKPKAPKLLIYEASKLASGVPSRFGSGSGSTFTLTIISSLPDDFAT
YYCQGYFYFISRTYVNSFGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
DSKSTYSLSLTLTSLKADYEKHKVYACEVTHQGLSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDITLMI SR
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV
MHEALHNRTQKSLSLSPG

>Sequence ID 60: SI-75X2 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCAACTCATGATCTATGATGTGATGATCGGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGACCAAGGTGACCGTCTTAGGCGGTGGCGG
TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCCTGGTCA
AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCCAAACATAAACCGCGATGGAAGTGCAGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAACGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGG
TCAGACGTCTGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAG
CATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTG
GGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACT
TATTACTGCCAAGGCTATTTTATTTTATTAGTCTGACTTATGTAAATTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
GGTGGCTGCCCTCTGTGTTTCTCTTCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACA
ACTTCTACCCAGAGAAGCCAAGGTGCAGTGGAAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGA
GGTGACCCACCAAGGCGCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGAGAGTGTGGAGGAGACCAAGACCCACACCTGCCCTC
CTGCCCCAGCCCCAGAAGCTGCTGGAGGCCCTCTGTGTTTCTCTTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACC
CCAGAAGTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGA
CAATGCCAAGACCAAGCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGC
TGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAG
CCCAGAGAGCCCCAGGTCTACACCCTGCCTCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAAGG
CTTCTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACT

CTGATGGCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCATG
CATGAGGCCCTGCACAACCGCTTACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 61: SI-7502 Chain A Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNSLR
AEDTAVYYCARDGSSSAITSNNIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPG

>Sequence ID 62: SI-7502 Chain A Nucleotide Sequence

GAGGTGCAGCTGGTTGAATCTGGCGGAGGATTGGTTCAGCCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCTTCTGGCTTCACCAT
CTCCACCAACGCCATGTCTGGGTCCGACAGGCTCCTGGCAAAGGCCTGGAATGGATCGGCGTGATCACCGGCAGAGATATTACCT
ACTACGCCTCCTGGGCCAAGGGCAGATTACCATCAGCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGAGA
GCCGAGGACACCGCGGTGTACTACTGTGCTAGAGATGGCGGCAGCAGCCATCACCTCCAACAATATTTGGGGCCAGGGCACCCCT
GGTCACTGTGTCTCTGCTAGCACAAAGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTG
CCCTGGGCTGCCTGGTGAAGGACTACTTCCAGAGCCTGTGACTGTGCTGGAAGTCTGGAGCCCTGACCTCTGGAGTGCACACC
TTCCCTGCTGTGCTGCAGAGCTCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTA
CATCTGCAATGTGAACCAAGCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCC
CTCCCTGCCCAGCCCCAGAGGCTGCTGGAGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGG
ACCCAGAAGTCACTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTCAACTGGTATGTGGATGGAGTGGAGGT
GCACAATGCCAAGACCAAGCCAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCCAGGACT
GGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGC
CAGCCCAGAGAGCCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAA
AGGCTTCTACCCAGTGAATTGTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGG
ACTCTGATGGCTCCTTCTTCTGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTCTGTC
ATGCATGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 63: SI-7502 Chain B Amino Acid Sequence

DVMTQSPSTLSASVGRVTINCAASESISSWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
YCGGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP
EVTCTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
REPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNRFTQKSLSLSPG

>Sequence ID 64: SI-7502 Chain B Nucleotide Sequence

GACGTGGTCATGACACAGAGCCCTTCCACACTGTCTGCCTCCGTGGGCGATAGAGTGACCATCAACTGTGAGGCCTCCGAGTCCAT
CTCCTCTTGGCTGGCTTGGTATCAGCAGAAGCCTGGCAAAGGCCCTTAAGCTGCTGATCTACGAGGCTTCCAAGCTGGCCTCTGGCG
TGCCCTCTAGATTTTCCGGCTCTGGCTCTGGCACCAGGTTTACCCTGACAATCTCCAGCCTGCAGCCTGACGACTTCGCCACCTAC
TACTGCCAAGGCTACTTCTACTTCATCTCCCGACCTACGTGAACCTCTTCCGGGAGGACCAAGGTGGAGATCAAGCGTACGGT
GGCTGCCCCCTCTGTGTTTCATCTTCCACCCAGTATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCTGCTCAACAAC
TCTACCCAGAGAAGCCAAGGTGCAAGTGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTGTCTCCACCCCTGACCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGAGGT
GACCCACCCAGGCTGAGCAGCCTGTGACCAAGAGCTTCAACCGAGGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCT
GCCCAGCCCCAGAAGCTGCTGGAGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCCA
GAAGTCACTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTCAACTGGTATGTGGATGGAGTGAAGTGCACAA
TGCCAAGACCAAGCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGA
ATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCC
AGAGAGCCCCAGGTCTACACCCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAAGGCTT
CTACCCAGTGAATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTG
ATGGCTCCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTCTGTCATGCAT
GAGGCCCTGCACAACCGCTTACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 65: SI-7507 Chain A Amino Acid Sequence

QVQLQESGGRLVQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLMNLSLRSE
DTAIYYCARGGYSSDIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS

SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPG

>Sequence ID 66: SI-7507 Chain A Nucleotide Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTGTCACTGACGTGTAAAAAAGCGGCATTGATCT
GTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGGCGATTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGAGGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAGAGCCCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGG
ACTACTTCCCAGAGCCTGTGACTGTGTCCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGC
TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAA
GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGG
CTGCTGGAGGCCCTCTGTGTTCCCTCTTCCCTCCCAAGCCCAAGGACACCCCTGATGATCTCCAGGACCCAGAAAGTCACCTGTGTG
GTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCC
CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTG
TACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACAT
TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAATAACAAGACACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTCTGTGCTGATGCATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGA

>Sequence ID 67: SI-7507 Chain B Amino Acid Sequence

DPQLTQSPSSLSATVGQRTVINCQSSQSVAKNNNLAWFQQKPGKPPKLLIYASTLAAGVPSRFSGSGSGTGQFTLTITRVQSEDF
TYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYLSSTLTLSKADYEKHVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLVWLKLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEA
LHNRFTQKSLSLSPG

>Sequence ID 68: SI-7507 Chain B Nucleotide Sequence

GATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGT
AGCGAAGAATAATAATTTGGCATGGTTCCAACAAAAACGGGTAAACCTCCTAACTCCTTATCTACTCAGCTTCAACCCTTGCCG
CGGTGTGCCCCAGCCGTTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCA
ACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGC
CCCCCTGTGTGTTATCTTCCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCTACC
CCAGAGAAGCCAGGTGCAGTGGAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTGTCTCCACCCCTGACCCCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGAGGTGACCCA
CCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAG
CCCCAGAAGCTGCTGGAGGCCCTCTGTGTTCCCTTCCCTCCCAAGCCCAAGGACACCCCTGATGATCTCCAGGACCCAGAAAGTC
ACCTGTGTGGTGGTGGATGTGTCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGCACAATGCCAA
GACCAAGCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGA
AGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAG
CCCCAGGTCTACACCCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTACCC
CAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAATAACAAGACACCCCTCCTGTGCTGGACTCTGATGGCT
CCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTCTGTGCTGATGCATGAGGCC
CTGCACAACCGCTTCAACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 69: SI-68P13 Chain A Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNNWPTTFPGTKLTVLGGGSGGGGSGGGGSGGGGSGVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
EWLGVIWSSGNTDYNTPFTSRFTITKDN SKNQVFKLRSVRADDTAIYCARALTYDYEFAYWGGTGLVTVSSGGGSGGGGSEV
QLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYQMNSLRAE
DTAVYYCARDGGSSAITSNNIWGGTGLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGGGGGSGGGGSDVMTQSPSSVSASVGRVITITCQASQNI RTYLSWYQQKPGKAPKLLIYAAANLASGVP

SRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGT DYVGGAFGGGTKLTVLGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQP
 GGSRLSCTASGFTISSYHMQWVRQAPGKGLEIYIGTISSGNVY YASSARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARD SG
 YSDPMWQGQTLTVTVSS

>Sequence ID 70: SI-68P13 Chain A Nucleotide Sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACGCGGACTTTCTCTTG CAGGGCAAGTCAATCCAT
 AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAAGTATGCAAGTGAAGTCTATTCCGGTA
 TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
 TACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTAGGCGGTGGCGGTAGTGGGGGAGG
 CGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
 CGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGGCAGGCACCCGGCAAGGTTTG
 GAATGGCTGGGTGTTATTTGGTCAGGTGGAAATACAGACTATAACACCCCTTTTACAAGTCGGTTCACAATTACGAAAGATAATTC
 CAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
 ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTGTAAACAGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
 CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCTGTG CAGCCTCTGGATTACCATCAGTAC
 CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACATACTACG
 CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATCCAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
 GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTCAC
 CGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCTTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
 CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCCAATCTTGTGACAAAACCTCACACATGCCCCACCGT
 GCCCAGCACCTGAAGCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCT
 GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGCGGTGGAGGTGCATAA
 TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGA
 ATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
 CGAGAACCACAGTGTATACCCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTT
 CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCG
 ACGGCTCCTTCTCTCTCTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
 GAGGCTCTGCAACACCACTACACGCAAGAGCCCTCTCCGTCTCCGGGTGGCGGCGGTTCAAGTGGTGGGGGATCCGACGT
 TGTGATGACGCGATCTCCTAGTTCAGTATCAGCCTCTGTTGGGGATCGAGTCAGGATTACATGCCAGCGAGCGAAAATATTAGGA
 CGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCTCATTTACGCCGTGCCAACTTGGCTAGTGGAGTACCT
 TCACGCTTTAGTGGGTGAGTTCTGGAACAGATTTACGTTGACGATCTCCGATTTGGAACCAGGGGACGCTGCCACGTATTATTG
 CCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTGGTGGTGGTGGTTCAG
 GCGGGGGGGGTTCCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCA GTTGGTTGAAAGTGGGGGGGACTCGTTCAGCCT
 GGAGGCTCTTTGCGACTTTCTGTACCGCTTCTGGGTTCACTATAAGTTTCATATCATATGCAATGGGTAAGACAGGCGCCTGGTAA
 GGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGCTTATTACGCCTCATCCGCGCGGGGGAGGTTTACAATTTCCAGGC
 CTTCTAGCAAAAACACGGTAGACTCTGCAAATGAACTCTCTTCGCGCTGAAGATACAGCAGTCTACTACTGCGCCAGGGATTACAGG
 TATTCTGACCCCATGTGGGGGCGAGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 71: SI-68P13 Chain B Amino Acid Sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHWYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
 CFQGSVYPFTFGQGTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLSTLCAFSGFLSTSGMGVWIRQPPGKG
 LEWLAHIWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGQTLTVTVSSGGGSGGGGSDV
 VMTQSPSTLSASVGRVTINCAQASEISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDGFATYYC
 QGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
 DSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEV
 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEA
 LHNRFTHQLSLSPGGGGSGGGGSDIQMTQSPSTLSASVGRVTITCAQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSR
 FSGSGSGTEFTLTISLQPDGFATYYCQGYSGWGNVDNVFGGTKVTVLGGGSGGGGSGGGGSGGGGSEVQLLES GGGLVQPGGS
 LSLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAACAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAF
 SFDYAMDLWGQTLTVTVSS

>Sequence ID 72: SI-68P13 Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTTCCGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAGATTTTGCAACTTATTAT
 TGTTTCCAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCTAGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTT CAGCCAGGACAGACCC

TTAGCCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTCGGCTGGATTCCGCAGCCTCCCGGCAAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGTGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTCGCGCGGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGACGGGACTCTCGTCACGGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
 GTGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
 TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAGCTCCTGATCTATGAAGCATCCAAACTGGCATCTGGGGTCCCAT
 CAAGGTTACAGCGCAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCACTTATTACTGC
 CAAGGCTATTTTTATTATTAGTCTGACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
 ACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATC
 CCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
 GACAGACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCCAAGTCACCCA
 TCAGGGCCTGAGTCTCGCCCGTACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCCAACCGTGCAGCAG
 CACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC
 ACATGCGTGGTGGTGGACGTGAGCCAGAACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA
 GACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCA
 AGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAA
 CCACAGGTGTACACCCTGCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGACGCTGTGGTGCCTGGTCAAAGGCTTCTATCC
 CAGCGACCTACCGCTGGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAAGACCACGCCTCCGTGCTGGACTCCGACGGCT
 CTTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCACAACAGATTACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTCAGAT
 GACACAGTCACCGTCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTCACACC
 TCAACTGGTATCAACAGAAACCCGTAAGCAGCAGAGCTGCTCATCTACAAGGCATCAACTCTTGCCCTCAGGTGTGCTAGTCGC
 TTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACTATTGTTCAGCA
 GGGTTATAGTTGGGAAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGGAGGAAGTGGCGCGGCG
 GAAGCGGAGGTGTGGCTCCGGCGGGGTGGAAGCGAAGTGCAATTTGCTCGAAAAGTGGTGGCGGACTGTGCAACCTGGTGGAAAG
 CTCTCACTCTCTTGCGCGCGGAGTGGTTTTAGCTTCAGTAGCGGTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCCCT
 TGAGTGGATTGCGTGTATCGCCCGGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTACAATCTCCAGGG
 ACAACTCAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTT
 AGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 73: SI-68P17 Chain A Amino Acid Sequence

DVMTQSPSTLSASVGRVTINCAQASESISWLAHYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLSLPDDFATY
 YCQGYFYFISRTYVNSFGGGTKVEIKGGGSGGGGSGGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSVMRQA
 PGKGLEWIGVITGRDITYYASWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGGSSAITSNNIWQGTTLVTVSSGGGGSG
 GGGSQVQLQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKLEWLGVIWSSGNTDYNTPFTSRFTITKDNSKNQVYFKL
 RSVRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSG
 VHTFPAVLQSSGLYSLSSVTVPSSSLGTQYICNVNHKPSNTKVKRVEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLM
 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISK
 AKGQPREPQVYTLPPSRDELTKNQVLSLCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSDVMTQSPSSVSASVGRVTITCAQASQNIPTYLSWYQQKPKAPKLLIYAAANL
 ASGVPSRFSGSGSGTDFTLTISLLEPGDAATYYCQSTYLGTIDYVGAFGGGKLTVLGGGGSGGGGSGGGGSGGGSEVQLVESGG
 GLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGGNVYASSARGRFTISRPSKNTVDLQMNLSRAEDTAVYYC
 ARDSGYSDPMWQGGLTVTVSS

>Sequence ID 74: SI-68P17 Chain A Nucleotide Sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
 TAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCAAGCTCCTGATCTATGAAGCATCCAAACTGGCATCTGGGG
 TCCCATCAAGGTTACAGCGGAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCACTTAT
 TACTGCCAAGGCTATTTTTATTATTATTAGTCTGACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGG
 CGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG
 TCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCGCCAGGCT
 CCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGTATACATACGCGAGCTGGGCGAAAGGCAGATTACCAT
 CTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGC
 GGTGGTGGATCACAAGTACAGTTCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGACTGTTTC
 AGGCTTTAGCCTTACGAACCTATGGAGTTCACTGGATTCCGGCAGGACCCCGCAAAGGTTTGAATGGCTGGGTGTTATTTGGTCAG
 GTGGAAATACAGACTATAACACCCCTTTACAAGTCGGTTACAAATTACGAAAGATAATTCCAAAAATCAAGTTTATTTCAAGTTG
 AGATCCGTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGTATTGGGGGCA
 AGGGAAGTCTTGTACAGTCTCCAGTGTAGCACCAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGG
 GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGGC
 GTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCAC

CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTC
 ACACATGCCCACCGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCCCTCATG
 ATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
 CGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTCTGC
 ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGGCGGCTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAA
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTATACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAAGCTGTCTCTG
 CGCCGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATAAGACCACGCCTC
 CCGTGTGGACTCCGACGGCTCCTTCTTCTCTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
 TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGCGCGCGGTTCAGGTGG
 TGGGGGATCCGACGTTGTGATGACGCAGTCTCCTAGTTTCACTATCAGCGTCTGTGGGGATCGAGTCACGATTACATGCCAGGCGA
 GCCAAAATATTAGGACGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAACTCCTCATTACGCCGCTGCCAACTTG
 GTCAGTGGATACCTTACCGTTTGTGGGTGAGTCTTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACCAAGGGGACGG
 TGCCACGTATTATTGCCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTG
 GTGGTGGTGGTTCAGGCGGGGGGGGTTCCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCACTTGGTTGAAAGTGGGGGG
 GGAATCGTTTCAAGCTGGAGGCTCTTTCGCACTTTCTGTACCGCTTCTGGGTTCACTATAAGTTTATATCATATGCAATGGGTAAAG
 ACAGGCGCCTGGTAAGGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGTCTATTACGCCCTCATCCGCGCGGGGAGGT
 TTACAATTTCCAGGCCTTCTAGCAAAAACACGGTAGATCTGCAATGAACTCTCTTCGCGCTGAAGATAACAGCAGTCTACTACTGC
 GCCAGGGATTCAAGGTATTCTGACCCCATGTGGGGCAGGGCACATTGTTTACCGTGTCTCTTGA

>Sequence ID 75: SI-68P17 Chain B Amino Acid Sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSNDHTLTISSEMPEDFATYY
 CFQGSVYPTFFGQGTQKTVLGGGGSGGGSGGGSGGGSGVTLKESGPGLVQPGQTLTLTCAFSGFSLSSTSGMGVWIRQPPGKG
 LEWLAIHWDDDKRYNPALKSRITISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFFDYWGQGLVTVSSGGGGSGGGGSEI
 VLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVYYC
 QQNNWPTTFPGTKLTVLRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS
 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTCTPPCPAPEAAGGFSVFLFPPKPKDTLMISRTPEVTCVTV
 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPREPQVYT
 LPPSRDELTKNQVSLWLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNR
 TQKSLSLSPGGGGSGGGGSDIQTQSPSTLSASVGDRTITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFSGSG
 SGTEFTLTISLQPDFATYYCQQGYSWGNVDNVFGGKTQKTVLGGGGSGGGSGGGSGGGGSEVQLLESGGGLVQPGGSLSLSC
 AASGFSFGYDMCWVRQAPGKGLEWIAICAAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDY
 MDLWQGGLTVTVSS

>Sequence ID 76: SI-68P17 Chain B Nucleotide Sequence

GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCACTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGAACCTATTAT
 TGTTTCCAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCTTAGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACTTGAAGGAATCTGGCCCCGGCCTTGTTTCAAGCAGGACAGACCC
 TTAGCCTCACCTGTGCCTTCACTGGTCTTCTCTTAGCACTAGCGGTATGGGGGTGGCTGGATTCGGCAGCCTCCCGGCAAAGGT
 CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAATAACAGTGTACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTCGCGCGGATGGAACCTCTGTT
 CTACTACTTTGATTATTTGGGGCAGGGGACTCTCTGTCAGGCTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAAATC
 GTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACCGCGCACTTTCTCTTGCAGGGCAAGTCAATCCATAGGGAC
 TAATATACATTGGTATCAACAAAAGCCAGGTAAACCAACCCAGGCTTTTATTAGTATGCAAGTGAAGTCTATTTCCGGTATCCCTG
 ACCGCTTCTCTGGATCAGGCAAGTGGCACAGAGTTCACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCCGTGTATTACTGC
 CAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTACGTACGGTGGCTGCACCATCTGTCTTCAT
 CTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAG
 TACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACTACAGC
 CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAAGCCGCGG
 GGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGTG
 GACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
 GGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGGC
 CGGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAACATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
 CTGCCCCCAAGCCGGATGAGTGAACCAAGACAGGTCAAGCTGTGGTGGTCAAGGCTTCTATCCAGCGACATCGCGGT
 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATA
 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACAGATT
 ACCGAGAAGAGCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTGAGTACACAGTCAACGTC
 TACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTTCAACCTCACTGGTATCAAC
 AGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCACTCTTGCCTCAGGTGTGCCTAGTTCGCTTCTCCGGGAGCGGG

TCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACTATTGTCAGCAGGGTTATAGTTGGGG
 AAATGTTGACAAATGTGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGAGGAAGTGGCGGCGCGGAAGCGGAGGTGGTG
 GCTCCGGCGGGGGTGGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGCCTCTCACTCTCTTGC
 GCGGCGAGTGGTTTTAGCTTCAGTAGCGGCTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGCCTTGAGTGGATTGCGTG
 TATCGCCGCGGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTCACAATCTCCAGGGACAACCTCAAAAAATA
 CATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTCAGCATTAGCTTCGATTATGCA
 ATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 77: SI-68P15 Chain A Amino Acid Sequence

EIVMTQSPSTLSASVGDRIITCQASESISSWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
 YCQGYFYFISRTYVNSFGQGTKLTVLGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSVMRQA
 PGKGLEWVGIVITGRDITYYASWAKGRFTISRDTSKNTVYLMNSLRAEDTAVYYCARDGGSSAITSNNIWQGTLLTVSSGGGSG
 GGGSQVQLQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPKGLEWLGVIWGGNTDYNTPFTSRFTITKDNSKNQVYFKL
 RSVRADDTAIYYCARALTYDYEFAYWQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
 VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPPCPAPEAAAGGPSVFLFPPKPKDTLM
 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI
 SKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSDVMTQSPSSVSASVGDRIITCQASQNIIRTYLSWYQQKPKAPKLLIYAAANL
 ASGVPSRFSGSGSGDTFTLTISDLEPGDAATYYCSTYLGTDYVGGAFGGGKLTVLGGGSGGGGSGGGGSEVQLVESGG
 GLVQPGGSLRLSCTASGFTISSYHMQWVRQAPKGLLEYIGTISGGNVYYASSARGRFTISRPSKNTVDLQMNSLRAEDTAVYYC
 ARDSGYSDDPMWQGTLLTVSS

>Sequence ID 78: SI-68P15 Chain A Nucleotide Sequence

GAAATCGTTATGACGCAGAGTCCCTCCACGCTCTCCGCTAGTGTGGGGATCGCGTCATTATCACATGCCAGGCCTCCGAGTCAAT
 CAGCAGCTGGCTTGCATGGTATCAACAGAAGCCGGGAAAAGCTCCTAAATTGCTGATCTATGAAGCGTCAAATTTGGCGTCTGGTG
 TCCCATCTAGGTTCTCCGGCTCTGGGTCTGGTGCGGAATTTACTTTGACAATCTCCAGTCTTCAACCAGACGATTTTCGTACCTAC
 TACTGCCAAGGGTATTTCTATTTTATAAGCCGGACATATGTAACTCCTTCGGCCAAGGAACAAAGTTGACTGTTCTTGGTGGCGG
 AGGCAGTGGTGGCGGGGCGAGCGAGGTGGTGGTTGAGGGGGTGGTGGGAGCGAAGTCCAATTGGTAGAAAGTGGCGGTGGTCTGG
 TGCAACCTCGGCGGATCTCTTCGCTCTCATGCGCGCTGTGTCGAGGCTTACTATTTCACTAATGCGATGAGCTGGGTTCGCCAGGCC
 CCCGGCAAAGGACTTGAGTGGGTGCGCGTCATCACCGGCAGGGACATTACATACTATGCGAGTTGGGCAAAGGGCAGGTTACGAT
 TAGCCGCGATACTTCAAAGAATACCGTTTACCTTCAAATGAATAGCTTGAGGGCGGAAGACACAGCTGTGTATTACTGCGCGAGGG
 ATGGAGGTAGTTCGCCATAACTTCCAACAACATATGGGACAAGGCACGCTGGTACTGTCTCGAGTGGCGGTGGAGGGTCCGGC
 GGTGGTGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTC
 AGGCTTTAGCCTTACGAAGTATGGAGTTCACTGGATTGCGCAGGCACCCGGCAAAGGTTTGAATGGCTGGGTGTTATTTGGTCAG
 GTGAAATACAGACTATAACACCCCTTTACAAGTCGGTTTACAATACGAAAGATAATTCCAAAAATCAAGTTTATTTCAAGTTG
 AGTACCGTCCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGTATTGGGGGCA
 AGGGACTCTTGTAACAGTCTCCAGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGG
 GCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCGGC
 GTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
 CCAGACCTACATCTGCAACGTGAATCACAAGCCGACGAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTC
 ACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATG
 ATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGG
 CGTGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAAGCTCCTCACCCTCTCTGC
 ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGCTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTATACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAAGCTGTCTCTG
 CGCGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTC
 CCGTGTGAGTCCGACGGCTCTTCTTCTCTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
 TGCTCCGTGATGATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTGGCGGCGGCGGTTCAAGTGG
 TGGGGGATCCGACGTTGTGATGACGCAGTCTCTAGTTTCAATATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCGA
 GCCAAAATATTAGACGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCTATTACGCCGCTGCCAACTTG
 GCTAGTGGAGTACCTTACGCTTTAGTGGGTCAAGTCTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACCAGGGGACGC
 TGCCACGTATTATTGCCAGTCCACCTACCTCGGACTGACTACGTTGGTGGGGGCTTGGCGGAGGAACAACTCACTGTACTTG
 GTGGTGGTGGTTCAAGCGGGGGGGGTTCGGCGGAGGCGGTTCTGGGGTGGAGGTTCCGAGGTTCACTTGGTTGAAAGTGGGGG
 GGACTCGTTACAGCTGGAGGCTCTTTCGCACTTCTTGTACCGCTTCTGGGTTCACTATAAGTTTATATCATATGCAATGGGTAAG
 ACAGGCGCCTGTTAAGGGACTTGAATACATAGGAACAAGCTCTGGTGGTAACGTCATTACGCTCATCCGCGCGGGGGAGGT
 TTACAATTTCCAGGCTTCTAGCAAAAACAGGTAGATCTGCAAAATGAACCTCTTTCGCGCTGAAGATACAGAGTCTACTACTGC
 GCCAGGATTACAGGTATTCTGACCCCATGTGGGGGACGGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 79: SI-68P15 Chain B Amino Acid Sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTIISSMEPEDFATYY
 CFQGSVYPFTFGQGTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLSTLTCAFSGFSLSTSGMGVWIRQPPGKG
 LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYDWGQGLTVTVSSGGGSGGGGSEI
 VLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLIKYASESISGIPDRFSGSGSGTEFTLTIISSVQSEDFAVYYC
 QQNNNNWPTTFPGPTKLTVLRTVAAPSVEFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS
 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGSPVFLFPPKPKDTLMISRTPEVTCVTV
 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYT
 LPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNR
 TQKSLSLSPGGGGSGGGGSDIQTQSPSTLSASVGRVITITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFSGSG
 SGTEFTLTIISSLPDDFATYYCQQGYSWGNVDNVFGGGTKVTVLGGGSGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLSLSC
 AASGFSFSSGYDMCWVRQAPGKLEWIAICIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYA
 MDLWGQGTLLTVSS

>Sequence ID 80: SI-68P15 Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTCCGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
 TGTTCAGGGGAGCGTGATCCCATTCACCTTCGGGCGAGGGACAAAAGTGACCGTCTAGGCGGTGGCGGTAGTGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTAGCCAGGACAGACCC
 TTAGCCTCACCTGTGCCTTCAGTGGTTCCTCTTAGCACTAGCGGTATGGGGGTGGCTGGATTCCGCGAGCCTCCCGGCAAGGT
 CTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGCGAGGGACTCTCGTACCGGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAAATC
 GTCCTTACACAACTCTCCTAGCACACTGAGTGTGAGCCCCGGCGAAGCGCGCACTTCTCTTGCAGGGCAAGTCAATCCATAGGGAC
 TAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAAGTATGCAAGTGAGTCTATTTCCGGTATCCCTG
 ACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTATTACTGC
 CAACAGAATAATAACTGGCCGACTACCTTCGGACCGGTACAAAGCTGACCGTTTACGTACGGTGGCTGCACCATCTGTCTTCAT
 CTTCGCCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAG
 TACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
 CTCAGCAGCACCTGACGTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTGGAGGACACACCTCACACATGCCCCACCGTGCCGACCTGAAGCCGCGG
 GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGT
 GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
 GGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCGAGGACTGGCTGAATGGCAAGGAGTACAAGTGG
 CGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
 CTGCCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
 GGAGTGGGAGAGCAATGGGAGCGCGGAGAACAACTACAAGACCACGCCCTCCCGTGGTGGACTCCGACGGCTCCTTCTCTATA
 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACAGATT
 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTCAGATGACACAGTCAACGTC
 TAGGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTCACACCTCAACTGGTATCAAC
 AGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCTCAGGTGTGCCTAGTCTCGCTTCTCCGGGAGCGGC
 TCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACTATTGTGAGCAGGGTTATAGTTGGGG
 AAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGAGGAAGTGGCGGCGCGGAAGCGGAGGTGGT
 GCTCCGGCGGGGTGGGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGCCTCTCACTCTCTTGC
 GCGGCGAGTGGTTTTAGCTTCACTAGCGGCTACGATATGTGCTGGGTAAAGACAGGCTCCTGGTAAAGGCTTGAAGGATTGCGTG
 TATCGCCGCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTACAATCTCCAGGACAACCTAAAAAATA
 CATTGTACCTCCAGATGAATAGCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTTAGCTTCGATTATGCA
 ATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 81: SI-68P18 Chain A Amino Acid Sequence

DVQMTQSPSTLSATVGRVITINCQASESISSWLAWYQQKPGQPPKLLIYEASKLASGVPSRFSGSGSGTEFTLTIISSLPQDDFATY
 YCQGYFYFISRTYVNSFGGGTRVEIKGGGSGGGGSGGGGSGGGGSGQLLESGGRLIKPGATLRLTCKTSGETIISTNAMS WVRQPP
 GKLEWIGVITGRDITYYASWAKGRFTISKTSINTVFLQMRSLRAEDTAVYYCARDGSSAITSNNIWRGTLTVTVSSGGGSGGGG
 GSQVQLQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKLEWLGVIWSSGNTDYNTPFTSRFTITKDN SKNQVYFKLRS
 VRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
 TFAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEAAGGSPVFLFPPKPKDTLMIS
 RTPEVTCVTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAK
 GQPREPQVYTLPPSRDELTKNQVSLCAVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLVSLKLTVDKSRWQQGNVFCSC
 VMHEALHNYHTQKSLSLSPGGGGSGGGGSDVMTQSPSSVSASVGRVITITCQASQNIIRTYLSWYQQKPGKAPKLLIYAAANLAS
 GVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTIDYVGGAFGGGKLTVLGGGSGGGGSGGGGSGGGGSEVQLVESGGGL

VQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISSGGNVYASSARGRFTISRPSSKNTVDLQMNSLRAEDTAVYYCAR
DSGYSDPMWQGTLTVTVSS

>Sequence ID 82: SI-68P18 Chain A Nucleotide Sequence

GATGTGCAGATGACCCAGAGCCCCGAGCACCCCTGAGCGCGACCGTGCGCCAGCGCGTGACCATTAACTGCCAGGCGAGCGAAAGCAT
TAGCAGCTGGCTGGCGTGGTATCAGCAGAAACCGGGCCAGCCGCCGAAACTGCTGATTTATGAAGCGAGCAAACCTGGCGAGCGGCG
TGCCGAGCCGCTTTAGCGGCAGCGCGAGCGGCACCGAATTTACCCTGACCATTAGCAGCCTGCAGAGCGATGATTTTGCAGCCTAT
TATTGCCAGGGCTATTTTTATTTTATTAGCCGCACCTATGTGAACAGCTTTGGCGGCGGCACCCGCGTGGAAATTAAAGGCGGTGG
CGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGCAGCTGCTGGAAGCGGCGGCGCCCTGATTA
AACCGGCGCGGACCCCTGCGCCTGACCTGCAAAACAGCGGCTTTACCATTAGCACCAACGCGATGAGCTGGGTGCGCCAGCCGCCG
GGCAAAGGCTTGAATGGATTGGCGTGATTACCGGCCGCGATATTACCTATTATGCGAGCTGGGCGAAAGGCGGCTTTACCATTAG
CAAAACAGCATTAACACCGTGTTTCTGCAGATGCGCAGCCTGCGCGCGGAAGATACCGCGGTGTATTATTGCGCGCGCGATGGCG
GCAGCAGCGCGATTACCAGCAACAACATTTGGGGCGCGGCACCCCTGGTGACCGTGAGCAGCGGCGGTGGAGGGTCCGGCGGTGGT
GGATCACAAGTACAGTTGCAGCAATCCGGTCCCGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTCAGGCTT
TAGCCTTACGAATATGGAGTTCACTGGATTCCGCGAGGCACCCGCGCAAAGGTTTGAATGGCTGGGTGTTATTTGGTCAGGTGGAA
ATACAGACTATAACACCCCTTTACAAGTCGGTTCACAATTACGAAAGATAATTCAAAAATCAAGTTTATTTCAAGTTGAGATCC
GTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGTATTGGGGGCAAGGGAC
TCTTGTAACAGTCTCCAGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAG
CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC
ACCTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTTGGGACCCAGAC
CTACATCTGCAACGTGAATCACAGCCCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTGTGACAAAACCTCACACAT
GCCCACCGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCCCTCATGATCTCC
CGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCACTGGTACGTGGACGGCGGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTTCCACCGTCCGCAACGAGG
ACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAACCACAGGTGTATACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGT
CAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGC
TGGACTCCGACGGCTCCTTCTCTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGCGGCGGTTACAGTGGTGGGG
ATCCGACGTTGTGATGCGCAGTCTCCTAGTTCACTGATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCGAGCCAAA
ATATTAGGACTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCCTATTACGCGCTGCCAAGTGGCTAGT
GGAGTACCTTCACGCTTTAGTGGGTGAGGTTCTGGAACAGATTTTACGTTGACGATCTCCGATTGGAACAGGGGACGCTGCCAC
GTATTATTGCCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTACTGTACTTGGTGGT
GTGGTTGAGGCGGGGGGGTTCGCGCGGAGGCGGTCTTGGGGGTGGAGGTTCCGAGGTTGAGTTGGTTGAAAGTGGGGGGGACTC
GTTGAGCCTGGAGGCTCTTTCGCACTTTCTTGTACCGCTTCTGGGTTCACTATAAGTTTCAATATCATATGCAATGGGTAAAGACAGGC
GCCTGGTAAGGGAAGTGAATACATAGGAACAATAAGCTCTGGTGGTAACGCTTATTACGCTCATCCGCGCGGGGGAGGTTTACAA
TTTCCAGGCTTCTAGCAAAAACCGGTAGATCTGCAAAATGAACCTCTTTCGCGCTGAAGATACAGCAGTCTACTACTGCGCCAGG
GATTGAGGTTATTCTGACCCCATGTGGGGGAGGCGACATTGGTTACCGTGTCTCTTGA

>Sequence ID 83: SI-68P18 Chain B Amino Acid Sequence

ENVLTQSPASLSASPERGVITITCSASSSVSYMHYQKPKGQAPKLWIYDTSKLASGVPSRFGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPFTFGQTKVTVLGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLSTLCAFSGFLSTSGMGVWIRQPPGKG
LEWLAIHWDDDKRYNPALKSRLTISKDTSKNQVLYQMNSLDAEDTAVYYCARMELWSYFFDYWGQGLTVTVSSGGGSGGGGSEI
VLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQKPKGKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVYYC
QQNNNWPTTFGPGTKLTVLRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS
LSSTLTLSKADYEEKHKVYACEVTHQGLSPVTKSFNRGECGGDKHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVTV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYT
LPISRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNR
TQKSLSLSPGGGGSGGGGSDIQTQSPSTLSASVGRVITITCQASQSISSHLNWYQKPKGKAPKLLIYKASTLASGVPSRFGSG
SGTEFTLTISLQPDFFATYYCQQGYSWGNDNVFGGGTKVTVLGGGSGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLSLSC
AASGFSFSSGYDMCWVRQAPGKLEWIAACIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYA
MDLWQGQGLTVTVSS

>Sequence ID 84: SI-68P18 Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCCTACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCCGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGTGATCCATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCTTAGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTGAGCCAGGACAGACCC
TTAGCCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGTTCGGCTGGATTCCGCAGCCTCCCGGCAAAGGT

CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGTGACTTGCAAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGACAGGGGACTCTCGTCACGGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAAATC
 GTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACGCGCGACTTTCTCTTGACGGGCAAGTCAATCCATAGGGAC
 TAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAGTATGCAAGTGAGTCTATTTCCGGTATCCCTG
 ACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACTACCATATCTAGTGTGCAATCAGAGGACTTCGCCGTGTATTACTGC
 CAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTACGTACGGTGGCTGCACCATCTGTCTTCAT
 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAG
 TACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
 CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAATCACACATGCCACCGTGCCAGCACCTGAAGCCGCGG
 GGGACCGTCACTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTCAATCTGGTGGTGGT
 GACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA
 GGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGGC
 CGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
 CTGCCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAGCCTCCCCTGCTGGACTCCGACGGCTCCTTCTTCTCTATA
 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACAGATT
 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTGAGATGACACAGTCACCGTC
 TACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTCACACCTCACTGGTATCAAC
 AGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCTCAGGTGTGCCTAGTCTGCTTCTCCGGGAGCGGC
 TCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACTATTGTGAGCAGGGTTATAGTTGGGG
 AAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGAAGTGTGTTGGGAGGGGGAGGAAGTGGCGCGCGCGGAAGCGGAGGTGGT
 GCTCCGGCGGGGTGGAAGCGAAGTGAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGCCTCTCACTCTCTTGC
 GCGCGAGTGGTTTATAGCTTACGTAGCGGCTACGATATGTGCTGGGTAAAGACAGGCTCCTGGTAAAGCCTTGAAGTGGATTGCGTG
 TATCGCGCGCGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTACAATCTCCAGGGACAACCTAAAAAATA
 CATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTTAGCTTCGATTATGCA
 ATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 85: SI-68P19 Chain A Amino Acid Sequence

DVVMTQSPSSLSASVGRVITISQASESISSWLAWYQKPKGPQAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLLEPEDFATY
 YCQGYFYFISRTYVNSFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGGGGSLVSGGGGLVKPGGSLRLSCAASGFTISTNAMSWVRQAP
 GKGLEWVGVIITGRDITYYASWAKGRFTISKTSKNTVYLMNSLRAEDTAVYYCARDGGSSAITSNNIWGGTGLTVTVSSGGGSGGG
 GSQVQLQSSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKLEWLGVIWSGNTDYNTPFTSRETITKDNSKNQVYFKLRS
 VRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVH
 TFFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKHTHTCPPEAPEAAGGFSVFLFPPKPKDTLMIS
 RPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGKEYKCAVSNKALPAPIEKTI SKAK
 GQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS
 VMHEALHNHYTQKLSLSLSPGGGGSGGGGSDVVMTQSPSSVSASVGRVITITQASQNIPTYLSWYQKPKGAPKLLIYAAANLAS
 GVPSPRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTDYVGGAFGGGTKLTVLGGGGSGGGGSGGGGSEVQLVESGGGL
 VQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGGNVYASSARGRFTISRPSSKNTVDLQMNLSLRAEDTAVYYCAR
 DSGYSDPMWQGTLTVTVSS

>Sequence ID 86: SI-68P19 Chain A Nucleotide Sequence

GATGTGGTGATGACCCAGAGCCCGAGCAGCCTGAGCGCGAGCGTGGGCGATCGCGTGACCATTAGCTGCCAGGCGAGCGAAAGCAT
 TAGCAGCTGGCTGGCGTGGTATCAGCAGAAACCGGGCCAGGCGCCGAAACTGCTGATTTATGAAGCAGCAAACTGGCGAGCGGCG
 TGCCGAGCCGCTTTAGCGGCAGCGGCAGCGGCACCGAATTTACCCTGACCATTAGCAGCCTGGAACCGGAAGATTTTGCACCTAT
 TATTGCCAGGGCTATTTTATTTTATTAGCCGCACCTATGTGAACAGCTTTGGCGGGCGCACCAAGTGGAAATTAAGGCGGTGG
 CGGTAGTGGGGGAGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGCAGCTGGTGGAAAGCGGGCGGCGGCTGGTGA
 AACCGGGCGGCAGCCTGCGCCTGAGCTGCGCGCGAGCGGCTTTACCATTAGCACCACCGCATGAGCTGGGTGCGCCAGGCGCGG
 GGCAAGGCGCTGGAATGGGTGGCGTGATTACCGGCCGCGATATTACCTATTATGCGAGCTGGGCGAAAGGCGCTTTACCATTAG
 CAAAACAGCAAAAACACCGTGTATCTGCAGATGAACAGCCTGCGCGCGGAAGATACCGCGGTGTATTATTGCGCGCGCATGGCG
 GCAGCAGCGCGATTACAGCAACAACATTTGGGGCCAGGGCACCCCTGGTGACCGTGAGCAGCGCGGTGGAGGGTCCGGCGGTGGT
 GGATCAAGTACAGTTGCAGCAATCCGGTCCCGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTCAGGCTT
 TAGCCTTACGAATATGGAGTTCACTGGATTCCGCGAGGACCCCGCAAAGTTTGAATGGCTGGGTGTTATTTGGTCAGGTGGAA
 ATACAGACTATAACACCCCTTTACAAGTCGGTTACAATTACGAAAGATAATTCCAAAAATCAAGTTTATTTCAAGTTGAGATCC
 GTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGTATTGGGGGCAAGGGAC
 TCTTGTAACAGTCTCCAGTGCTAGACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAG
 CGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGCGGTGCAC
 ACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGAC
 CTACATCTGCAACGTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACAT

GCCCACCGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCC
 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
 GGTGCATAATGCCAAGACAAAGCCGCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCCTCTGCACCAGG
 ACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAA
 GGGCAGCCCCGAGAACACAGGTGTATACCCTGCCCCCATCCGGGATGAGGTGACCAAGAACCAGGTACGCTGTCTTGC GCGGT
 CAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGC
 TGGACTCCGACGGCTCCTTCTTCTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCCTCTCCCTGTCTCCGGGTGGCGGGCGGCTTCAAGTGGTGGGGG
 ATCCGACGTTGTGATGACGCAGTCTCCTAGTTCAGTATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCAGGCCAAA
 ATATTAGGACGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCCTCATTTACGCCGCTGCCAATTGGCTAGT
 GGAGTACCTTCACGCTTTAGTGGGTCAAGTTCGGAACAGATTTACGTTGACGATCTCCGATTGGAACAGGGGACGCTGCCAC
 GTATTATTGCACTCCACCTACCTCGGGACTGACTACGTTGGTGGGCGTTCGGCGGAGGAACAAAACCTCACTTGGTGGTG
 GTGGTTCAAGCGGGGGGGTTCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCAAGTGGTTGAAAGTGGGGGGGACTC
 GTTCAGCCTGGAGGCTCTTTCGCACTTTCTTGTACCGCTTCTGGGTTCACTATAAGTTCATATCATATGCAATGGGTAAACAGGC
 GCCTGGTAAGGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGTCTATTACGCCTCATCCGCGCGGGGAGGTTTACAA
 TTTCCAGGCCCTCTAGCAAAAACACGGTAGATCTGCAAAATGAATCTCTTCGCGCTGAAGATACAGCAGTCTACTACTGCGCCAGG
 GATTCAAGGTATTCTGACCCCATGTGGGGGCGAGGACATTGGTTACCGTGTCTCTTGA

>Sequence ID 87: SI-68P19 Chain B Amino Acid Sequence

ENVLTSQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
 CFQGSVYPFTFGQTKVTVLGGGSGGGGSGGGGSGGGGSGVTLLKESGPGLVQPGQTLSLTCAFSGFLSTSGMGVWIRQPPGKG
 LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYDWGQGLVTVSSGGGSGGGGSEI
 VLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVSQSEDFAVYYC
 QQNNWPTTFGPGTKLTVLRVTVAAPSVFIFFPSDEQLKSGTASVCLLNFFYPREKAVQWKVDNALQSGNSQESVTEQDSKSTYS
 LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPKPKDLMISRTEPVTCVVV
 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYT
 LPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNR
 TQKSLSLSPGGGGSGGGGSDIQTQSPSTLSASVGRDVTITCQASQSISSHLNHWYQQKPKAPKLLIYKASTLASGVPSRFSGSG
 SGTEFTLTISLSLPDDFATYYCQQGYSWGNVDNVFGGKTVTVLGGGSGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLSLSC
 AASGFSFSSGYDMCWVRQAPGKLEWIAICIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYA
 MDLWGGGTGLTVTVSS

>Sequence ID 88: SI-68P19 Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGACAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTGCAACTATTAT
 TGTTTCCAGGGGAGCGTGATCCCATTCACCTTCGGGCAGGGGACAAAAGTGACCGTCCTAGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTAGCCAGGACAGACCC
 TTAGCCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGGTGCGCTGGATTCCGCAGCCTCCCGGCAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAATCAAGTGTACTTGCAAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGACGGGACTCTCGTACCGGTCTCGATGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAAATC
 GTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGCGCAAGCGCGACTTTCTCTGAGGGCAAGTCAATCCATCAGGGAC
 TAATATACATTGGTATCAACAAAAGCCAGGTAAACCAACCCAGGCTTTTGATTAAGTATGCAAGTGAAGTCTATTTCCGGTATCCCTG
 ACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCCGTGTATTACTGC
 CAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTACGTACGGTGGCTGCACCATCTGTCTTCAT
 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAG
 TACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
 CTCAGCAGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC
 GCGCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGG
 GGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTG
 GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGA
 GGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGGC
 CGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
 CTGCCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT
 GGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATA
 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACAGATT
 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTGAGATGACACAGTACCGTCT
 TACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTCACACCTCAACTGGTATCAAC
 AGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCTCAGGTGTGCCTAGTTCGCTTCTCCGGGAGCGGC
 TCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCAACCCGACGACTTCGCCACATACTATTGTGACGAGGGTTATAGTTGGGG

AAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGGAGGAAGTGGCGGCGCGGAAGCGGAGGTGGTG
GCTCCGGCGGGGGTGGAAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGGAAAGCCTCTCACTCTCTTGC
GCGGCGAGTGGTTTTAGCTTCAGTAGCGGCTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCCCTTGAGTGGATTGCGTG
TATCGCCGCCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTCACAATCTCCAGGGACAACCTCAAAAAATA
CATTTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTTAGCTTCGATTATGCA
ATGGATCTTTGGGGCCAGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 89: SI-68P16 Chain A Amino Acid Sequence

DPVLTQSPSSLSASVGDRTVITSCQSSQSVAKNNNLAWFQQKPGQAPKLLIYASSTLAAGVPSRFSGSGSGTDFTLTISVQPEDFA
TYTCSARDSGNIQSFEGGKKEIKGGGSGGGGSGGGGSGGGGSGGGGSLVSGGLVKPGLSLRLSCAASGIDLSSNAIGWVRQAPGK
GLEWVGVIFGSGNTYYASWAKGRFTISRKNTVYLQMNSLRRAEDTAVYYCARGGYSSDIWGQGLTVTVSSGGGSGGGGSGVQLQQ
SGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKLEWLGVIWSSGNTDYNTPFTSRFTITKDNSKNQVYFKLRSVRADDTAI
YYCARALTYDYEFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTCPCPPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLVSKLTVDKSRWQQGNVFSVSMHEALHN
HYTQKSLSLSPGGGGSGGGGSDVMTQSPSSVSASVGDRTVITCQASQNIPTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSG
SGSGTDFTLTISDLEPGDAATYYCQSTYLGTDYVGGAFGGGKLTFLVGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLR
LSCTASGFTISSYHMQWVRQAPGKLEYIGTISSGGNVYASSARGRFTISRPSKNTVDLQMNSLRRAEDTAVYYCARDGYSDDPM
WGQGLTVTVSS

>Sequence ID 90: SI-68P16 Chain A Nucleotide Sequence

GATCCAGTTCTGACACAAAGTCCATCCAGCCTGTCTGCCTCAGTCGGCGACAGAGTGACCATCAGTTGCCAGAGCTCACAGTCTGT
GGCTAAGAACAACAACCTTGGCGTGGTTCCAACAGAAACCTGGACAGGCTCCGAAATTGCTGATCTATTCTGCTTCCACGCTTGCTG
CTGGTGTTCCTTCCCGCTTTTCAGGTAGTGGTAGCGGACAGACTTCACTTTGACTATAAGCAGCGTGCAGCCTGAAGATTTTGC
ACCTACTATTGTCTGCTAGAGACAGTGGAATATTCAGTCCTTTGGGGGGGGAACGAAGGTGGAATAAAGGGCGCGCGAGGGGTC
TGGTGGGGGTGGCAGTGGTGGTGGAGGAAGTGGTGGCGGTGGTCCCAACAGTTGGTTGAGTCTGGTGGCGGTCTCGTTAAGCCTG
GAGGGTCCCTTCGGCTTAGTTGTGCGGCCTCTGGGATCGACCTGTCTAGCAACGCTATAGGATGGGTACGGCAAGCTCCGGGCAAA
GGCTTTGAGTGGTTCGGCTTATTTTGGGAGCGGTAAATACGTACTACGCCAGCTGGGCAAAAGGTAGTTCACTATCAGTCGATC
AAAGAACACGGTATATCTTCAGATGAACAGTCTCGGGGCGGAGGACACCGCGGTTTATTATTGCGCAAGGGGGGGATACTCCTCAG
ACATATGGGGCCAAGGTACTTTGGTGACGGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAGTACAGTTGCAGCAA
TCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTACGGCTTTAGCCTTACGAAGTATGGAGTTCA
CTGGATTCCGCGAGGCACCCGGCAAGGTTTGGAAATGGCTGGGTGTATTTGGTCAAGTGGAAATACAGACTATAACACCCCTTTTA
CAAGTCGGTTACAATTACGAAAGATAATTCCAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCCGCGCGGACGACACTGCGATC
TACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAAAGTCTCCAGTGTCTAG
CACCAGGGCCCATCGGCTTATTTTGGGAGCGGTAAATACGTACTACGCCAGCTGGGGGCAACAGCGGCCCTGGGCTGCCTGGTCAAGG
ACTACTTCCCGGAACCGGTGACGGTGTCTGGAAGTCAAGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCC
TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA
GCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAG
CCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTG
GTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCACTGGTACGTGGACGGCGGTGGAGGTGCATATGCCAAGACAAAGCC
GCGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCTCAGCTGCTGACAGGACTGGTGAATGCCAAGGAGTACA
AGTGGCGGGTCTCCAACAAGGCCCTCCAGCCCCATCGAGAAAACCTCTCAAAGCCAAAGGGGACGCCCGAGAACCACAGGTG
TATACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTTCTATCCAGCGACAT
CGCCGTGGAGTGGGAGAGCAATGGGAGCCGGAGAACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC
TCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTGGCGGCGCGGTTCAAGTGGTGGGGGATCCGACGTTGTGATGACGCAGTC
TCCTAGTTTCAATATCAGCGTCTGTTGGGGATCGAGTCAGGATTACATGCCAGGCGAGCCAAATATTAGGACGTATCTGTCTTGGT
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TCAGGTTCTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACAGGGGACGCTGCCACGTATTATTGCCAGTCCACCTACCT
CGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAACTCACTGTACTTGGTGGTGGTGGTTCAGGCGGGGGGGTCCG
GCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCACTGGTTGAAAGTGGGGGGGACTCGTTTACGCTGGAGGCTCTTTGCGA
CTTTCTTGTACCCTTCTGGGTTCACTATAAGTTCATATCATATGCAATGGGTAAGACAGGCGCCTGGTAAGGGACTTGAATACAT
AGGAACAATAAGCTCTGGTGGTAACGTCTATTACGCCCTCATCCGCGCGGGGAGGTTTACAATTTCCAGGCTCTTAGCAAAAACA
CGGTAGATCTGCAATGAAGTCTCTTCCGCTGAAGATACAGCAGTCTACTACTGCGCCAGGGATTGAGGATTCTGACCCCATG
TGGGGGACGGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 91: SI-68P16 Chain B Amino Acid Sequence

ENVLTQSPASLSASPERVTITCSASSSVSYMHWYQQKPGQAPKLLIYDTSKLASGVPSRFSGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPFTFGQTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLSTLCAFSGFLSTSGMGVWIRQPPGKG

LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYDYWGQGLVTVSSGGGGSGGGGSEI
 VLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLTKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVYYC
 QQNNNWPTTFPGTKLTVLRVVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS
 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGCGGDKHTCPCPAPAEAAAGPSVFLFPPKPKDTLMSRTPEVTCVVV
 DVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYT
 LPSPRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVSMHEALHNR
 TQKLSLSLSPGGGGSGGGGSDIQMTQSPSTLSASVGDRTITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFSGSG
 SGTEFTLTISLQPDFFATYYCQQGYSWGNDNVFGGGTQKTVLGGGGSGGGGSGGGGSGGGGSEVQLLESGLLVQPGGSLSLSC
 AASGFSFSSGYDMCWVRQAPGKGLEWIAICIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYA
 MDLWGQGLTVTVSS

>Sequence ID 92: SI-68P16 Chain B Nucleotide Sequence

AAAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
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 CTAGCCGCTTCAGTGGTTCCGGCTCAGGCAACGATCACACCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
 TGTTCACAGGGGAGCGTGTACCCATTCACTTCGGGCAGGGGACAAAAGTGACCGTCTAGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGGCGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTCAGCCAGGACAGACCC
 TTAGCCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGGTGCGGTGGATTGCGCAGCCTCCCGCAAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGTGACTTGCAAATGAATAGCCTTGACGCGGAGGATACGGCTGTATATTATTCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGAGGGGACTCTCGTCACGGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAAATC
 GTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAACCGCGCACTTTCTCTTGCAAGGCAAGTCAATCCATAGGGAC
 TAATATACATTTGGTATCAACAAAAGCCAGGTAAACCAACCCAGGCTTTTGATTAAGTATGCAAGTGAGTCTATTTCCGGTATCCCTG
 ACCGCTTCTCTGATCAGGCAGTGGCACAGAGTTCACTACCTACCATATCTAGTGTGCAATCAGAGGACTTCGCCGTGTATTACTGC
 CAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTACGTACGGTGGCTGCACCATCTGTCTTCAT
 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAG
 TACAGTGGAAGGTGGATAACGCCCTCCAATCGGTAAGTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC
 CTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCCATCAGGGCCTGAGCTC
 GCGCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGCCAGACCTGAAGCCGCGG
 GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTACATCGGTGGTGGTG
 GACGTGAGCCAGCAAGACCTTCAAGTCACTGGTACGTGGACGGCGTGGAGGTGCATAATGCAAGACAAAGCCGCGGGA
 GGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCG
 CGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC
 CTGCCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
 GGAGTGGGAGAGCAATGGGCGAGCCGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATA
 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTCTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACAGATT
 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTGACATGACACAGTCAACGCT
 TACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTCACACCTCAACTGGTATCAAC
 AGAAACCCGGTAAAGCACCGAAGTGTCTCATCTACAAGGCATCAACTCTTGCTCAGGTGTGCCTAGTTCGCTTCTCCGGGAGCGGC
 TCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCAACCCGACGACTTCGCCACATACTATTGTGACGAGGGTTATAGTTGGGG
 AAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGAGGAAGTGGCGGCGCGGAAGCGGAGGTGGTG
 GCTCCGGCGGGGGTGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGCCTCTCACTCTCTTGC
 GCGGCGAGTGGTTTTAGCTTCAGTAGCGGCTACGATATGTGCTGGTAAGACAGGCTCCTGGTAAAGGCCCTTGAAGTGGATTGCGTG
 TATCGCCCGCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTCACAATCTCCAGGGACAACCAAAAAATA
 CATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTTAGCTTCGATTATGCA
 ATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 93: SI-75P5 Chain A Amino Acid Sequence

EVQLQESGGGLVQAGDSLSSCLVSGRFSNSYTMGWFRQAPGKEREFVAAAILWSGPITYYADSVKGRFTISRDNKNTVYLQMNSL
 KPEDTAVYYCAALGLVLAPGNVYSYWGQGTQVTVSSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVR
 QAPGKGLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDGGSSAITSNNIWQGTGLTVTVSSASTK
 GPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS
 NTKVDKRVPEKSCDKHTCPCPAPAEAAAGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRE
 EQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAV
 EWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSVSMHEALHNYTQKLSLSLSPGGGGSGGGGSDVVMQTSPS
 SVSASVGDRTITCQASQNIIRTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTI SDLEPGDAATYYCQSTYLG
 DYVGGAFGGGTGLTVLGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKGLEIYGT
 ISSGGNVYYASSARGRFTISRPSKNTVLDLQMNSLRAEDTAVYYCARDSGYSDPMWGQGLTVTVSS

>Sequence ID 94: SI-75P5 Chain A Nucleotide Sequence

GAGGTGCAGCTGCAGGAGTCTGGCGGCGGCCTGGTGCAGGCTGGGGACAGCCTGAGCCTGTCTGCCTGGTGTCTGGCCGCTCCTT
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 CCTACTATGCTGACTCTGTGAAGGGCGCTTACCATCTCCAGAGACAATGCCAAGAACACTGTGTACCTGCAGATGAACAGCCTG
 AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGCCCTGGGAGTGTGGTGTGGCCCCCTGGCAATGTGTACAGCTACTGGGG
 CCAGGGCACCCAGGTGACTGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAG
 GCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCCGC
 CAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACATACTACGCGAGCTGGGCGAAAGGCAGATT
 CACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACAGGCTGTGTATTACTGTG
 CGAGAGACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTCACCGTGTCTCAGCTAGCACCAAG
 GGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTT
 CCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGAC
 TCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGCCGAGC
 AACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGGCCAGCACCTGAAGCCGCGGG
 GGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGG
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 GAGCAGTACAACAGCACGTACCGTGTGGTGCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGC
 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTATACCC
 TGCCCCATCCCGGATGAGCTGACCAAGAACAGGTACGCGTGTCTGCGCCGTCAGGCTTCTATCCCAGCGACATCGCCGTG
 GAGTGGGAGAGCAATGGGCAGCCGAGAACTACAAGAACAGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTCGTGAG
 CAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA
 CGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGCGCGGTTTCAAGTGGTGGGGGATCCGACGTTGTGATGACGCAGTCTCCTAGT
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 AAAGCCTGGTAAGGCTCCAAAACCTCCTCATTTACGCCGCTGCCAAGTGGCTAGTGGAGTACCTTACGCTTTAGTGGGTGAGGTT
 CTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACAGGGGACGCTGCCACGTATTATTGCCAGTCCACCTACCTCGGGACT
 GACTACGTTGGTGGGGCGTTTGGCGGAGGAACAACTCACTGTACTTGGTGGTGGTGGTTTCAAGCGGGGGGGTCCGGCGGAGG
 CGGTTCTGGGGGTGGAGGTTCCGAGGTTCAAGTGGTTGAAAGTGGGGGGGACTCGTTACGCTGGAGGCTCTTTCGCGACTTTCTT
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 ATAAGCTCTGGTGGTAACGTCTATTACGCCTCATCCGCGCGGGGGAGGTTTACAATTTCCAGGCCTTCTAGCAAAAACACGGTAGA
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 AGGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 95: SI-75P5 Chain B Amino Acid Sequence

QVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIADSVNGRFTISRDNKNTLYLQMDSL
 KPEDTAVYYCAADLQYGSWFPQRS SA EYDYWGQGT VTVVS SGGGSGGGGSDVMTQSPSTLSASVGRVTINCAQASESISSWLAW
 YQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDGFATYYCQGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVF
 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLS
 SPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 EEQYNSTYRVVSVLTIVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIA
 VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNRFTQKLSLSLPGGGGSGGGGSDIQMTQSP
 STLSASVGRVTITCAQASQSISSHLNWKYQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDGFATYYCQQGYSW
 GNVDNVFGGGKTVTLVGGGGSGGGGSGGGGSGGGGSEVQLLESGLVQPGGSLSLSCAASGFSFSSGYDMCWVRQAPGKGLEWIA
 CIAAGSAGITYDANWAKGRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARSAFSDYAMDWLGQGLTVTVSS

>Sequence ID 96: SI-75P5 Chain B Nucleotide Sequence

CAGGTGCAGCTGGTGCAGTCTGGCGGAGGCCTGGTGCAGGCTGGGGGACAGCCTGAGCCTGAGCTGTGCCTTCTCTGGCCGCACCTT
 CTCCATGTACACCATGGGCTGGTTCCGCCAGGCCCCAGGGAAGGAGAGAGAGTTTGTGGCTGCCAACAGAGGCAGAGGCCTGAGCC
 CAGACATTGCTGACTCTGTGAATGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCTGCAGATGGACAGCCTG
 AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGA
 CTACTGGGGCCAGGGCACCACTGTGACTGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTCGTGATGACCCAGT
 CTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAGTTGGTTAGCCTGG
 TATCAGCAGAAACCAGGGAAAGCCCCAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGGTCCCATCAAGGTTGAGCGG
 CAGTGGATCTGGGACAGAATTCATCTCACCATCAGCAGCCTGCAGCCTGATGATTTGCAACTTATTACTGCCAAGGCTATTTTT
 ATTTTATTAGTCTACTTATGTAATTTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTC
 ATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAA
 AGTACAGTGAAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACA
 GCCTCAGCAGCACCCCTGACGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGCGCTGAGC
 TCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCCACCGTGGCCAGCACCTGAAGCCGC
 GGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGG
 TGACGTCAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGG
 GAGGAGCAGTACAACAGCACGTACCGTGTGGTGCAGCTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG
 CGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACA

CCCTGCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTACGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
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 TAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACAGAT
 TCACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTAGATGACACAGTCACCG
 TCTACGCTCTCAGCCTCAGTAGGGGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTACACCTCAACTGGTATCA
 ACAGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCCTCAGGTGTGCCTAGTCGCTTCTCCGGGAGCG
 GCTCCGGTACTGAGTTTACTTTGACGATATCTCCCTCCAACCCGACGACTTCGCCACATACTATTGTGACAGGGTTATAGTTGG
 GGAAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGACTGTGTTGGGAGGGGAGGAAGTGGCGCGCGCGGAAGCGGAGGTGG
 TGGCTCCGGCGGGGTGGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGCCTCTCACTCTCTT
 GCGCGGCGAGTGGTTTTAGCTTCAGTAGCGGCTACGATATGTGCTGGGTAAAGACAGGCTCCTGGTAAAGGCCTTGAGTGGATTGCG
 TGTATCGCCGCGGGTCTGCTGGTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTCACAATCTCCAGGGACAACCTCAAAAAA
 TACATTGTACCTCCAGATGAATAGCCTGAGAGCCGGAAGACACCGCATCTACTATTGCCGAAGGTCAGCATTTAGCTTCGATTATG
 CAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTGA

>Sequence ID 97: SI-75P8 Chain A Amino Acid Sequence

EVQLQESGGGLVQAGDSLSSLVSGRSFNSYTMGWFRAQPGKEREFVAAILWSGPTTYADSVKGRFTISRDNKNTVYLMNSL
 KPEDTAVYYCAAALGVLVLPAGNVSYWQGTQVTVSSGGGSGGGGSGVQLQESGGRLVQPEPLSLTCKTSGIDLSSNAIGWVR
 QAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLMNSLRSEDTAIYYCARGGYSSDIWGQGLVTVSSASTKGPSVFPL
 APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKR
 VEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDLWLNKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLCAVKGFYPSDIAVEWESNGQ
 PENNYKTTTPVLDSGFFLVSKLTVDKSRWQQGVNFVSCSMHEALHNHYTQKSLSLSPGGGGSGGGGSGVQLQSGPGLVKPSE
 TLSITCTVSGFSLTNYGVHWIRQAPGKGLEWLVGIWSGGNTDYNTPFTSRFTITKDNSKNQVYFKLRSVRADDTAIYYCARALTY
 DYEFAWYWGQGLTVTVSSGGGSGGGGSGGGGSGGGGSEIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIK
 YASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVYYCQNNNNWPTTFPGTKLTVL

>Sequence ID 98: SI-75P8 Chain A Nucleotide Sequence

GAGGTGCAGCTGCAGGAGTCTGGCGGCGGCCTGGTGCAGGCTGGGGACAGCCTGAGCCTGTCCTGCCTGGTGTCTGGCCGCTCCTT
 CAACCTCCTACACCATGGGCTGGTTCCGCGCAGGCCCTGGGAAGGAGCGGGAGTTTGTGGCTGCCATCCTGTGGAGTGGCCCCACCA
 CCTACTATGCTGACTCTGTGAAGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACTGTGTACCTGCAGATGAACAGCCTG
 AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGCCCTGGGAGTGCTGGTGTGGCCCCCTGGCAATGTGTACAGCTACTGGGG
 CCAGGGCACCCAGGTGACTGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAGTGCAAGTGAAGAAAGTGGTGGTA
 GACTGGTTTCAAGCTGGTGAACCTTGTCACTGACCTGTAAAACAAGCGGCATTGATCTGTCTCTAACGCCATCGGATGGGTCCGA
 CAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACGCAAGCTGGGCAAAAGGGCGATT
 TACGATATACGAGGACACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAGGATACCGCGATATATTACTGTGCCAGAG
 GGGGTACTCCTCTGATATCTGGGGGACAGGTACACTGGTTACAGTTTTCATCCGCTAGCACCAAGGCCCTCTGTGTTCCTCTG
 GCCCCCTCCTCCAAGAGCACCTCTGGAGGACTGCTGCCCTGGGCTGCCTGGTGAAGGACTACTTCCAGAGCCTGTGACTGTGTC
 CTGGAATCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGCTCTGGCCTCTACAGCCTGTCTCTGTGG
 TCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAAGCCCTCCAACACCAAGGTGGACAAGAGA
 GTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCTGCCAGCCCCAGAGGCTGCTGGAGGGCCCTCTGTGTTCTCTT
 CCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCAGAAGTCACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAG
 AAGTGAAGTTCACTGGATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCCAGAGAAGAGCAGTACAACCTCCACCTAC
 CGAGTGGTGTCTGTGCTGACTGTGCTGCACAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCC
 TGCCCCCATTTAGAAGACCATCTCCAAGGCCAAGGCCAGGCCAGAGAGCCCCAGGTCTACACCTGCCTCCCTCCAGAGATGAGC
 TGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAG
 CCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGCTCTCCAGCTGACTGTGGACAAGAG
 CCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGATGCATGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGA
 GCCCTGGAGGAGGAGGAGGCTCTGGAGGAGGAGGATCCCAAGTTCAGTTGCAGCAGTCTGGCCCTGGCCTGGTCAAGCCTTCTGAG
 AACTGTCCATCACCTGTACCGTGTCCGGCTTCTCCCTGACCAATTACGGCGTGCACTGGATCAGACAGGCCCTGGCAAAGGACT
 GGAATGGCTGGGAGTGATTTGGAGCGCGGCAACACCGACTACAACACCCCTTTACCAGCCGTTTACCATACCAAGGACAACCT
 CCAAGAACCAGGTGTACTTCAAGCTGCGGAGCGTGCAGGCTGATGACACCGCCATCTACTACTGTGCTCGGGCCCTGACCTACTAC
 GACTACGAGTTTGTCTTACTGGGGCCAGGGCACCTGGTCAAGTTTCTTCTGGTGGTGGTGGTTCAGGCGGGGGGGTTCCGGCGG
 AGGCGGTTCTGGGGGTGGAGGTTCCGAGATCGTGTGACCCAGTCTCCTTCCACACTGTCTGTGTCTCCCGGCGAGAGGCCACCT
 TCAGCTGTAGAGCCTCTCAGTCCATCGGCACCAACATCCACTGGTATCAGCAGAAGCCCGGCAAGCCTCCTCGGCTGCTGATTAAG
 TACGCTCCGAGTCCATCAGCGGCATCCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCAGGTTTACCCTGACCATCTCCTCCGT
 GCAGTCCGAGGATTTCCGCGTGTACTACTGCCAGCAGAACAACACTGGCCACCACCTTTGGACCCGGCACCAAGCTGACCGTGC
 TGTGA

>Sequence ID 99: SI-75P8 Chain B Amino Acid Sequence

QVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIADSVNGRFTISRDNAKNTLYLQMDSL
 KPEDTAVYYCAADLQYGSWPPQRS SA EYDYWGQGT VTVSSGGGGSGGGGSDPQLTQSPSSLSATVGQRTVINCQSSQSVAKNNNL
 AWFQQKPGKPKPKLLIYASASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDFATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIF
 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLSSP
 VTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
 QYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE
 WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNRFTQKSLSLSPGGGGSGGGGSQVQLQESGGG
 LVKPGGSLSLSCAASGFTTFSSYMSWVRQAPGKGLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYC
 ARDRGVGYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSQSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLM
 IYDVSDRPSGVSDRFSGSKSGNTASLIISGLQADDEADYYCSSYGSSTHVI FGGGTKVTVL

>Sequence ID 100: SI-75P8 Chain B Nucleotide Sequence

CAGGTGCAGCTGGTGCAGTCTGGCGGAGGCCTGGTGCAGGCTGGGGGCAGCCTGAGCCTGAGCTGTGCCTTCTCTGGCCGCACCTT
 CTCCATGTACACCATGGGCTGGTTCCGCCAGGCCCCAGGGAAGGAGAGAGAGTTTGTGGCTGCCAACAGAGGCAGAGGCCTGAGCC
 CAGACATTGCTGACTCTGTGAATGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCTGCAGATGGACAGCCTG
 AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGA
 CTACTGGGGCCAGGGCACCCTGTGACTGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGATCCTCAATTGACCCAGT
 CCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGTAACAATCAATTGCCAGTCAAGCCAGTCCGTAGCGAAGAATAATAATTTG
 GCATGGTTCCAACAAAAACCGGTAAACCTCCTAACTCCTTATCTACTCAGCTTCAACCCCTGCCGCGGGTGTGCCAGCCGGTT
 CTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCAACCTACTATTGTCTGCAC
 GGATTCCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGCCCCCTCTGTGTTCATCTTC
 CCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCTACCCAGAGAAGCCAAGGTGCA
 GTGGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTGT
 CCTCCACCCTGACCTGTCCAAGGCTGACTATGAGAAGCACAAAGTGTATGCCTGTGAGGTGACCCACCAGGGCCTGAGCAGCCCT
 GTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAAGCTGCTGGAGG
 CCCCTCTGTGTTCTTCTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAGTCACTGTGTGGTGGTGGATG
 TGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAGTGACAATGCCAAGACCAAGCCAGAGAAGAG
 CAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGT
 GTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTCTACACCTGCTG
 CTCCCTCCAGAGATGAGCTGACCAAGAACCAGTGTCCCTGTGGTGGCTGAAAGGCTTCTACCCAGATGACATTGCTGTGGAG
 TGGGAGAGCAATGGCCAGCCAGAGAACAACACTACAAGACCCCCCTCTGTGCTGGACTCTGATGGCTCTTCTCTCTGACAGCAA
 GCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCTGCTCTGTGATGCATGAGGCCCTGCACAACCGCTTCAACC
 AGAAGAGCCTGAGCCTGAGCCCTGGAGGAGGAGGAGGCTCTGGAGGAGGAGGATCCAGGTGCAGCTGCAGGAGTGGGGGGAGGC
 CTGGTCAAGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCA
 GGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAACATAAACCGCGATGGAAGTGCGAGTTACTATGTGGACTCTGTGAAGGGCCGAT
 TCACCATCTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGT
 GCGAGAGATCGTGGGGTGGGTACTTTCGATCTCTGGGGCCGTGGCACCCTGGTCACCGTGTCTAGCGGTGGAGGCGGTTACGGCGG
 AGGTGGTTCGGCGGTGGCGGCTCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCTGGACAGTCGATCACCATCT
 CCTGCACTGGAACAGCAGTACGTTGGTGGTTATAACTTTGTCTCTGGTACCAACAACACCCAGGCAAAGCCCCAACTCATG
 ATCTATGATGTGAGTATCGGCCCTCAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTC
 TGGCCTCCAGGCTGACGACGAGGCTGATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCA
 AGGTGACCGTCTCTATAA

>Sequence ID 101: SI-75X4 Chain A Amino Acid Sequence

EVQLQESGGGLVQAGDSL SLSCLVSGRFSNSYTMGWFRQAPGKEREFVAAILWSGPTTYADSVKGRFTISRDNAKNTVYLQMNSL
 KPEDTAVYYCAALGVLV LAPGNVYSYWGQGTQVTVSSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMS
 WVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMSLSRSED TAVYYCARDGGSSAITSNNIWQGT LVTVSSASTK
 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS
 NTKVDKRVPEPKCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAV
 EWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPG

>Sequence ID 102: SI-75X4 Chain A Nucleotide Sequence

GAGGTGCAGCTGCAGGAGTCTGGCGGCGGCCTGGTGCAGGCTGGGGACAGCCTGAGCCTGTCCTGCCTGGTGTCTGGCCGCTCCTT
 CAACTCCTACACCATGGGCTGGTTCCGCCAGGCCCCCTGGGAAGGAGCGGGAGTTTGTGGCTGCCATCCTGTGGAGTGGCCCCACCA
 CTTACTATGCTGACTCTGTGAAGGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACTGTGTACCTGCAGATGAACAGCCTG

AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGCCCTGGGAGTGCTGGTGCTGGCCCCCTGGCAATGTGTACAGCTACTGGGG
 CCAGGGCACCCAGGTGACTGTCTCGAGCGGAGGAGAGGCTCTGGAGGAGGAGGCAGTGAGGTGCAGCTGGTGGAGAGTGGAGGAG
 GCCTGGTGCAGCCTGGAGGCAGCCTGCGGCTGTCTGTGCTGCCTCTGGCTTCACCATCTCCACCAATGCCATGTCTGGGTGCGC
 CAGGCCCCCTGGCAAGGGCCTGGAGTGGATTGGAGTCATCACTGGCAGAGACATCACCTACTATGCCTCCTGGGCCAAAGGCCGCTT
 CACCATCTCCAGAGACAACAGCAAGAACACCTGTACCTGCAGATGAGCAGCCTGCGCAGTGAGGACACAGCTGTGTACTACTGTG
 CCCGAGATGGAGGCAGCAGTGCCATCACCTCCAACAACATCTGGGGCCAGGGCACCTGGTCACTGTGTCTCTGCTAGCACAAA
 GGCCCCCTGTGTTCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGTGCTGCTGGTGAAGGACTACTT
 CCCAGAGCCTGTGACTGTGTCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGCTCTGGCC
 TCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAAGCCCTCC
 AACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGGCTGCTGG
 AGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCCAAGATCACCTGTGTGGTGGTGG
 ATGTGTCCCATTGAAGAGTGAAGTTCAATGGTATGTGGAGTGGAGGTGCACAATGCCAAGACCAAGCCCAAGAGAA
 GAGCAGTACAACCTACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGC
 TGTGTCCAACAAGGCCCTGCTGCCCTTATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTCTACACCC
 TGCTTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACATTGCTGTG
 GAGTGGGAGAGCAATGGCCAGCCAGAGAACAACATAAGACCACCCCTCCTGTGCTGGAGTCTGATGGCTCCTTCTCTCTGGTCTC
 CAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTCATGCATGAGGCCCTGCACAACCACTACA
 CCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 103: SI-75X4 Chain B Amino Acid Sequence

QVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIADSVNGRFTISRDNANTLYLQMDSL
 KPEDTAVYYCAADLQYGSWQRRSSAEYDYWGQGTVTVSSGGGSGGGGSDVMTQSPSTLSASVGDRTVINCQASESISWLA
 YQKPGKAPKLLIYEASKLASGVPSRFSGSGSTEFTLTISLQPDFATYYCQGYFYFISRTYVNSFGGGTKVEIKRTVAAPS
 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLS
 SPVTKSFNRGECGGDKTHTCPPCPAEPAAAGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
 EEQYNSTYRVVSVLTVHLQDNLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYP
 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVSMHEALHNRTQKSLSLSPG

>Sequence ID 104: SI-75X4 Chain B Nucleotide Sequence

CAGGTGCAGCTGGTGAGTCTGGCGGAGGCCTGGTGCAGGCTGGGGGCAGCCTGAGCCTGAGCTGTGCCTTCTCTGGCCGCACCTT
 CTCCATGTACACCATGGGCTGGTTCGCCAGGCCCCAGGGAAGGAGAGAGAGTGTGGCTGCCAACAGAGGCAGAGGCCTGAGCC
 CAGACATTGCTGACTCTGTGAATGGCCGCTTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCTGCAGATGGACAGCCTG
 AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGA
 CTACTGGGGCCAGGGCACCACTGTGACTGTCTCGAGCGGAGGAGGAGGCTCTGGAGGAGGAGGCAGTGATGTGGTGTGATACCCAGA
 GCCCTCCACCCTGTCTGCCTCTGTGGGAGACAGAGTGACCATCAACTGCCAGGCCAGTGAGAGCATCTCCTCCTGGCTGGCCTGG
 TACCAGCAGAAGCCAGGCCAGGCCCAAGCTGCTCATATGAAGCCTCCAAGCTGGCCTCTGGAGTGGCCTCCCGCTTCTCTGG
 CTCTGGCTCTGGCACAGAGTTCACCTGACCATCTCCAGCCTGCAGCCAGATGACTTTGCCACCTACTACTGCCAGGGCTACTTCT
 ACTTCATCTCCAGGACCTATGTGAACAGCTTTGGAGGAGGCACCAAGGTGGAGATCAAGCGTACGGTGGCTGCCCCCTCTGTGTTT
 ATCTTCCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCTACCCAGAGAAGCCAA
 GGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACGCAAGGACAGCACCTACA
 GCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAGGTGTATGCCTGTGAGGTGACCCACCAGGGCCTGAGC
 AGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACCTGCCCTCCCTGCCAGCCAGAGAGCTGCTG
 TGGAGGCCCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAAGTCACTGTGTGGTGG
 TGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGCACAATGCCAAGACCAAGCCAGA
 GAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTG
 TGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTCTACA
 CCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAAGGCTTCTACCCAGTGACATTGCT
 GTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACATAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTCTCTGTGA
 CAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGTCATGCATGAGGCCCTGCACAACCGCT
 TCAACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 105: SI-75X17 Chain A Amino Acid Sequence

EVQLQESGGGLVQAGDSLSSLVSGRFSNSYTMGWFRQAPGKEREFVAAILWSGPTTYADSVKGRFTISRDNANTVYVYLMNSL
 KPEDTAVYYCAALGLVLAAPGNVYSYWGQGTQVTVSSGGGSGGGGQVQLQESGGRVLPGEPLSLTCKTSGIDLSSNAIGWVR
 QAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTVYLYKMNLSRSEDTAIYYCARGGYSSDIWGQGTLVTVSSASTKGPSVFLP
 APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKR
 VEPKSCDKTHTCPPCPAEPAAAGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVHLQDNLNGKEYKCAVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLCAVKGFYP
 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSVSMHEALHNHYTQKSLSLSPG

GAGGTGCAGCTGCAGGAGTCTGGCGGGCGGCTGGTGCAGGCTGGGGACAGCCTGAGCCTGTCTGCTGGTGTCTGGCCGCTCCTT
CAACTCCTACACCATGGGCTGGTTCGGCCAGGCCCCCTGGGAAGGAGCGGGAGTTTGTGGCTGCCATCCTGTGGAGTGGCCCCACCA
CCTACTATGCTGACTCTGTGAAGGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACACTGTGTACCTGCAGATGAACAGCCTG
AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGCCCTGGGAGTGTGCTGTGCTGGCCCCCTGGCAATGTGTACAGCTACTGGGG
CGAGGGACCCACAGTGACTGTCTGAGCGCGGTGGAGGCTCCGGCGGTGGTGGATCACAAGTCAGTTGCAAGAAAGTGGTGGTA
GACTGGTTACGCCCTGGTGAACCCCTGTGCTACTGACGTGTAAAAACAAGCGCGATTGATCTGTCTCTAAAGCCATCGGATGGGTCCGA
CAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACGCAAGCTGGGCAAAAGGGCGATT
TACGATATCACGGAGCACCTCTACAGTTTATTTGAAAAAGAACTCCCTCCGGTCCGAGGATACCGCGATATATTACTGTGCCAGAG
GGGGGTACTCCTCTGATATCTGGGGGCGAGGTACACTGGTTACAGTTTCATCCGCTAGCACCAAAGGCCCTCTGTGTTCCCTCTG
GCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCTGGTGAAGGACTACTTCCAGAGCCTGTGACTGTGTC
CTGGAACCTGGAGCCCTGACCTCTGGAGTGACACCTTCCCTGCTGTGCTGACAGAGCTCTGGCCCTACAGCCTGTCTCTGTGG
TCACTGTGCCCTCCTCCAGCCTGGGACCCAGACCTACATCTGCAATGTGAACCAAGCCCTCCAACACAAGGTGGACAAGAGA
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CCCTCCCAAGCCCCAAGGACACCCTGATGATCTCCAGGACCCCAAGTCACTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAG
AAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCCCAAGAGAAGAGCAGTACAACCTCACCTAC
CGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCC
TGCCCCCATTTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCCAAGAGGCCCAAGGTCTACACCCTGCCCTCCCTCCAGAGATGAGC
TGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCCAAGTACATTTGCTGTGGAGTGGGAGAGCAATGGCCAG
CCAGAGAACCAACTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTTGGTCTCCAAGCTGACTGTGGACAAGAG
CCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGATGCATGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGA
GCCCTGGATGA

QVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIADSVNGRFTISRDNAKNTLYLQMDSL
KPEDTAVYYCAADLQYGSWFPQRSSAEYDYWGQTTTVTS SGGGSGGGGSDPQLTQSPSSLSATVGQRTVINCSSQSVAKNNNL
AWFQQKPGKPKLLIYASSTLAAGVPSRFSGSGSGTQFTLTITRVQSEDFATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIF
PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGCEGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSYTRVVSVLTVLHQLDNLNGEYKCAVSNKALPAPIEKTIKAKGQPREPQVYDPSRDELTKNQVSLWCLVKGFYPSDIAVE
WESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGVNFSQCMVHEALHNRFETOKSLSLSPG

CAGGTGCAGCTGGTGCAGTCTGGCGGAGGCCCTGGTGCAGGCTGGGGGCAGCCTGAGCCTGAGCTGTGCCTTCTCTGGCCGCACCTTCTCCATGTACACCATGGGCTGGTTCGCCCAGGCCCCAGGGAAGGAGAGAGAGTTTGTGGCTGCCAACAGAGGCAGAGGCCCTGAGCCAGACATTGCTGACTCTGTGAATGGCCGCTTACCATTCTCCAGAGACAATGCCAAGAACACCCTGTACCTGCAGATGGACAGCCCTGAAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGCTACTTGGGGCCAGGGCCACCATCTGTGACTGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGATCCTCAATTGACCCAGTCCCCTAGTAGCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGTAGCGAAGAATAATAATTTGCGATGGTTCACAACAAAAACCGGGTAAACCTCCTAACTCCTTATCTACTACGCTTCAACCCCTTGGCGGGGTGTGCCACAGCCGGTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCAACCTACTATTGTTCTGCACGGGATTCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGCCCCCTCTGTGTTTCATCTTCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCTACCCAGAGAAGCCAAGGTGCAGTGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTGTCCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAAGTGTATGCCTGTGAGGTGACCCACCAAGGCCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCCAGGAGAGTGTGGAGGACAAAGCCACACCTGCCCTCCCTGCCAGCCCCAGAGTCTGTGGAGCCCCCTAGGTTCTCTCTTCTCCCAAGCCCCAAGGACCCCTGATGATCTCCAGGACCCAGAAGTCAACCTGTGTGTTGGTGGATGTGTCCTCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGAAGTGCACAATGCCAAGACCAAGCCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTCTACACCCTGCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGGAAACAACACTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTACAGCAA

QVQLQESGGRLVQPGEPLSLTCKTSGIDLSSNAIGWVRQAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLMNLSRSE
DTAIYYCARGYSSDIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTCTCPCPAPEAAGGSPVFLPPKPKDITLMSRTPEVTCV

VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPGGGGGSGGGGSEVQLQESGGGLVQAGDSLSSLCLVSGRSFNSYTMGWFRQAPGKEREFVAAILWSGPTTYADSV
KGRFTISRDNAKNTVYLQMSLKPEDTAVYYCAALGVLVLPAGNVYSYWGQGTQVTVSS

>Sequence ID 110: SI-75X19 Chain A Nucleotide Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTGTCACTGACGTGTAAACAAGCGGCATTGATCT
GTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGGCGATTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGAGGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAAAGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGG
ACTACTTCCCAGAGCCTGTGACTGTGTCCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGC
TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAA
GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGG
CTGCTGGAGGCCCTCTGTGTTCCCTCTTCCCTCCCAAGCCCAAGGACACCCCTGATGATCTCCAGGACCCAGAAAGTCACTGTGTG
GTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCC
CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCCTCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTG
TACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCCAGTGACAT
TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGATGATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGAGGAGGAGGAGGCTCTGGAGGAGGAGGATCCGAGGTGCAGCTGCAGGAGTC
TGGCGGCGGCCTGGTGCAGGCTGGGGACAGCCTGAGCCTGTCTGCTGGTGTCTGGCCGCTCCTTCAACTCCTACACCATGGGCT
GGTTCGCGCAGGCCCTGGGAAGGAGCGGGAGTTTGTGGCTGCCATCCTGTGGAGTGGCCCCACCACCTACTATGCTGACTCTGTG
AAGGGCCGCTTCAACATCTCCAGAGACAATGCCAAGAACACTGTGTACCTGCAGATGAACAGCCTGAAGCCAGAGGACACAGCTGT
GTACTACTGTGCTGCTGCCCTGGGAGTGTGGTGTGGCCCTGGCAATGTGTACAGCTACTGGGGCCAGGGCACCCAGGTGACTG
TGCTAGCTGA

>Sequence ID 111: SI-75X19 Chain B Amino Acid Sequence

DPQLTQSPSSLSATVQQRVTINCQSSQSVAKNNNLAWFQQKPGKPKKLLIYSASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDFA
TYYSARDSGNIQSFGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEA
LHNRFTQKSLSLSPGGGGGSGGGGQVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIA
DSVNGRFTISRDNAKNTLYLQMDSLKPEDTAVYYCAADLQYGSWPPQRSSAEYDYWGQGTITVTVSS

>Sequence ID 112: SI-75X19 Chain B Nucleotide Sequence

GATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGT
AGCGAAGAATAAATTTGGCATGGTTCCAACAAAAACCGGGTAACCTCCTAACTCCTTATCTACTCAGCTTCAACCCTTGCCG
CGGTGTGCCAGCCGCTTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCA
ACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGC
CCCCTCTGTGTTTCATCTTCCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCTCAACAACCTTCTACC
CCAGAGAAGCCAAAGTGCAGTGGAAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTGTCTCCACCTGACCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGTATGCCTGTGAGGTGACCCA
CCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAG
CCCAGAAAGCTGCTGGAGGCCCTCTGTGTTCCCTCTTCCCTCCCAAGCCCAAGGACACCCCTGATGATCTCCAGGACCCAGAAAGTC
ACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGCACAATGCCAA
GACCAAGCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGA
AGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCCTCTCCAAGGCCAAGGGCCAGCCAGAGAG
CCCCAGGTCTACACCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTACCC
CAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACACCCCTCCTGTGCTGGACTCTGATGGCT
CCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGATGCATGAGGCC
CTGCACAACCGCTTCAACCAGAAGAGCCTGAGCCTGAGCCTGGAGGAGGAGGCTCTGGAGGAGGAGGATCCCAGGTGCAGCT
GGTGCAGCTCTGGCGGAGGCTGGTGCAGGCTGGGGGAGCCTGAGCCTGAGCTGTGCTTCTCTGGCCGACCTTCTCCATGTACA
CCATGGGCTGGTTCCGCCAGGCCCCAGGGAAGGAGAGAGTGTGGTGTGCCAACAGAGGCAGAGGCTGAGCCCAGACATTGCT
GACTCTGTGAATGGCCGCTTCAACATCTCCAGAGACAATGCCAAGAACCCTGTACCTGCAGATGGACAGCCTGAAGCCAGAGGA
CACAGCTGTGTACTACTGTGCTGCTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGACTACTGGGGCC
AGGGCACCACTGTGACTGTGTCTAGCTGA

>Sequence ID 113: SI-75X9 Chain A Amino Acid Sequence

QVQLQESGGRLVQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSE
DTAIYYCARGGYSSDIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFPYSDIAVEWESNGQPENNYKTTPFVLDSGDSFFLVSKLTVDKSRWQQGNVFSCSVMEALHN
HYTQKSLSLSPG

>Sequence ID 114: SI-75X9 Chain A Nucleotide Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCTTGTCACTGACGTGTAAACAAGCGGCATTGATCT
GTCCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGGCGATTTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGGTACTCCTCTGATATCTGGGGGCAGGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAAAGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGG
ACTACTTCCCAGAGCCTGTGACTGTGTCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGC
TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAA
GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGG
CTGCTGGAGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAGTCACCTGTGTG
GTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCC
CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTC
TACACCTTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAGGCTTCTACCCAGTGACAT
TGCTGTGGAGTGGAGAGCAATGGCCAGCCAGAGAACCACTACAAGACCAACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGCATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 115: SI-75X9 Chain B Amino Acid Sequence

QVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIADSVNGRFTISRDNKNTLYLQMDSL
KPEDTAVYYCAADLQYGSWPPQRSSAEYDYWGQGTTVTVSSGGGGSGGGGSDPQLTQSPSSLSATVQGRVTINCQSSQSVAKNNNL
AWFQQKPGKPPKLLIYASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDFATYYCSARDSGNIQSFGGGTREVEIKRTVAAPSVFIF
PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGECGGDKHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE
WESNGQPENNYKTTPFVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNRTQKSLSLSPG

>Sequence ID 116: SI-75X9 Chain B Nucleotide Sequence

CAGGTGCAGCTGGTGCAGTCTGGCGGAGGCCTGGTGCAGGCTGGGGGCAGCCTGAGCCTGAGCTGTGCCTTCTCTGGCCGCACCTT
CTCCATGTACACCATGGGCTGGTTCGCCAGGCCCCAGGGAAGGAGAGAGAGTTTGTGGCTGCCAACAGAGGCAGAGGCCTGAGCC
CAGACATTGCTGACTCTGTGAATGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACCCTGTACCTGCAGATGGACAGCCTG
AAGCCAGAGGACACAGAGTGTACTACTGTGCTGTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGA
CTACTGGGGCCAGGGCACCCTGTGACTGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGATCCTCAATTGACCCAGT
CCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGTAACAATCAATTGCCAGTCAAGCCAGTCCGTAGCGAAGAATAATAATTTG
GCATGGTTCCAACAAAAACCGGTAACCTCCTAACTCCTTATCTACTCAGCTTCAACCCTTGCCGCGGGTGTGCCAGCCGGTT
CTCAGGCTCAGGTCCGGGACTCAATTTACCTTACCATCACTCGCGTCCAAAGTGAAGATTTTGCAACCTACTATTGTCTGCAC
GGGATTCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGCCCCCTCTGTGTTTCATCTTC
CCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCCTGCTCAACAACCTTCTACCCAGAGAAGCCAAGGTGCA
GTGGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTGT
CCTCCACCCTGACCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGTATGCCTGTGAGGTGACCCACCAGGGCCTGAGCAGCCCT
GTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAAGCTGCTGGAGG
CCCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAGTCACCTGTGTGGTGGTGGATG
TGTCCCATGAAGACCCAGAAGTGAAGTCAACTGGTATGTGGATGGAGTGAAGTGCACAATGCCAAGACCAAGCCAGAGAAGAG
CAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGT
GTCCAACAAGGCCCTGCCTGCCCATTTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTCTACACCCTGC
CTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGGCTGAAAGGCTTCTACCCAGTGACATTGCTGTGGAG
TGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCAACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGTACAGCAA
GCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGCATGAGGCCCTGCACAACCGCTTCAACC
AGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 117: SI-75X11 Chain A Amino Acid Sequence

EVQLQESGGGLVQAGDSL SLSCLVSGRSFNSYTMGWFRQAPGKEREFVAAILWSGPTTYADSVKGRFTISRDNAKNTVYLQMNSL
KPEDTAVYYCAALGVLVLAPGNVYSYWGQGTQVTVSSGGGGSGGGGSQVQLQESGGRLVQPGPELSLTCKTSGIDLSSNAIGWVR
QAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLMNLSRSEDTAIYYCARGGYSSDIWGQGTLVTVSSASTKGPSVFPL
APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDLNGLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

>Sequence ID 118: SI-75X11 Chain A Nucleotide Sequence

GAGGTGCAGCTGCAGGAGTCTGGCGGCGGCCTGGTGCAGGCTGGGACAGCCTGAGCCTGTCTGCTGCTGGTGTCTGGCCGCTCCTT
CAACTCCTACACCATGGGCTGGTTCGCCAGGCCCCCTGGGAAGGAGCGGGAGTTTGTGGCTGCCATCCTGTGGAGTGGCCCCACCA
CCTACTATGCTGACTCTGTGAAGGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACACTGTGTACCTGCAGATGAACAGCCTG
AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGCCCTGGGAGTGTCTGGTGTCTGGCCCCCTGGCAATGTGTACAGCTACTGGGG
CCAGGGCACCCAGGTGACTGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAAGTGCAGTTGCAAGAAAGTGGTGGTA
GACTGGTTTCAGCCTGGTGAACCTTGTCACTGACGTGTAAACAAGCGGCATTGATCTGTCTCTAACGCCATCGGATGGGTCCGA
CAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACATACTACGCAAGCTGGGCAAAAGGGCGATT
TACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAGGATACCGCGATATATTACTGTGCCAGAG
GGGGGTACTCCTCTGATATCTGGGGGCAGGGTACACTGGTTACAGTTTCATCCGCTAGCACCAAGGCCCTCTGTGTTCCTCTG
GCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGTGCCCTGGGCTGCCTGGTGAAGGACTACTTCCAGAGCCTGTGACTGTGTC
CTGGAATCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGCTCTGGCCTCTACAGCCTGTCTCTGTGG
TCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAAGCCCTCCAACACCAAGGTGGACAAGAGA
GTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGGCTGCTGGAGGCCCTCTGTGTTCTCTCT
CCCTCCCAAGCCCAAGGACACCTGATGATCTCCAGGACCCAGAAGTCACTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAG
AAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCCAGAGAAGAGCAGTACAACCTCCACCTAC
CGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCC
TGCCCCCATTTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGC
TGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAG
CCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCTGGTCTCCAAGCTGACTGTGGACAAGAG
CCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGATGCATGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGA
GCCCTGGATGA

>Sequence ID 119: SI-75X11 Chain B Amino Acid Sequence

DPQLTQSPSSLSATVGQVRVTINCQSSQSVAKNNNLAWFQQKPGKPKPLLIYSASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDF
TYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEA
LHNRFTQKSLSLSPG

>Sequence ID 120: SI-75X11 Chain B Nucleotide Sequence

GATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGT
AGCGAAGAATAATAATTTGGCATGGTTCCAACAAAAACCGGGTAACCTCCTAAACTCCTTATCTACTCAGCTTCAACCCCTTGCCG
CGGGTGTGCCAGCCGGTTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAAGATTTTGCA
ACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGC
CCCCCTCTGTGTTTCATCTTCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCTGCTCAACAACCTTCTACC
CCAGAGAAGCCAAAGGTGCAGTGAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTGTCTCCACCCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGATGCTGTGAGGTGACCCA
CCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAG
CCCCAGAAGCTGTGGAGGCCCTCTGTGTTCTCTTCCCTCCCAAGCCCAAGGACACCCCTGATGATCTCCAGGACCCCAAGAGTC
ACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGAAGTGCACAATGCCAA
GACCAAGCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGA
AGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCCTGCCCCCATTTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAG
CCCCAGGTCTACACCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTACCC
CAGTGACATTGCTGTGGAGTGGAGAGCAATGGCAGCAGCAGAGAACACTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCT
CCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTGTGTCATGCATGAGGCC
CTGCACAACCGCTTCAACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 121: SI-75X15 Chain A Amino Acid Sequence

QVQLQESGGRLVQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSE
DTAIYYCARGGYSSDIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSKDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDITLMSRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSVMEALHN
HYTQKSLSLSPG

>Sequence ID 122: SI-75X15 Chain A Nucleotide Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTACAGCCTGGTGAACCCCTGTCACTGACGTGTAAAAACAAGCGGCATTGATCT
GTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGTCTGGAGTGGATCGGAGTTATCTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGGCGATTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGCAGGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAAAGGCCCTCTGTGTTCCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCTGGTGAAGG
ACTACTTCCCAGAGCCTGTGACTGTGCTCCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTCCCTGCTGTGCTGCAGAGC
TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAA
GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCCTGCCCAGCCCCAGAGG
CTGCTGGAGGGCCCCCTCTGTGTTCCCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAGTCACCTGTGTG
GTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCC
CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
AGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATTCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTC
TACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACAT
TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACACTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGATGCATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 123: SI-75X15 Chain B Amino Acid Sequence

DPQLTQSPSSLSATVGQVRVTINCQSSQSVAKNNNLAWFQQKPGKPPKLLIYSASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDF
TYYSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDITLMSRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEAL
LHNRFTQKSLSLSPGGGGSGGGGSQVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIA
DSVNGRFTISRDNAKNTLYLQMDSLKPEDTAVYYCAADLQYGSWPPQRSSAEYDYWGQGTITVTVSS

>Sequence ID 124: SI-75X15 Chain B Amino Acid Sequence

GATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGT
AGCGAAGAATAATAATTTGGCATGGTTCCAACAAAACCGGGTAACCTCCTAAACTCCTTATCTACTCAGCTTCAACCCTTGCCG
CGGGTGTGCCAGCCGGTTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCA
ACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAACGTACGGTGGCTGC
CCCCTCTGTGTTTCATCTTCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCTGCTCAACAACCTTCTACC
CCAGAGAAGCCAAAGGTGCAGTGGAAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTGTCTCCACCCTGACCCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGTATGCCTGTGAGGTGACCCA
CCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAG
CCCCAGAAGCTGTGAGAGGCCCTCTGTGTTCCCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCAGAAAGTC
ACCTGTGTGGTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAAAGTGCACAATGCCAA
GACCAAGCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGA
AGGAGTACAAGTGTGCTGTGTCCACAAGGCCCTGCCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAG
CCCCAGGTCTACACCCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTACCC
CAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACACTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCT
CCTTCTTCCCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGATGCATGAGGCC
CTGCACAACCGCTTCACCCAGAAGAGCCTGAGCCTGAGCCCTGGAGGAGGAGGAGGCTCTGGAGGAGGAGGATCCAGGTGCAGCT
GGTGCAGTCTGGCGGAGGCCTGGTGCAGGCTGGGGGCAGCCTGAGCCTGAGCTGTGCCTTCTCTGGCCGACCTTCTCCATGTACA
CCATGGGCTGGTTCCGCCAGGCCCCAGGGAAGGAGAGAGATTTGTGGCTGCCAACAGAGGCAGAGGCCTGAGCCCAGACATTGCT
GACTCTGTGAATGGCCGCTTCAACATCTCCAGAGACAATGCCAAGAACCCTGTACCTGCAGATGGACAGCTGAAGCCAGAGGA
CACAGCTGTGTACTACTGTGCTGCTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGACTACTGGGGCC
AGGGCACCACTGTGACTGTGTCTAGCTGA

>Sequence ID 125: SI-75X13 Chain A Amino Acid Sequence

QVQLQESGGRLVQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKGLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSE
DTAIYYCARGGYSSDIWQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDITLMSRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPREPQV
YTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSVCSVMHEALHN
HYTQKSLSLSPGGGGSGGGSEVQLQESGGGLVQAGDSLSSLSCVSGRSFNSYTMGWFRQAPGKEREFVAAILWSGPTTYADSV
KGRFTISRDNKNTVYQLQMNLSLKPEDTAVYYCAAALGVLVLAPGNVYSYWGQGTQVTVSS

>Sequence ID 126: SI-75X13 Chain A Nucleotide Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTGTCACTGACGTGTAAACAAGCGGCATTGATCT
GTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGGCGATTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGCAGGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAAAGGCCCCCTGTGTTCCTCTGGCCCCCTCCTCCAAGAGCACCTCTGGAGGCACTGCTGCCCTGGGCTGCCCTGGTGAAGG
ACTACTTCCCAGAGCCTGTGACTGTGTCTGGAACCTCTGGAGCCCTGACCTCTGGAGTGCACACCTTCCCTGCTGTGCTGCAGAGC
TCTGGCCTCTACAGCCTGTCTCTGTGGTCACTGTGCCCTCCTCCAGCCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAA
GCCCTCCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGTCTGTGACAAGACCCACACCTGCCCTCCCTGCCAGCCCCAGAGG
CTGCTGGAGGCCCCCTGTGTTCCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCCAAGAGTCACTGTGTG
GTGGTGGATGTGTCCCATGAAGACCCAGAAGTGAAGTTCAACTGGTATGTGGATGGAGTGGAGGTGCACAATGCCAAGACCAAGCC
CAGAGAAGAGCAGTACAACCTCCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGAAGGAGTACA
AGTGTGCTGTGTCCAACAAGGCCCCCTGCTGCCCTCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTC
TACACCCTGCCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTCTGTGCTGTGAAAGGCTTCTACCCAGTGACAT
TGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCTCCTTCTTCC
TGGTCTCCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGAGGCCCTGCACAAC
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCTGGAGGAGGAGGAGGCTCTGGAGGAGGAGGATCCGAGGTGCAGCTGCAGGAGTC
TGGCGGCGGCTGGTGCAGGCTGGGGACAGCCTGAGCCTGTCTGCTGCTGGCCGCTCCTTCAACTCCTACACCATGGGCT
GGTTCGCGCAGGCCCCCTGGGAAGGAGCGGGAGTTTGTGGCTGCCATCCTGTGGAGTGGCCCCACCCTACTATGCTGACTCTGTG
AAGGGCCGCTTACCATCTCCAGAGACAATGCCAAGAACACTGTGTACCTGCAGATGAACAGCCTGAAGCCAGAGGACACAGCTGT
GTACTACTGTGCTGCTGCCCTGGGAGTGTGCTGCTGGCCCCCTGGCAATGTGTACAGCTACTGGGGCCAGGGCACCCAGGTGACTG
TGCTAGCTGA

>Sequence ID 127: SI-75X13 Chain B Amino Acid Sequence

DPQLTQSPSSLSATVQGRVTINCQSSQSVAKNNNLAWFQQKPGKPKPKLLIYSASTLAAGVPSRFSGSGSGTQFTLTITRVQSEDF
TYYCSARDSGNIQSFGGTRVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDITLMSRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPRE
PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSVCSVMHEA
LHNRFTQKSLSLSPG

>Sequence ID 128: SI-75X13 Chain B Nucleotide Sequence

GATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGT
AGCGAAGAATAATAATTTGGCATGGTTCCAACAAAAACCGGGTAACCTCCTAACTCCTATCTACTCAGCTTCAACCCCTTGCCG
CGGGTGTGCCAGCCGGTTCTCAGGCTCAGGTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCA
ACCTACTATTGTCTGACAGGGATTCCGGGAACATACAGTCTTTGGGGGTGGAACCTCGGGTGGAGATAAAAACGTACGGTGGCTGC
CCCCCTGTGTTCATCTTCCCACCCAGTGATGAGCAGCTGAAGAGTGGCACAGCCTCTGTGGTGTGCTGCTCAACAACCTTCTACC
CCAGAGAAGCCAAAGGTGCAGTGGAAAGGTGGACAATGCCCTGCAGAGTGGCAACAGCCAGGAGAGTGTGACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTGTCTCCACCCCTGACCCCTGTCCAAGGCTGACTATGAGAAGCACAAAGGTGTATGCCTGTGAGGTGACCCA
CCAGGGCCTGAGCAGCCCTGTGACCAAGAGCTTCAACCGAGGAGAGTGTGGAGGAGACAAGACCCACACCTGCCCTCCCTGCCAG
CCCCAGAAGCTGCTGGAGGCCCCCTGTGTTCCTCTTCCCTCCCAAGCCCAAGGACACCCTGATGATCTCCAGGACCCCAAGATC
ACCTGTGTGGTGGTGGATGTGTCATGAAGACCCAGAAGTGAAGTGAAGTGGTATGTGGATGGAGTGGAAAGTGCACAATGCCAA
GACCAAGCCCAGAGAAGAGCAGTACAACAGCACCTACCGAGTGGTGTCTGTGCTGACTGTGCTGCACCAGGACTGGCTGAATGGGA
AGGAGTACAAGTGTGCTGTGTCCAACAAGGCCCTGCCTGCCCCATTGAGAAGACCATCTCCAAGGCCAAGGGCCAGCCAGAGAG
CCCCAGGTCTACACCTGCCTCCCTCCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTGAAGGCTTCTACCC
CAGTGACATTGCTGTGGAGTGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACCACCCCTCCTGTGCTGGACTCTGATGGCT
CCTTCTTCTGTACAGCAAGCTGACTGTGGACAAGAGCCGCTGGCAGCAGGGCAATGTGTTCTCCTGCTCTGTGCATGCATGAGGCC
CTGCACAACCGCTTACCCAGAAGAGCCTGAGCCTGAGCCCTGGATGA

>Sequence ID 129: SI-38P11 Chain A Amino Acid Sequence

QIVLSQSPAILSASPGKEVTMTCRASSSVSYIHWFOQKPGSSPKPIYATSNLASGVFVRFSGSGSGTSYSLTISRVEAEDAATYY
 CQOWTSNPPTFGGGTKLTVLGGGSGGGGSGGGGSGGGGSGVQLQPPGAELVKPGASVKMCKASGYFTSYNMHWVKQTPGRGLE
 WIGAIYPNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWAGTTVTVSSGGGSGGGGSE
 VQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRA
 EDTAVYYCARDGGSSAITSNNIWGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
 PAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTHTCPPEAPEAAGGPSVFLFPPKPKDTLMISRT
 PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSV
 HEALHNHYTQKSLSLSPGGGSGGGGSDVMTQSPSSVSASVGDRTVITCQASQNIIRTYLSWYQQKPKAPKLLIYAAANLASGV
 PSRFSGSGSGTDTLTISDLEPGDAATYYCQSTYLGTDYVGGAFGGTKLTVLGGGSGGGGSGGGGSEVQLVESGGGLVQ
 PGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISSGNVYASSARGRFTISRPSSKNTVDLQMNSLRAEDTAVYYCARDS
 GYSDFPMWGQGLTVTVSS

>Sequence ID 130: SI-38P11 Chain A Nucleotide Sequence

CAGATCGTGCTGAGCCAGAGCCCCGCCATCCTGAGCGCCAGCCCCGCGCAGAAGGTGACCATGACCTGCCGGGCCAGCAGCAGCGT
 GAGCTACATCCACTGGTTCCAGCAGAAGCCCGGCAGCAGCCCCAAGCCCTGGATCTACGCCACCAGCAACCTGGCCAGCGCGTGC
 CCGTGCGGTTCCAGCGCAGCGGCAGCGGCACCAGCTACAGCCTGACCATCAGCCGGTGGAGGCCGAGGACGCCGCCACCTACTAC
 TGCCAGCAGTGGACCAGCAACCCCCACCTTCGGCGGCGGCACCAAGCTGACCGTGCTGGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAGCTGCAGCAGCCCGCGCCGAGCTGGTGAAGCCCGCGCCAGCG
 TGAAGATGAGCTGCAAGGCCAGCGGTACACCTTACCAGCTACAACATGCACTGGGTGAAGCAGACCCCCGCGCGGGCCTGGAG
 TGGATCGGCGCCATCTACCCCGGCAACGGCGACACCAGCTACAACCAGAAGTTCAAGGGCAAGGCCACCTGACCGCCGACAAGAG
 CAGCAGCACCGCTACATGCAGCTGAGCAGCCTGACCAGCGAGGACAGCGCCGTGTACTACTGCGCCGGAGCACCTACTACGGCG
 GCGACTGGTACTTCAACGTGTGGGCGCGCGCACCCAGCTGACCGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAG
 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAG
 TACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGTATATCACATACT
 ACGCCGAGCTGGGCGAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTCAAATGAACAGCCTGAGAGCC
 GAGGACACGCTGTGTATTACTGTGCGAGAGACGGTGGTCTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTTGGT
 CACCGTGCCTCAGTACAGCAACCAAGGCCATCGGTCTTCCCTTCCGACCCCTCCTCCAAGAGCACCTCTGGGGGCGACGCGGCC
 TGGGCTGCCTGGTCAAGACTACTTCCCGAACCCTGACGGTGTGCTGGAACCTCAGGCGCCCTGACAGCGCGCTGCACGCTTC
 CCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACAT
 CTGCAACGTGAATACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCAC
 CGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCACTCTTCTTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
 TAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 TGAATGGCAAGGAGTACAAGTGGCGGTCTCCAACAAAGCCCTCCAGCCCTCAGAGCCCACTCAGAGAAACCAAGGCGAG
 CCCCCGAGAACCACAGGTGTATACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGG
 CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGCAACTACAAGACCAGCCTCCCGTGTGGACT
 CGGACGGCTCCTTCTTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGCGCGGTTACAGGTGGTGGGGGATCCGA
 CGTTGTGATGACGCAGTCTCCTAGTTAGTATCAGCGTCTGTGGGGATCGAGTCACGATTACATGCCAGGCGAGCCAAATATTA
 GGACGTATCTGTCTGGTATCAACAAAGCCTGGTAAGGCTCCAAACCTCCTCATTACGCCGCTGCCAACTTGGCTAGTGGAGTA
 CCTTACGCTTGTAGTGGGTCTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACAGGGGACGCTGCCACGTATTA
 TTGCCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAACTCACTGTACTTGGTGGTGGTGGT
 CAGGCGGGGGGGTTCGGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCAAGTTGGTTGAAAGTGGGGGGGACTCGTTTCA
 CCTGGAGGCTCTTGGGACTTTCTGTACCGCTTCTGGGTTCACTATAAGTTCAATATCATATGCAATGGGTAAAGACAGGCGCCTGG
 TAAGGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGCTTATTACGCCTCATCCGCGCGGGGAGGTTTACAATTTCCA
 GGCCTTCTAGCAAAAACAGGTAGATCTGCAATGAACCTCTTCTCGCGCTGAAGATACAGCAGTCTACTACTGCGCCAGGGATTCA
 GGTATTCTGACCCCATGTGGGGGAGGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 131: SI-38P11 Chain B Amino Acid Sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSMEPEDFATYY
 CFQGSVYFPFTFGQGTQKTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLSTLCAFSGFSLTSGMGVWGIQPPGK
 LEWLAIHWDDDKRYNPALKSRITISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFFDYWGQGLTVTVSSGGGSGGGGSDV
 VMTQSPSTLSASVGDRTVINCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYC
 QGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
 DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPEAPEAAGGPSVFLFPPKPKDTLMISRTPEV
 TCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSV
 LHNRTQKSLSLSPGGGSGGGGSDIQMTQSPSTLSASVGDRTVITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSR

FSGSGSGTEFTLTISLQPDDEFATYYCQOQYSWGNVDNVFGGGKVTVLGGGSGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGS
LSLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAACIAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARSAF
SFDYAMD LWGQGLTVTVSS

>Sequence ID 132: SI-38P11 Chain B Nucleotide Sequence

AAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCCGGCTCAGGCAACGATCACACCCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCTAGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTGTTCAGCCAGGACAGACCC
TTAGCCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTGGCTGGATTCCGGCAGCCTCCCGGCAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAAATCAAGTGTACTTGCAAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTCGCGCGGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGAGGGGACTCTCGTCACGGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
GTGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCTGATCTATGAAGCATCCAACTGGCATCTGGGGTCCCAT
CAAGGTTACGCGGAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGC
CAAGGCTATTTTTATTATTTAGTCTGACTTATGTAATTTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
ACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATC
CCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
GACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGCCAG
CACCTGAAGCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC
ACATGCGTGGTGGAGCTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATGCCAA
GACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCA
AGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAA
CCACAGGTGTACACCCTGCCCCCAAGCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT
CCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
CTGCACAACAGATTACGAGAGAGCCCTCTCCTGCTCCGGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCCGACATTACAGT
GACACAGTACCCCTCATCGCTCTCAGCCTCAGTAGGCTGATAGGTTGACTACCTGCCAAGCCTCCCAATCTATAAGTTACACCC
TCAACTGGTATCAACAGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCTCAGGTGTGCTAGTCGC
TTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACTATTGTGACGA
GGGTTATAGTTGGGGAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTACTGTGTTGGGAGGGGAGGAAGTGGCGGCGGCG
GAAGCGGAGGTGGTGGCTCCGGCGGGGGTGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGC
CTCTCACTCTCTTGCGCGGCGAGTGGTTTTAGCTTCAGTAGCGGCTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCC
TGAGTGGATTGCTGTATCGCCGCGGGTCTGGTATAACATACGATGCAAACCTGGGCGAAAGGGCGCTTCACAATCTCCAGGG
ACAACTCAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTCAGCATTT
AGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 133: SI-76PM1 Chain A Amino Acid Sequence

QIVLSQSPAILASAPGKVTMTCRASSSVSYIHWFOQKPGSSPKPWIYATSNLASGVFVRFSGSGSGTSYSLTISRVEAEDAATYY
CQQTWSNPPTFGGKTLTVLGGGSGGGGSGGGGSGGGGSGVQLQPGAEVLKPGASVKMSCKASGYTFTSYNMHWVQKTPGRGLE
WIGAIYPNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVSSGGGSGGGGSE
VQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKCLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNLSRA
EDTAVYYCARDGSSAITSNNIWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEAAGPSVFLFPPKPKDITLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQ
PREPQVYTLPPSRDELTKNQVSLCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLVSKLTVDKSRWQQGNVFSVSM
HEALHNHYTQKSLSLSPGGGGSGGGGSDVVMQTQSPSSVSASVGRVITITQASQNIRTYLSWYQQKPKAPKLLIYAAANLASGV
PSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTLDYVGGAFGGGTKLTVLGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQ
PGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGGNVYASSARGRFTISRPSKNTVDLQMNLSRAEDTAVYYCARDS
GYSDPMWQGLTVTVSS

>Sequence ID 134: SI-76PM1 Chain A Nucleotide Sequence

CAGATCGTGCTGAGCCAGAGCCCCGCCATCCTGAGCGCCAGCCCCGGCGAGAAGGTGACCATGACCTGCCGGGCCAGCAGCAGCGT
GAGCTACATCCACTGGTTCCAGCAGAAGCCCGGCAGCAGCCCCAAGCCCTGGATCTACGCCACCAGCAACCTGGCCAGCGGCGTGC
CGTGCGGTTACGCGGCAGCGGCAGCGGCACCAGTACAGCCTGACCATCAGCCGGTGGAGGCCGAGGACGCCGCCACCTACTAC
TGCCAGCAGTGGACCAGCAACCCCCCACCTTCGGCGGCGGCACCAAGCTGACCGTGCTGGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAGCTGCAGCAGCCCGCGCCGAGCTGGTGAAGCCCGGCGCCAGCG

TGAAGATGAGCTGCAAGGCCAGCGGCTACACCTTACCAGCTACAACATGCACTGGGTGAAGCAGACCCCGCGGGGCTGGAG
 TGGATCGGCGCCATCTACCCCGGCAACGGCGACACCAGCTACAACCAGAAGTTCAAGGGCAAGGCCACCTGACCGCCGACAAGAG
 CAGCAGCACCGCTACATGCACTGAGCAGCCTGACCAGCGAGGACAGCGCCGTGTACTACTGCGCCCGGAGCACCTACTACGGCG
 GCGACTGGTACTTCAACGTGTGGGGCGCCGGCACCACCGTGACCGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAG
 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCATCAG
 TACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGATCGAGTATTACTGGTCGTGATATCACATACT
 ACGCGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
 GAGGACACGGCTGTGATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGT
 CACCGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
 TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGCGCCCTGACCAGCGCGGTGCACACCTTC
 CCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
 CTGCAACGTGAATCACAAAGCCAGCAACACCAAGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCAC
 CGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGACACCTCATGATCTCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCA
 TAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGC
 TGAATGGCAAGGAGTACAAGTGC CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG
 CCCCAGAACACAGGTGTATACCCTGCCCCATCCCGGGATGAGTGAACAAAGACAGGTGACCGTGTCTGCGCGGTCAAAGG
 CTTCTATCCAGCGACATCGCGGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACACCGCTCCCGTGGTGGACT
 CGACGGCTCTTCTTCTCTCGTGAGCAAGCTCACCGTGGACAAGACAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCTCTCCCTGTCTCCGGGTGGCGGCGGGGTTGAGGTGGTGGGGGATCCGA
 CGTGTGATGACGAGTCTCTTAGTTAGTATCAGCGTCTGTTGGGATCGAGTACGATTACATGCCAGGCGAGCCAAAATATTA
 GGACGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCCTCATTTACGCGCTGCCAACTTGGCTAGTGGAGTA
 CCTTCACGCTTTAGTGGGTGAGTTCTGGAACAGATTTTACGTTGACGATCTCCGATTTGGAACAGGGGACGCTGCCACGTATTA
 TTGCCAGTCCACCTACCTCGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTCACTGTACTTGGTGGTGGTGGT
 CAGCGGGGGGGGTTCGCGCGGAGGCGGTTCTGGGGGTGGAGGTTCCGAGGTTCAAGTTGAGTTGAAAGTGGGGGGGACTCGTTACG
 CCTGGAGGCTCTTTCGACTTTCTGTACCGCTTCTGGGTTCACTATAAGTTTATATCATATGCAATGGGTAAGACAGCGCGCTGG
 TAAGGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGTCTATTACGCTCATCCGCGCGGGGGAGGTTTACAATTTCCA
 GGCTTCTAGCAAAAACAGGTAGATCTGCAATGAAGTCTCTTCGCGCTGAAGATACAGCAGTCTACTACTGCGCCAGGGATTCA
 GGGTATTCTGACCCCATGTGGGGCAGGGCACATTGGTTACCGTGTCTCTTGA

>Sequence ID 135: SI-76PM1 Chain B Amino Acid Sequence

ENVLTSQSPASLSASPERVITITCSASSSVSYMHYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSEMEPEDFATYY
 CFQGSVYPFTFGQGTQKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLSTLCAFSGFSLSSTSGMGVWIRQPPGKG
 LEWLAIHWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYFDYWGQGLVTVSSGGGSGGGGSDV
 VMTQSPSTLSASVGDRTVINCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDDEFATYYC
 QGYFYFISRTYVNSFGCGTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
 DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPCPAPEAAGGSPVFLFPPKPKDTLMI SRTPEV
 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCSVMHEA
 LHNRFTHQKSLSPGGGGSGGGGSDIQMTQSPSTLSASVGDRTVITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSR
 FSGSGSGTEFTLTISLQPDDEFATYYCQQGYSGWNVNDFVGGGTQKVTVLGGGSGGGGSGGGGSGGGGSEVQLLESGLVQPGGS
 LSLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAF
 SFDYAMD LWGQGLTVTVSS

>Sequence ID 136: SI-76PM1 Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 TAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
 TGTTCACAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCTTAGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTAGCCAGGACAGACCC
 TTAGCCTCACCTGTGCCTTCAGTGGTCTTCTCTTAGCACTAGCGGTATGGGGTTCGGCTGGATTCCGCAGCCTCCCGGCAAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCGCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGACAGGGGACTCTCGTCACGGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
 GTGATGACCAAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
 TTGGTTAGCCTGGTATCAGCAGAAACAGGAAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAAACTGGGCATCTGGGTCCCAT
 CAAGGTTACAGCGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGC
 CAAGGCTATTTTTATTTTATTAGTCTGACTTATGTAAATCTTTCGGCTGTGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
 ACCATCTGTCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATC
 CCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
 GACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCCA

TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCCACCGTGCCCGAG
CACCTGAAGCCGCGGGGGGACCGTCAGTCTTCCTCTTCCCCCACCACCAAGGACACCGTCATGATCTCCCGGACCGCTGAGGTC
ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCGTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA
GACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA
AGGAGTACAAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAA
CCACAGGTGTACACCGTCCCCCAAGCCGGGATGAGCTGACCAAGAACAGGTACAGCCTGTGGTGCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT
CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
CTGCACAACAGATTACGCGAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTGATGAT
GACACAGTCACCGTCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTACACCC
TCAACTGGTATCAACAGAAACCCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCTCAGGTGTGCCTAGTCGC
TTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTCCCTCCAACCCGACGACTTCGCCACATACTATTGTGACGA
GGGTATAGTTGGGGAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTACTGTGTTGGGAGGGGGAGGAAGTGGCGCGGCG
GAAGCGGAGGTGGTGGCTCCGGCGGGGGTGAAGCGAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGC
CTCTCACTCTCTTGCAGCGGAGTGGTTTTAGCTTCAGTAGCGGTACGATATGTGCTGGGTAAAGACAGGCTCCTGGTAAAGGCCT
TGAGTGGATTGCGTGTATCGCCGCGGGTCTGCTGGTATAACATACGATGCAACTGGGCGAAAGGGCGCTTCACAATCTCCAGGG
ACAACCTCAAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTT
AGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 137: SI-68X2 Chain A Amino Acid Sequence

DIQMTQSPSSLSASVGRVTITCQASQDISNYLNWYQQKPKGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLPEDIATY
FCQHFHDLPLAFGCGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGK
CLEWIGHIYYSNTNYPNPSLKSLRTISIDTSKTQFSLKLSVTAADTAIYYCVRDRVTGAFDIWGQTMVTVSTGGGSGGGGSEV
QLVESGGGLVQPGLSLRLSCAASGFTISTNAMSWMVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAE
DTAVYYCARDGGSSAITSNNIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPP
AVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKPKCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDLMISRTF
EVTQVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQP
REPQVCTLPSPRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>Sequence ID 138: SI-68X2 Chain A Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTACCATCACTTGCCAGGCGAGTCAGGACAT
CAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAACTCCTGATCTACGATGCATCCAATTTGGAAACAGGGG
TCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACTTTACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
TTCTGTCAACACTTTGATCATCTCCCGCTCGCTTTCCGGCTGTGGGACCAAGGTGGAAATTAAAGGCGGTGGCGGTAGTGGGGGAGG
CGGTTCTGGCGGGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAGCTGCAGGAGTCCGGGCCAGGACTGGTGAAGCCTTCGGAGA
CCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCGTGACAGTGGTGATTACTACTGGACCTGGATCCGGCAGTCCCAGGGAAG
TGCTGGAGTGGATTGGACACATCTATTACAGTGGGAACACCAATTATAACCCCTCCCTCAAGAGCCGACTCACCATATCAATTGA
CACGTCCAAGACTCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCGGACACGGCCATTTATTACTGTGTGCGAGATCGAGTGA
CTGGTGCTTTTGATATCTGGGGCCAAGGGACAATGGTCAACCGTGTGCAGAGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGATATCACATACTACG
CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTCAC
CGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG
GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTGTGACAAAACCTCACACATGCCCACCGT
GCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCACCACCAAGGACACCCCTCATGATCTCCCGGACCCCT
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
TGCCAAGACAAAGCCGCGGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGA
ATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTGTACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTT
CTATCCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCG
ACGGCTCCTTCTTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAG

>Sequence ID 139: SI-68X2 Chain B Amino Acid Sequence

QSAITQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLLMIYDVSDRPSGVSDRFSGSKSGNTASLIISGLQADDEA
 DYYCSSLSSSTHVFICGCTKVTVLGGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLRLSCAASGFTFSSYMSWVRQAP
 GKCLEWVANINRDGSASYYVDSVKGRFTISRDDAKNSLYLQMNLSLRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSTGGGSGGGG
 SDVMTQSPSTLSASVGDRTVINCQASESISWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFAT
 YYCQGYFYFISRTYVNSFSGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYFPREAKVQWKVDNALQSGNSQESVTEQ
 DSKDSTYSLSSLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPCPAPEAAGGFSVFLFPPKPKDTLMISRT
 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV
 MHEALHNHYTQKSLSLSPGK

>Sequence ID 140: SI-68X2 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACAGCAGTGACGT
 TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCAAACCTCATGATCTATGATGTGACGTGACGGCCCT
 CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
 GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCTGTGGGACCAAGGTGACCGTCTAGGCGGTGGCGG
 TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCGGTGGTCA
 AGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
 GGAAGTGCCTGGAGTGGGTGGCAACATAAACCCGATGGAAGTGGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
 CTCCAGAGACGACGCCAAGAAGTCACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCAACGTGTGACAGGCGGTGGAGGGTCCGGCGGTGGTGA
 TCAGAGCTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAG
 CATTAGCAGTTGGTTAGCTGGTATCAGCAGAAACACAGGAAAGCCCCCTAAGCTCTGATCTATGAAGCATCCAACTGGCATCTG
 GGTCCCATCAAGGTTAGCGGCGAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACT
 TATTACTGCCAAGGCTATTTTTATTTTATTAGTCTACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
 GGTGGCTGCACCATCTGTCTTCTATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATA
 ACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAG
 GACAGACAGGACAGCACCTACAGCCTCAGCAGCACCTGACCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTCGCA
 AGTACCCATCAGGGGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAACTCACACATGCCAC
 CGTGCCACAGCAGTGAAGCGCGGGGGGACCGTCACTCTTCTTCCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
 TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCAGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACAGGACTGGC
 TGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAG
 CCCCAGAACACAGGTGTACACCTGCCCCCATGTGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGG
 CTTCTATCCCAGCAGCATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACT
 CGGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATAG

>Sequence ID 141: SI-68E1 Chain A Amino Acid Sequence

DIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATY
 FCQHFDFHPLAFGCGTKVEIKGGGSGGGSGGGSGGGSGVQLQESGGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGK
 CLEWIGHIYYSGNTNYPNLSKRLTISIDTSKTQFSLKLSVTAADTAIYYCVRDRTVGAFDIWDGQTMVTVSTGGGSGGGGSEV
 QLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKLEWIGVITGRDITYASWAKGRFTISRDNKNTLYLQMNLSLRAE
 DTAVYYCARDGGSSAITSNNIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
 AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPSCKDHTCPCPAPEAAGGFSVFLFPPKPKDTLMISRT
 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
 REPQVCTLPPSRDELTKNQVSLCAVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSV
 MHEALHNHYTQKSLSLSPGGGGSGGGGSRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKCLEYIGTISGGNVYYA
 SSARGRFTISRPSKNTVDLQMNLSLRAEDTAVYYCARDSGYSDPMWQGLVTVSSGGGSGGGSGGGSGGGSGGGSDVMTQSPSS
 VSASVGDRTVITCQASQNIPTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGT
 D YVGGAFGCGTKVEIK

>Sequence ID 142: SI-68E1 Chain A Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACAT
 CAGCAACTATTTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAACTCCTGATCTACGATGCATCCAATTTGGAAACAGGGG
 TCCCATCAAGGTTAGTGAAGTGGATCTGGGACAGATTTTACTTTCAACATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
 TTCTGTCAACACTTTGATCATCTCCGCTCGCTTTCGGCTGTGGGACCAAGGTGGAATTAAGGCGGTGGCGGTAGTGGGGGAGG
 CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAGCTGCAGGAGTCCGGGCCAGGACTGGTGAAGCCTTCGGAGA
 CCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCGTGAGCAGTGGTGATTACTACTGGACCTGGATCCGGCAGTCCCCAGGGAAG

TGCCTGGAGTGGATTGGACACATCTATTACAGTGGGAACACCAATTATAACCCCTCCCTCAAGAGCCGACTCACCATATCAATTGA
 CACGTCCAAGACTCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCGGACACGGCCATTTATTACTGTGTGCGAGATCGAGTGA
 CTGGTGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTGTGCGACAGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
 CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
 CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGAAGGGGTGGAGTGGATCGGAGTCATTACTGGTCTGTATATCACATACTACG
 CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATTCCAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
 GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCTGGTCAC
 CGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
 CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTGTGACAAAACCTCACACATGCCACCGT
 GCCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCT
 GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
 TGCCAAGACAAAGCCGCGGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTACGCGTCTCACCCTCTGCACCAGGACTGGCTGA
 ATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
 CGAGAACCACAGGTGTGTACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTT
 CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCG
 ACGGCTCCCTTCTTCTGTGAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGAGAT
 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCGGT
 GCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACTGCCTCTGGATTACCATCAGTAGCT
 ACCACATGCAGTGGTCCGGCAGGCACCTGGGAAGTGCCTGGAGTACATCGGAACCATTAGTAGTGGTGGTAATGTATACTACGCA
 AGCTCCGCTAGAGGCAGATTACCATCTCCAGACCTCGTCCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGA
 CACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCTATGTGGGGCCAGGGAACCCCTGGTCACCGTCTCTTCAGGCG
 GTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCC
 GTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTGTGAGGCCAGTCAGAACATTAGGACTTACTTCTGGTATCAGCAGAA
 ACCAGGGAAAGCCCTAAGCTCTGATCTATGCTGCAGCCAATCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTG
 GGACAGATTTCACTCTACCATCAGCGACTTGGAACTGGCGATGCTGCAACTTACTATTGTAGTCTACCTATCTTGGTACTGAT
 TATGTTGGCGGTGCTTTCGGCTGTGGACCAAGGTGGAGATCAAATGA

>Sequence ID 143: SI-68E1 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSDDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
 DYYCSSYSSSTHVFICGCTKVTVLGGGSGGGGSGGGGSGGGGSGVQLQESGGGLVKPGGSLRLSCAASGFTFSSYMSWVRQAP
 GKLEWVANINRDGSASYYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSTGGGSGGGG
 SDVMTQSPSTLSASVGRVTINCAQASESISSWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFAT
 YYCQGYFYFISRTYVNSFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
 DSKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGFSVFLFPPKPKDLMISRT
 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQ
 PREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV
 MHEALHNHYTQKSLSLSPGK

>Sequence ID 144: SI-68E1 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTGCATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
 TGGTGGTTATACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCAAACTCATGATCTATGATGTGAGTATCGGCCCT
 CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
 GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCTGTGGGACCAAGGTGACCGTCTAGGCGGTGGCGG
 TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAATTGCAGGAGTCCGGGGGAGGCGTGGTCA
 AGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
 GGAAGTGCCTGGAGTGGGTGGCAACATAAACC CGATGGAAGTGCAGGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
 CTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCGGTGGCACCCCTGGTCACCGTGTGCGACAGGCGGTGGAGGGTCCGGCGGTGGTGA
 TCAGACGTCTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAG
 CATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCTGATCTATGAAGCATCCAAACTGGCATCTG
 GGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACT
 TATTACTGCCAAGGCTATTTTATTTTATTAGTCTGACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
 GGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCTCTGTTGTGTGCTGCTGAATA
 ACTTCTATCCCAAGAGAGGCAAGAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAG
 GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGA
 AGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCAC
 CGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCACTCTTCTTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
 TAATGCCAAGACAAAGCCGCGGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTACGCGTCTCACCCTCTGCACCAGGACTGGC

TGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
 CCCCAGAAACCACAGGTGTACACCTGCCCCCATGTCTGGGATGAGCTGACCAAGAACAGGTGAGCCTGTGGTGCCTGGTCAAAGG
 CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACT
 CCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAG

>Sequence ID 145: SI-68E2 Chain A Amino Acid Sequence

DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPKGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLPEDIATY
 FCQHFDHPLPLAFGCGTKVEIKGGGSGGGSGGGSGGGSGGVQVQLQESGPGLVKPSSETLSLTCTVSGGSVSSGDYYWTWIRQSPGK
 CLEWIGHIYYSGNTNYPNPSLKSRLTISIDTSKTQFSLKLSVTAADTAIYYCVRDRVTGAFDIWGGQTMVTVSTGGGSGGGSEV
 QLVESSGGGLVQPGGSLRLSCAASGFTISTNAMS WVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNSLRAE
 DTA VYYCARDGSSAITSNNIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPP
 AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSKDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRT
 EVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQP
 REPQVCTLPSPRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMH
 EALHNHYTQKSLSLSPGK

>Sequence ID 146: SI-68E2 Chain A Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTACCATCACTTGCCAGGCGAGTCAGGACAT
 CAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAACTCCTGATCTACGATGCATCCAATTTGGAACAGGGG
 TCCCATCAAGGTTTCAGTGAAGTGGATCTGGGACAGATTTTACTTTACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
 TTCTGTCAACACTTTGATCATCTCCCGCTCGCTTTCGGCTGTGGACCAAGGTGGAATTAAGGCGGTGGCGGTAGTGGGGGAGG
 CGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGA
 CCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCGTGAGCAGTGGTGATTACTACTGGACCTGGATCCGGCAGTCCCCAGGGAAG
 TGCTGGAGTGGATTGGACACATCTATTACAGTGGGAACACCAATTATAACCCCTCCCTCAAGAGCCGACTCACCATATCAATTGA
 CACGTCCAAGACTCAGTTCTCCCTGAAGCTGAGTCTGTGACCGCTGCGGACACGGCCATTTATTACTGTGTGCGAGATCGAGTGA
 CTGGTGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTGTGCAGAGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
 CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
 CAATGCAATGAGCTGGGTCGGCGGAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGATATCACATACTACG
 CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
 GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTTGGTCAC
 CGTGTCTCAGCTAGCACCAAGGGCCATCGGTCTTCCCCCTGGCACCTCTCCTCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG
 GCTGCTGTGCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
 CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTGTGACAAACTCACACATGCCACCGT
 GCCAGCACCTGAAGCCGCGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGGACCCCT
 GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
 TGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAAGCTCCTCACCCTCTGCACCAGGACTGGCTGA
 ATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
 CGAGAACCACAGGTGTGTACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTT
 CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCG
 ACGGCTCCTTCTTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAG

>Sequence ID 147: SI-68E2 Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
 DYYC SSSYSSSTHVIFGCGTKVTVLGGGSGGGSGGGSGGGSGGVQVQLQESGGGLVKPGGSLRLSCAASGFTSSYYMSWVRQAP
 GKLEWVANINRDGSASYYVDSVKGRTISRDDAKNSLYLQMNSLR AEDTAVYYCARDRGVGYFDLWGRGTLTVSTGGGSGGGG
 SDVVM TQSPSTLSASVGDRTINCQASESISSWLAWYQQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISSLPDDFAT
 YYCQGYFYFISRTYVNSFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYFPREAKVQWKVDNALQSGNSQESVTEQ
 DSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRT
 PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVM
 HEALHNHYTQKSLSLSPGGGSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTSSSGYDMCWVRQAPGKCLEWIAACIAGSAG
 ITYDANWAKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCARSAFSDYAMD LGWQGLTVTVSSGGGSGGGSGGGSGGGSDI
 QMTQSPSTLSASVGDRTITCQASQSISSHLN WYQQKPKGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISSLPDDFATYYC
 QQGYSWGNVDNVFGCGTKVEIK

>Sequence ID 148: SI-68E2 Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
 TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCAACTCATGATCTATGATGTGATGATCGGCCCT
 CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
 GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCTGTGGGACCAAGGTGACCGTCTAGGCGGTGGCGG
 TAGTGCGGGGAGGCGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCGGGGGAGGCGCTGGTCA
 AGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
 GGGAAAGTGCTGGAGTGGGTGGCCAAACATAAACCCGCGATGGAAGTGCAGGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
 CTCCAGAGACGACGCCAAGAAGTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTGTGACAGGCGGTGGAGGGTCCGGCGGTGGTGG
 TCAGACGTCTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAG
 CATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACAGGGAAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTG
 GGTCCCCTGCAAGGTTCAAGCGGCTGGATCTGGCGCAGAACTCTCACCATCAGCAGCCTGACGCTGATGATTTTGCAACT
 TATTACTGCCAAGGCTATTTTTATTTTATTAGTCTGACTTATGTAATTTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
 GGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATA
 ACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG
 GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGA
 AGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCAC
 CGTGCCAGCAGCTGCAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACC
 CCTGAGGTCACATGCGTGGTGGTGGAGCTGAGCCAGAGACCTCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGGTGGAGGTGCA
 TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCAGTACCGTGTGGTCAAGCTCTCACCCTCTGCACCCAGGACTGGC
 TGAATGGCAAGGAGTACAAGTGCAGGCTCTCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
 CCCCCGAGAACCACAGGTGTACACCTGCCCCCATGTCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGG
 CTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGGTGGACT
 CCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGA
 GGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCA
 GTAGCGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGTGCCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTGGT
 ATCACTTACGACGCAACTGGGCGAAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAG
 CCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGCGCTTTTCGTTGACTACGCCATGGACCTCTGGGGCCAGGGAA
 CCCTGGTCACCGTCTCGTCTGGTGGAGGCGGTTTCAGGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGACATC
 CAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTC
 CCACCTTAAACTCGTATCAGCAGAAACAGGGAAGCCCTAAGCTGCTGATCTATATAAGGCATCCACTCTGGCATCTGGGTCCCCT
 CAAGGTTTCAGCGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGC
 CAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCTGCGGGACCAAGGTGGAGATCAATAG

>Sequence ID 149: SI-68P1 Chain A Amino Acid Sequence

DIQMTQSPSSLSASVGRVITITCQASQDISNYLNWYQQKPKGKAPKLLIYDASNLETGVPSPRFSGSGSGTDFTFTISSLQPEDIATY
 FCQHFHDLPLAFGCGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGK
 CLEWIGHIYYSGNTNYPNPSLKSLRLTISIDTSKTQFSLKLSVTAADTAIYYCVRDRVTGAFDIWGQTMVTVSTGGGSGGGGSEV
 QLVESSGGLVQPGSLRLSCAASGFTISTNAMSWVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRAE
 DTAIVYYCARDGSSAITSNNIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTSGVHTFP
 AVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVKPKCDKHTCPPEPAEAAGGPSVFLFPPKPKDTLMISRT
 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
 REPQVCTLPPSRDELTKNQVSLTCAVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFCSTMH
 EALHNHYTQKSLSLSPGGGGSGGGGSRSLVESGGGLVQPGSLRLSCTASGFTISSYHMQWVRQAPGKCLEYIGTISGGNVYYA
 SSARGRFTISRPSKNTVDLQMNLSLRAEDTAVYYCARDGSGYSDPMWGQGLVTVSSGGGSGGGGSGGGGSGGGGSDVMTQSPSS
 VSASVGRVITITCQASQNIIRTYLSWYQQKPKGKAPKLLIYAAANLASGVSPRFSGSGSGTDFTLTISDLPEGDAATYYCQSTYLGT
 D YVGAFAFCGCTKVEIK

>Sequence ID 150: SI-68P1 Chain A Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACAT
 CAGCAACTATTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCCTAACTCCTGATCTACGATGCATCCAATTTGGAAACAGGGG
 TCCCATCAAGGTCAGTGGAAAGTGGATCTGGGACAGATTTTACTTTACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
 TTCTGTCAACACTTTGATCATCTCCCGCTCGCTTTTCGGCTGTGGGACCAAGGTGGAAATTAAAGGCGGTGGCGGTAGTGGGGGAGG
 CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGA
 CCTGTCCCTCACCCTGCTCTGCTGGTGGCTCCGTCAGCAGTGGTGATTACTACTGGACCTGGATCCGGCAGTCCCAGGGAAG
 TGCTTGGAGTGGATTGGACACATCTATTACAGTGGGAACACCAATTATAACCCCTCCCTCAAGAGCCGACTCACCATATCAATTGA
 CACGTCCAAGACTCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCGGACACGGCCATTTATTACTGTGTGCGAGATCAGTGGA
 CTGGTGTCTTTGATATCTGGGGCCAAAGGGACAATGGTCACCGTGTGACAGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTG
 CAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTAC
 CAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGATATCACATACTACG

CGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAG
 GACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTCAC
 CGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGG
 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCG
 GTATCCACGATCCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
 CAACGTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACATGCCACCGT
 GCCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCT
 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
 TGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCCTCTGCACCAGGACTGGCTGA
 ATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCC
 CGAGAACCACAGGTGTGTACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGTCTGCGCGCTCAAAGGCTT
 CTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACCTACAAGACCACCGCTCCCGTGTGACTCCG
 ACGGCTCCTTCTTCTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCGGTC
 GCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACTGCCTCTGGATTACCATCAGTAGCT
 ACCACATGCAGTGGGTCCGGCAGGCACCTGGGAAGTGCCTGGAGTACATCGGAACCATTAGTAGTGGTGGTAATGTATACTACGCA
 AGCTCCGCTAGAGGCAGATTACCATCTCCAGACCCTCGTCCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGA
 CAGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCTTATGTGGGGCCAGGGAACCCCTGGTACCCTCTCTTCCAGCG
 GTGGCGGTAGTGGGGGAGGCGGTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCC
 GTGTCTGCATCTGTAGGAGACAGAGTACCATCACCTGTGAGGCCAGTCAAGACATTAGGACTTACTTATCCTGGTATCAGCAGAA
 ACCAGGGAAAGCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTG
 GGACAGATTTCTACTCTCACCATCAGCGACTTGGAACTGGCGATGCTGCAACTTACTATTGTGAGTCTACCTATCTTGGTACTGAT
 TATGTTGGCGGTGCTTTCGGCTGTGGGACCAAGGTGGAGATCAAATGA

>Sequence ID 151: SI-68Pl Chain B Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSDDVGGYNFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
 DYCCSSYSSSTHVFICGKTVTLGGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLRLSCAASGFTFSSYWMSWVRQAP
 GKCLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGLVTVSTGGGGSGGGG
 SDVVMTQSPSTLSASVGDRTINCAQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDDEFAT
 YYCQGYFYFI SRTYVNSFGGGKVEIKRTVAAPSVFIFPPSDEQLKSTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
 DSKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSPVTKSFNRGECGGDKHTHTCPCPAPEAAGGSVFLFPKPKDTLMI SRT
 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQ
 PREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVM
 HEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKCLEWIAICAAAGSAG
 ITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMD LWGQGLVTVSSGGGGSGGGSGGGSGGGSGGGSDI
 QMTQSPSTLSASVGDRTITCQASQSISSHLNWIYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDDEFATYYC
 QQGYSWGNVDNVFGCGTKVEIK

>Sequence ID 152: SI-68Pl Chain B Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
 TGGTGGTTATACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGGCCCAAACCTCATGATCTATGATGTCAGTGATCGGCCCT
 CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCTCCTGATCATCTCTGGCTCCAGGCTGACGACGAGGCT
 GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCCGGCTGTGGGACCAAGGTGACCGTCTAGCGGTGGCGG
 TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCCGGGGGAGGCCTGGTCA
 AGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
 GGAAGTGCCTGGAGTGGGTGGCCAACATAAACCCGATGGAAGTGCGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
 CTCCAGAGACGACGCCAAGAATCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
 ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTGTGACAGGCGGTGGAGGGTCCGGCGGTGGTGA
 TCAGACGTCTGTGATGACCCAGTCTCCTTCCACCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAG
 CATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGGCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTG
 GGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCT
 TATTACTGCCAAGGCTATTTTATTTTATTAGTCGTACTTATGTAAATTCTTTCCGGCGGAGGGACCAAGGTGGAGATCAAACGTAC
 GGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATA
 ACTTCTATCCCAGAGAGGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAG
 GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCCA
 AGTCACCATCAGGGCCTGAGCTCGCCCTCACAAAGAGCTTCAACAGCGGAGAGTGTGGAGGCGCAAAAACCTCACACATGCCAC
 CGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACC
 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
 TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCCTCTGCACCAGGACTGGC
 TGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG
 CCCCAGAACACAGGTGTACACCCTGCCCCCATGTCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGG

CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT
 CCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATG
 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGA
 GGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCA
 GTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGTGCCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTGGT
 ATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAG
 CCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTTTTCGTTGACTACGCCATGGACCTCTGGGGCCAGGGAA
 CCCTGGTCACCGTCTCGTCTGGTGGAGGCGGTTACAGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGACATC
 CAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCAACATCACTTGCCAGGCCAGTCAGAGCATTAGTTC
 CCACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCAT
 CAAGGTTACAGCGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCTATTACTGC
 CAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCTGCGGGACCAAGGTGGAGATCAAAATAG

>Sequence ID 153: SI-49R26 Chain A Amino Acid Sequence

FLNSLFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNWAYESQASCMSQNASLLKVYSKEDQDLLKLKVSYHWMGLVHIPTN
 GSWQWEDGSILSPNLLTIIEMQKGDALYASSFKGYIENCSTPNYICMORTVASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPPCPAPEAAG
 GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCA
 VSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLVS
 KLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPG

>Sequence ID 154: SI-49R26 Chain A Nucleotide Sequence

TTTCTTAATTCCCTTTTCAACCAAGAGGTTAGATCCCTTGACTGAAAGCTATTGCGGCCCTTGTCCGAAAACTGGATATGTTA
 CAAGAATAATTGTTACCAATCTTCGACGAAAGCAAGAACTGGTATGAGAGTCAGGCGTCTTGATGAGTCAGAATGCCAGCCTGC
 TTAAGGTTTATTCAAAGAAGACCAGGATCTGCTTAAGTTGGTAAAGACTACCACTGGATGGGGCTGGTACATATCCCAACGAAT
 GGGTCATGGCAGTGGGAGGACGGTCTATTCTGAGTCCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGCCCTGTA
 TGCATCATCCTTCAAGGGGTACATCGAGAACTGCAGTACCCCAAATACCTACATTTGTATGCAAAGAACGGTTGCTAGCACCAAGG
 GCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
 CCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCTGACAGCGCGCTGCACACCTTCCCGGCTTCCTACAGTCTCAGGACT
 CTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGCCAGCA
 ACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGG
 GGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGA
 CGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG
 AGCAGTACGCCAGCACGTACCGTGTGGTGCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCG
 GTCTCCAACAAGCCCTCCCAGCCCCATCGAGAAAACCTCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTGTACCCT
 GCCGCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGCTGCGCCGTCAAAGGCTTCTATCCAGCGACATCGCCGTGG
 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCGTGAGC
 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC
 GCAGAAGAGCCTCTCCCTGTCTCCGGTTAA

>Sequence ID 155: SI-49R26 Chain B Amino Acid Sequence

FLNSLFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNWAYESQASCMSQNASLLKVYSKEDQDLLKLKVSYHWMGLVHIPTN
 GSWQWEDGSILSPNLLTIIEMQKGDALYASSFKGYIENCSTPNYICMORTVRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY
 PREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCP
 APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG
 KEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSG
 SFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPG

>Sequence ID 156: SI-49R26 Chain B Nucleotide Sequence

TTCTTAAACTCATTATTCAACCAAGAAGTTCAAATTCCTTGACCGAAAGTTACTGTGGCCCATGTCCTAAAACTGGATATGTTA
 CAAAAATAACTGTACCAATTTTTTGATGAGAGTAAAACTGGTATGAGAGCCAGGCTTCTTGATGTCTCAAAATGCCAGCCTTC
 TGAAAGTATACAGCAAAGAGGACCAGGATTTACTTAAACTGGTGAAGTACATATCATTGGATGGGACTAGTACACATTCCAACAAAT
 GGATCTTGGCAGTGGGAAGATGGCTCCATTCTCTCAACCACTTCAACAAATTAATGAAATGCAGAGGGAGACTGTGCCTCTA
 TGCTCTGAGCTTTAAAGGCTATATAGAAAACCTGTCAACTCCAAATACGTACATCTGCATGCAAAGGACTGTGCGTACGGTGGCTG
 CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTAT
 CCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAA
 GGACAGCACCTACAGCCTCAGCAGCACCTGACGTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACC
 ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGCCCA
 GCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT

CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
AGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACCTACCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGC
AAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGA
ACCACAGGTGTACACCCTGCCCCATGTGCGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCCTGGTCAAAGGCTTCTATC
CCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGC
TCTTCTTCTCTATAGCAAGCTCACCCTGGACAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC
TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA

>Sequence ID 157: SI-49R27 Chain A Amino Acid Sequence

EIVMTQSPSTLSASVGRVITTCQASESISSWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
YQGYFYFISRTYVNSFGCGTKLTVLSTGSGSKPGSGEGSTKGEVQLVESGGGLVQPGGSLRLSCTASGFTISTNAMSWVRQAPG
KCLEWVGVIITGRDITYYASWAKGRFTISRDTSKNTVYLMNSLRAEDTAVYYCARDGGSSAITSNNIWWQGTLLTVSTGGGGSGGG
GSFLNSLFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNWYESQASCMSQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIP
TNGSWQWEDGSILSPNLLTIEMQKGDALYASSFKGYIENCSTPNTYICMQRVTASTKGPSVFLAPSSKSTSGGTAAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTIKAKGQPREPQVCTLPFSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTFPVLDSDGSFFL
VSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPG

>Sequence ID 158: SI-49R27 Chain A Nucleotide Sequence

GAGATCGTGATGACACAATCTCCATCTACGCTCTCCGCTCAGTGGGCGATAGAGTAATTATTACTTGTCAAGCCTCAGAGAGCAT
TTCATCATGGCTCGCTTGGTATCAGCAAAAGCCTGGGAAGGCCCAACTTCTCATCTATGAAGCATCAAAGCTGGCCTCTGGGG
TTCGCTCTCGCTTCTCCGGGTCCGCGAGTGGTGACAGAGTTTACGTTGACTATATCTTCTTTGCAACCTGACGATTTCCGAACATAT
TATTGCCAGGGATACTTTTATTTTATTTCCGAACATATGTTAACTCTTTTGGGTGCGGGACCAAACTCACTGTGCTGGGGTCTAC
CGGTAGTGGTTCTAAGCCTGGTTCAGGCGAAGGCAGTACGAAAGGGGAAGTGCAACTGGTTCGAAAGCGGTGGAGGGCTTGTTCAC
CTGGAGGAAGCCTCCGCTTGTCTGTCACGGCTAGCGGCTTTACAATAAGTACGAACGCCATGAGCTGGGTCCGGCAGGCTCCAGGT
AAGTGTCTCGAATGGGTGGGGGTGCATAACAGGCAGGGACATTACCTACTACGCCAGTTGGGCCAAGGGTCGATTTACCATTTCTAG
AGATACATCCAAGAACACGGTGTACCTCCAGATGAATTCTCTTAGGGCGGAAGACACAGCAGTATACTACTGCGCGCGAGATGGCG
GGAGCAGTGCAGTCCAACAACATCTGGGGTCAGGGCACTCTGTGTCAGGCTGTCGACTGGCGGTGGAGGGTCCGGCGGTGGT
GGATCATTTCTTAATTCCCTTTTCAACCAAGAGGTTGAGATCCCTTGACTGAAAGCTATTGCGGCCCTTGTCCGAAAACTGGAT
ATGTTACAAGAATAATTGTTACCAATTCTTCGACGAAAGCAAGAACTGGTATGAGAGTCAGGCGTCTTGTATGAGTCAGAATGCCA
GCCTGCTTAAGGTTTATTCAAAGAAGACCAGGATCTGCTTAAGTTGGTAAAGAGCTACCACTGGATGGGGCTGGTACATATCCCA
ACGAATGGGTGATGCGAGTGGGAGGACGGTTCTATTTGAGTCCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGC
CCTGTATGCATCATCCTTCAAGGGGTACATCGAGAACTGCAGTACCCCAAATACCTACATTTGTATGCAAAGAACGGTTGCTAGCA
CCAAGGGGCCATCGGTCTTCCCTTGGCACCCCTCCTCAAAGACACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
TACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCTGACCAAGCGGCTGCACACCTTCCCGGTGTCTTACAGTCTCT
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCC
GCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
GGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC
GGGAGGAGCAGTACGCCAGCAGTACCGTGTGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
TGCGCGGTCTCCAAACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGATGTG
TACCCTGCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCTGTCTGCGCGGTCAAAGGCTTCTATCCGACGCGATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGACTCCGACGGCTCTTCTCTCTC
GTGAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA

>Sequence ID 159: SI-49R27 Chain B Amino Acid Sequence

FLNSLFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNWYESQASCMSQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIPTN
GSWQWEDGSILSPNLLTIEMQKGDALYASSFKGYIENCSTPNTYICMQRVTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY
PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCP
APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG
KEYKCAVSNKALPAPIEKTIKAKGQPREPQVYTLFPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTFPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPG

>Sequence ID 160: SI-49R27 Chain B Nucleotide Sequences

TTCTAAACTCATTATTCAACCAAGAAGTTCAAATTCCTTGACCGAAAGTTACTGTGGCCCATGTCTAAAACTGGATATGTTA
CAAAAATAACTGTACCAATTTTTTATGATGAGAGTAAAACTGGTATGAGAGCCAGGCTTCTTGTATGTCTCAAAATGCCAGCCTTC
TGAAAGTATACAGCAAGAGGACCAGGATTTACTTAAACTGGTGAAGTCATATCATTGGATGGGACTAGTACACATTCACAAAT

GGATCTTGGCAGTGGGAAGATGGCTCCATTCTCTACCCAACTACTAACAATAATTGAAATGCAGAAAGGAGACTGTGCACTCTA
 TGCTTCGAGCTTTAAAGGCTATATAGAAAACCTGTTCAACTCCAAATACGTACATCTGCATGCAAAGGACTGTGCGTACGGTGGCTG
 CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAAATTCTAT
 CCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAA
 GGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGAGCACTACAGAAACACAAAGTCTACGCCTGCCAAGTCAACC
 ATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAACTCACACATGCCACCGTGGCCA
 GCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGACCCCTGAGGT
 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATGCCA
 AGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGC
 AAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGA
 ACCACAGGTGTACACCTGCCCCATGTCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATC
 CCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCGAGCCGGAGAGCAACTACAAGACCACGCTCCCGTGGCTGGACTCCGACGGC
 TCCTTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC
 TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA

>Sequence ID 161: SI-49R25 Chain A Amino Acid Sequence

EIVMTQSPSTLSASVGDRIITCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
 YCQGYFYFISRTYVNSFGCGTKLTVLSTGSGSKPGSGEGSTKGEVQLVESGGGLVQPGGSLRLSCTASGFTISTNAMSWVRQAPG
 KCLEWVGIVITGRDITYYASWAKGRTISRDTSKNTVYLMQNSLRAEDTAVYYCARDGSSAITSNNIWGGTGLTVTVSTGGGSGGG
 GSFLNSLFNQEVQIPLTESYCGPCPNWICYKNNCYQFFDESKNWEYQASCMQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIP
 TNGSWQWEDGSILSPNLLTIEMQKGDALYASSFKGYIENCSTPNTYICMQRVASTKGPSVFLAPSSKSTSGGTAAAGCLVKD
 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNPKVDKRVPEKSCDKHTHTCPPEAPEA
 AGGFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
 CAVSNKALPAPIEKTIISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLL
 VSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPG

>Sequence ID 162: SI-49R25 Chain A Nucleotide Sequence

GAGATCGTGATGACACAATCTCCATCTACGCTCTCCGCTCAGTGGGCGATAGAGTAATTATTACTTGTCAAGCCTCAGAGAGCAT
 TTATCATGGCTCGCTGGTATCAGCAAAAGCCTGGGAAGGCCCAAACTTCTCATCTATGAAGCATCAAAGCTGGCTCTGGGG
 TTCCGTCTCGCTTCTCCGGGTCCGGCAGTGGTGCAGAGTTTACGTTGACTATATCTTCTTTGCAACCTGACGATTTTCGCAACATAT
 TATTGCCAGGGATACTTTTATTTTATTTCCCGAACATATGTTAACTCTTTGGGTGCGGGACCAAACTCACTGTGCTGGGGTCTAC
 CGGTAGTGGTTCTAAGCCTGGTTCAGGCGAAGGCAGTACGAAAGGGGAAGTGCAACTGGTCGAAAGCGGTGGAGGGCTGTTCAC
 CTGGAGGAAGCCTCCGCTTGTCTGCACGGCTAGCGGCTTTACAATAAGTACGAACGCCATGAGCTGGTCCGGCAGGCTCCAGGT
 AAGTGTCTCGAATGGGTGGGGTGCATAACAGGCAGGGACATTACCTACTACGCCAGTTGGGCCAAGGGTCGATTTACCATTTCTAG
 AGATACATCCAAGAACACGGTGTACCTCCAGATGAATTCTCTTAGGGCGGAAGACACAGCAGTATACTACTGCGCGCGAGATGGCG
 GGAGCAGTGGATCACATCCAACACATCTGGGTCAAGGCACCTTGTGCACGGTGTGACTGGCGGTGGAGGGTCCGGCGGTGGT
 GGATCATTTCTTAATTCCTTTTCAACCAAGAGGTTGAGATCCCTTGACTGAAAGCTATTGCGGCCCTTGTCCGAAAACTGGAT
 ATGTTACAAGAATAATTGTTACCAATTCTTCGACGAAAGCAAGAACTGGTATGAGAGTCAGGCGTCTTGTATGAGTCAGAATGCCA
 GCCTGCTTAAGGTTTATTCAAAAGAAGACCAGGATCTGCTTAAGTTGGTAAAGAGCTACCACTGGATGGGGCTGGTACATATCCCA
 ACGAATGGGTCTATGGCAGTGGGAGGACGGTTCTATTCTGAGTCCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGC
 CCTGTATGCATCATCCTTCAAGGGGTACATCGAGAAGTGCAGTACCCCAAAATACCTACATTTGTATGCAAAGAACGGTTGTAGCA
 CCAAGGGCCCATCGGTCTTCCCTTGGCACCCTCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
 TACTTCCCCAACCCGGTGCAGGTGTCGTGGAACCTCAGGCGCCCTGACGAGCGCGTGCACACCTTCCCGGTCTCTTACAGTCTC
 AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAAGCC
 GCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
 GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC
 GGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
 TGGCGGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTG
 TACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCGCTCAAAGGCTTCTATCCAGCGACATCG
 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTC
 GTGAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA

>Sequence ID 163: SI-49R25 Chain B Amino Acid Sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSEMEPEDFATYY
 CFQGSVYPFTFGQGTLEIKGSTGSGSKPGSGEGSTKQVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVWIRQPPGKGLE
 WLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLMQNSLDAEDTAVYYCARMELWSYFYDYWGQGLTVTVSTGGGSGGGGSLNS
 LFNQEVQIPLTESYCGPCPNWICYKNNCYQFFDESKNWEYQASCMQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIPTNGSWQ
 WEDGSILSPNLLTIEMQKGDALYASSFKGYIENCSTPNTYICMQRVTRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREA

KVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEA
 AGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
 CAVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL
 YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPG

>Sequence ID 164: SI-49R25 Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
 TGTTCACAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAATTGGAGATAAAGGGAAGTACTGGTTCTGGGTCTAAACC
 CGGTTCCGGCGAAGGTAGTACTAAAGGACAGGTCACATTGAAGGAATCTGGCCCCGCTTGTTCAGCCAGGACAGACCCTTAGGC
 TCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGTTCGGCTGGATTTCGGCAGCCTCCCGCAAAGGTCTTGAG
 TGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAA
 AATCAAGTGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGTCTTACT
 ACTTTGATTATTGGGGGCGAGGGGACTCTCGTCACGGTGTGCACTGGCGGTGGAGGGTCCGGCGGTGGTGGATCATTCCTAAACTCA
 TTATTCAACCAAGAAGTTCAAATTCCTTGACCGAAAGTTACTGTGGCCCATGTCTAAAAACTGGATATGTTACAAAAATAACTG
 CTACCAATTTTTTATGAGAGTAAAACTGGTATGAGAGCCAGGCTTCTTGATGTCTCAAAATGCCAGCCTTCTGAAAGTATACA
 GCAAAGAGGACCAGGATTTACTTAAACTGGTGAAGTCATATCATTTGGATGGGACTAGTACACATTCACAAATGGATCTTGGCAG
 TGGGAAGATGGCTCCATTCTCTCACCAACCTACTAACAATAATTGAAATGCAGAAGGGAGACTGTGCACTCTATGCCTCGAGCTT
 TAAAGGCTATATAGAAAAGTGTCAACTCCAATACGTACATCTGCATGCAAAGGACTGTGCGTACGGTGGCTGCACCATTCTGTCT
 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCC
 AAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTA
 CAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCCAAGTCAACCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAAGCC
 GCGGGGGGACCGTCAGTCTTCTCTTCCCCCACCACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
 GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC
 GGAGGAGCAGTACGCCAGCAGTACCGTGTGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC
 TGCGCGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTA
 CACCCTGCCCCCATGTGGGATGAGCTGACCAAGAACCAGGTCAAGCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
 CCGTGGAGTGGGAGAGCAATGGGAGCCGGAGAACACTACAAGACCACGCCTCCGTGCTGGACTCCGACGGCTCCTTCTTCTCCT
 TATAGCAAGTCAACCGTCAAGAGCAGGTGGCAGAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTTAA

>Sequence ID 165: SI-49P_x Chain A Amino Acid Sequence

EIVMTQSPSTLSASVGRVITTCQASESISWLAWYQQKPKGAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
 YCQGYFYFISRTYVNSFGCGTKLTVLGSTGSGSKPGSGEGSTKGEVQLVESGGGLVQPGGSLRLSCTASGFTISTNAMSWSVRQAPG
 KCLEWVGVIITGRDITYYASWAKGRFTISRDTSKNTVYLMNSLRAEDTAVYYCARDGSSAITSNNIWQGTLLTVSTGGGGSGGG
 GSFLNSLFNQEQIPLTESYCGPCPNWICYKNNCYOFFDESKNYESQASCMSQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIP
 TNGSQWQWEDGSILSPNLLTIEMQKGDALYASSFKGYIENCSTPNTYICMQRVASTKGPSVFPLAPSSKSTSGGTAAALGCLVKD
 YFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEA
 AGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
 CAVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLCAVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL
 VSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPG

>Sequence ID 166: SI-49P_x Chain A Nucleotide Sequence

GAGATCGTGATGACACAATCTCCATCTACGCTCTCCGCTCAGTGGGCGATAGAGTAATTATTACTTGTCAAGCCTCAGAGAGCAT
 TTCATCATGGCTCGCTGGTATCAGCAAAAGCCTGGGAAGGCCCCAACTTCTCATCTATGAAGCATCAAAGCTGGCTCTGGGG
 TTCCGTCTCGCTTCTCCGGGTCGGCAGTGGTGCAGAGTTTACGTTGACTATATCTTCTTTGCAACCTGACGATTTTCGCAACATAT
 TATTGCCAGGGATACTTTTATTTTATTTCCCGAACATATGTTAACTCTTTTGGGTGCGGGACCAAACCTCACTGTGCTGGGGTCTAC
 CGGTAGTGGTTCTAAGCCTGGTTCAGGCGAAGGAGTACGAAAGGGGAAGTGCAACTGGTTCGAAAGCGGTGGAGGGCTTGTTCAC
 CTGGAGGAAGCCTCCGCTTGTCTGCACGGCTAGCGGCTTTACAATAAGTACGAACGCCATGAGCTGGGTCCGGCAGGCTCCAGGT
 AAGTGTCTCGAATGGGTGGGGTGCATAACAGGCAGGGACATTACCTACTACGCCAGTTGGGCCAAGGGTCGATTTACCATTTCTAG
 AGATACATCCAAGAACACGGTGTACCTCCAGATGAATTCTCTTAGGGCGGAAGACACAGCAGTATACTACTGCGCGCGAGATGGCG
 GGAGCAGTGGCATCATACCAACATCTGGGTCAAGGCACTTGTACCGGTGTCGACTGGCGGTGGAGGGTCCGGCGGTGGT
 GGATCATTTCTTAATTCCTTTTCAACCAAGAGGTTTCAGATCCCCCTTGACTGAAAGCTATTGCGGCCCTTGTCCGAAAAACTGGAT
 ATGTTACAAGAATAATTGTTACCAATTCTTCGACGAAAGCAAGAACTGGTATGAGAGTCAGGCGTCTTGTATGAGTCAGAATGCCA
 GCCTGCTTAAGGTTTATTCAAAGAAGACCAGGATCTGCTTAAGTTGGTAAAGAGCTACCACTGGATGGGGCTGGTACATATCCCA
 ACGAATGGGTCTAGGAGTGGGAGGACGGTTCTATTCTGAGTCCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGC
 CCTGTATGCATCATCCTTCAAGGGGTACATCGAGAACTGCAGTACCCCAAAATACCTACATTTGTATGCAAAGAACGGTTGCTAGCA
 CCAAGGGGCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC

TACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTC
 AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCC
 GCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
 GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGC
 GGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
 TGCGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTG
 TACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTTCTATCCCAGCGACATCG
 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTCCTC
 GTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTTAA

>Sequence ID 167: SI-49P_x Chain B Amino Acid Sequence

ENVLTQSPASLSASPERVTITCSASSSVSYMHWYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
 CFQGSVYPFTFGQGTKEIKSTGSGSKPGSGEGSTKGQVTLKESGPGLVQPQGLRLTCAFSGFLSTSGMGVGVIRQPPGKGLE
 WLAHIWDDDKRYPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYDWGQGLTVTVSTGGGSGGGGSFLNS
 LFNQEVQIPLTESYCGPCPNWICYKNNCYQFFDESKNWEYQASCMQNASLLKVYSKEDQDLLKLKVSYHWMGLVHIPNWSWQ
 WEDGSILSPNLLTIEMQKGDICALYASSFKGYIENCSTPNTYICMQRTVVRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
 KVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPFPAPEA
 AGGFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
 CAVSNKALPAPIEKTI SKAKGQPREPQVYTLPPCDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL
 YSKLTVDKSRWQQGNVFSQSMHEALHNYTKQKSLSPGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMC
 WVRQAPGKCLEWIAAGSAGITYDANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMDLDWGQGLTVTVSS
 GGGSGGGSGGGSGGGSDIQMTQSPSTLSASVGDRTITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFSGSG
 SGTEFTLTISSLQPDFFATYYCQQGYSWGNVDNVFGCGTKVEIK

>Sequence ID 168: SI-49P_x Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
 CTATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTTCCGGCTCAGGCAACGATCACACCCCTTACGATTTCCAGTATGGAACCCGAGATTTTGAACCTATTAT
 TGTTTCCAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAATTGGAGATAAAGGGAAGTACTGGTTCTGGGTCTAAACC
 CGGTTCCGGCGAAGGTAGTACTAAAGGACAGGTACATTGAAGGAATCTGGCCCCGCGCTTGTTCAGCCAGGACAGACCCTTAGGC
 TCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTGCGCTGGATTCGGCAGCCTCCCGGCAAAGGTCTTGAG
 TGTTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAA
 AATCAAGTGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGTCTTACT
 ACTTTGATTATTGGGGGCAGGGGACTCTCGTCACGGTGTCTGACTGGCGGTGGAGGGTCCGGCGGTGGTGGATCATTTCTAAACTCA
 TTATTCAACCAAGAAGTTCAAATTCCTTGACCGAAAGTTACTGTGGCCCATGTCTTAAAACTGGATATGTTACAAAAATAACTG
 CTACCAATTTTTTGATGAGAGTAAAACTGGTATGAGAGCCAGGCTTCTGTATGTCTCAAATGCCAGCCTTCTGAAAGTATACA
 GCAAAGAGGACAGGATTTACTTAACTGGTGAAGTCATATCATTTGGATGGGACTAGTACACATTCACAAATGGATCTTGGCAG
 TGGAAGATGGCTCCATTCTCTACCCAACTACTAACAATAATTGAAATGCAGAAGGGAGACTGTGCACTCTATGCCTCGAGCTT
 TAAAGGCTATATAGAAAAGTGTCAACTCCAAATACGTACATCTGCATGCAAAGGACTGTGCGTACGGTGGCTGCACCATCTGTCT
 TCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCGAGAGGCC
 AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTA
 CAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCTGA
 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCC
 GCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
 GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGC
 GGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
 TGGCGGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTA
 CACCCTGCCCCATGTGCGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTCCTC
 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTG
 GGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCACTAGCGGGTACGACATGTGC
 TGGGTCCGCGCAGGCTCCAGGGAAGTGCCTGGAGTGGATCGCATGATTGCTGCTGGTAGTGTGGTATCACTTACGACGCGAAGT
 GCGGAAAGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
 CCGTATATTACTGTGCGAGATCGGCGTTTTCTGTTGACTACGCCATGGACCTCTGGGGCCAGGGAACCCCTGGTACCGTCTCGTCT
 GGTGGAGGCGGTTTACGGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGACATCCAGATGACCCAGTCTCCTTC
 CACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCCTCACTTAACTGGTATCAGC
 AGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTACGCGCAGTGG

TCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGG
TAATGTTGATAATGTTTTTCGGCTGCGGGACCAAGGTGGAGATCAAAATAG

>Sequence ID 169: SI-49P8 Chain A Amino Acid Sequence

EIVMTQSPSTLSASVGDRIITCQASESISSWLAWYQQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
YCGQYFYFISRTYVNSFGCGTKLTVLGSTGSGSKPGSGEGSTKGEVQLVESGGGLVQPGGSLRLSCTASGFTISTNAMSVMRQAPG
KCLEWVGIVITGRDITYYASWAKGRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARDGGSSAITSNNIWQGGTLVTVSTGGGSGGG
GSFLNSLFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNYESQASCMSQNASLLKVYSKEDQDLLKLKVS YHWMGLVHIP
TNGSWQWEDGSILSPNLLTIEMQKGDICALYASSFKGYIENCSTPNTYICMQRVASTKGPSVFPPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKHTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTIKAKGQPREPQVCTLPPSRDELTKNQVLSLCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL
VSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPGGGGSGGGGSRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWV
RQAPGKCLEYIGTISGGNVYASARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARDGSDPMWQGGTLVTVSSGGGSGGG
GGSGGGSGGGGSDVMTQSPSSVSASVGDRTITCQASQNIITYLSWYQQKPKGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTL
TISDLEPGDAATYYCQSTYLGTDYVGGAFGCGTKVEIK

>Sequence ID 170: SI-49P8 Chain A Nucleotide Sequence

GAGATCGTGATGACACAATCTCCATCTACGCTCTCCGCTCAGTGGGCGATAGAGTAATTATTACTTGTCAAGCCTCAGAGAGCAT
TTCATCATGGCTCGCCTGGTATCAGCAAAAGCCTGGGAAGGCCCCCAAACCTTCTCATCTATGAAGCATCAAAGCTGGCCTCTGGGG
TTCCGTCTCGCTTCTCCGGGTCCGGCAGTGGTGACAGATTTACGTTGACTATATCTTCTTTGCAACCTGACGATTTTCGAACATAT
TATTGCCAGGGATACTTTTATTTTATTTCCCGAACATATGTTAACTCTTTTGGGTGCGGGACCAAACCTCACTGTGCTGGGGTCTAC
CGGTAGTGGTTCTTAAGCCTGGTTCAGGCGAAGGCAGTACGAAAGGGGAAGTGCAACTGGTTCGAAAGCGGTGGAGGGCTTGTTC AAC
CTGGAGGAAGCCTCCGCTTGTCTGCACGGCTAGCGGCTTTACAATAAGTACGAACGCCATGAGCTGGGTCCGGCAGGCTCCAGGT
AAGTGTCTCGAATGGGTGGGGGTGATAACAGGCAGGGACATTACCTACTACGCCAGTTGGGCCAAGGGTCGATTTACCATTCTAG
AGATACATCCAAGAACACGGTGTACCTCCAGATGAATTCTCTTAGGCGCGGAAGACACAGCAGTATACTACTGCGCGCGAGATGGCG
GGAGCAGTGCGATCACATCCAACAACATCTGGGGTCAGGGCACTCTGTACAGGTGTCGACTGGCGGTGGAGGGTCCGGCGGTGGT
GGATCATTTCTTAATTCCTTTTCAACCAAGAGGTTGAGATCCCTTGACTGAAAGCTATTGCGGCCCTTGTCCGAAAACTGGAT
ATGTTACAAGAAATTAATTGTTACCAATTCTTCGACGAAAGCAAGAACTGGTATGAGAGTCAGGCGCTTGTATGAGTCAGAATGCCA
GCCTGCTTAAGGTTTATTCAAAGAAGACAGGATCTGCTTAAGTTGGTAAAGAGCTACCACTGGATGGGGCTGGTACATATCCCA
ACGAATGGGTGATGGCAGTGGGAGGACGGTCTTATTCTGAGTCCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGC
CCTGTATGCATCATCCTTCAAGGGGTACATCGAGAACTGCAGTACCCCAAAATACCTACATTTGTATGCAAAGAACGGTTGCTAGCA
CCAAGGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
TACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTTACAGTCCTC
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCGAAAGCAAGAACTGTGACAAAACCTCACACATGCCACCGGTGCCAGCACCTGAAGCC
GCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC
GGGAGGAGCAGTACGCCAGCAGTACCGTGTGGTCAAGCTCCTCAGCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAG
TGCGCGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTG
TACCTTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCTGCTCCTGCGCCGTCAAAGGCTTCTATCCAGCGACATCG
CCGTGGAGTGGGAGAGGAGGAGCGGAGAGCAACAGTACAGACACGCTCCCGTGTGAGTCCGACGGCTCCGCTCTTCTTCTCTC
GTGAGCAAGCTCAGCGTGAAGAGCAGGTGGCAGAGGGAACGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCGGTGCTGGTGGAGTCTGGGG
GAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACTGCCTCTGGATTACCATCAGTAGCTACCACATGCAGTGGGTC
CGGCAGGCACCTGGGAAGTGCCTGGAGTACATCGGAACATTAGTAGTGGTGGTAATGTATACTACGCAAGCTCCGCTAGAGGCAG
ATTACCATCTCCAGACCCTCGTCCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACT
GTGCGAGAGACTCTGGTTATAGTGATCCTATGTGGGGCCAGGGAACCTGGTCACCGTCTCTTCAGGCGGTGGCGGTAGTGGGGGA
GGCGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG
AGACAGAGTCACCATCACCTGTGAGGCCAGTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACAGGGAAGCCCTTA
AGCTCCTGATCTATGCTGCAGCAATCTGGCATCTGGGGTCCCATCAAGGTTCAAGCGGAGTGGATCTGGGACAGATTTCACTCTC
ACCATCAGCGACTTGAACCTGGCGATGCTGCAACTTACTATTGTCACTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTT
CGGCTGTGGGACCAAGGTGGAGATCAAATGA

>Sequence ID 171: SI-49P8 Chain B Amino Acid Sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSEMEPEDFATYY
CFQGSVYPFTFGQGTKEIKGSTGSGSKPGSGEGSTKQVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVWIRQPPGKGLE
WLAHIWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYDYWGQGTIVTVSTGGGSGGGGSLNS
LFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNYESQASCMSQNASLLKVYSKEDQDLLKLKVS YHWMGLVHIPTNGSWQ
WEDGSILSPNLLTIEMQKGDICALYASSFKGYIENCSTPNTYICMQRVTRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA

>Sequence ID 172: SI-49P8 Chain B Nucleotide Sequence

>Sequence ID 173: SI-49PM1 Chain A Amino Acid Sequence

>Sequence ID 174: SI-49PM1 Chain A Nucleotide Sequence

TTTCTTAATTCCTTTTCAACCAAGAGGTTTCTGATCCCCCTTGACTGAAAGCTATTGCGGCCCTTGTCCGAAAACTGGATATGTTA
CAAGAATAATTGTTACCAATTCCTCGACGAAAGCAAGAACTGGTATGAGAGTCAGGCGTCTTGTATGAGTCAGAATGCCAGCCTGC
TTAAGGTTTATTCAAAGAAGACCAGGATCTGCTTAAGTTGGTAAAGAGCTACCACTGGATGGGGCTGGTACATATCCCAACGAAT
GGGTATGGCAGTGGGAGGACGGTTCTATTCTGAGTCCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGCCCTGTA
TGCATCATCCTTCAAGGGGTACATCGAGAACTGCAGTACCCCAAATACCTACATTTGTATGCAAAGAACGGTTGGAGGCGGTGGCT
CAGGCGGAGGCGGCTCAGGAGGTGGCGGTTTCAAGAGGCGGCGGATCTTTCCTAAACTCATTATTCAACCAAGAAGTTCAAATTCCTC
TTGACCGAAAGTTACTGTGGCCCATGTCTTAAAACTGGATATGTTACAAAATAACTGCTACCAATTTTTTGTATGAGAGTAAAAA
CTGGTATGAGAGCCAGGCTTCTTGTATGTCTCAAATGCCAGCCTTCTGAAAGTATACAGCAAAGAGGACCAGGATTTACTTAAAC
TGGTGAAGTCATATCATTGGATGGGACTAGTACACATTCCAACAAATGGATCTTGGCAGTGGGAAGATGGCTCCATTCTCTCACC
AACCTACTAACAATAATTGAAATGCAGAAGGGAGACTGTGCACTCTATGCCTCGAGCTTTAAAGGCTATATAGAAAACCTGTTCAAC
TCCAAATACGTACATCTGCATGCAAAGGACTGTGGTGCAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGG
AGCTTGGGGGAGGCTTGGTCCAGCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTTGGATTACCATCAGTACCAATGCAATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACATACTACGCGAGCTGGGC
GAAAGGCAGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTG
TGTATTACTGTGCGAGAGACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGTCACCGTGTCTCTCA
GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCTCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTCTAC
AGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGGCCAAATCTTGTGACAAAACCTCACACATGCCACCCTGCCAGCAC
TGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACAT
GCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTGCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGA
GTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
AGGTGTGTACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGGCTTCTATCCCAGC
GACATCGCGGTGAGTGGGAGAGCAATGGGCAGCGGAGAACCACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTT
CTTCTCGTGAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCGGTGCTGGTGGAG
TCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACTGCCTCTGGATTACCATCAGTAGCTACCACATGCA
GTGGGTCCGGCAGGCACCTGGGAAGTGCCTGGAGTACATCGGAACCATAGTAGTGGTGGTAATGTATACTACGCAAGCTCCGCTA
GAGGCAGATTACCATCTCCAGACCCTCGTCCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTG
TATTACTGTGCGAGAGACTCTGGTTATAGTGATCTATGTGGGGCCAGGGAACCTGGTCACCGTCTCTTCAAGCGGTGGCGGTAG
TGGGGGAGGCGGTCTTGGCGGGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCCGTGCTGCTG
CTGTAGGAGACAGAGTACCATCACCTGTGAGGCCAGTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGAAA
GCCCCAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGATTT
CACTCTCACCATCAGCGACTTGAACCTGGCGATGCTGCAACTTACTATTGTGAGTACCTATCTTGGTACTGATTATGTTGGCG
GTGCTTTTCGGCTGTGGGACCAAGGTGGAGATCAATGA

>Sequence ID 175: SI-49PM1 Chain B Amino Acid Sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHYQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPFTFGQTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLSTLCAFSGFSLSTSGMGVWIRQPPGKG
LEWLAIHWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFYFDYWGQGTLLTVTVSSGGGSGGGGSDV
VMTQSPSTLSASVGDRTVINCQASESISWLAHYQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYC
QGYFYFISRTYVNSFGGKTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGECGDKTHTCPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEA
LHNRFTQKSLSLSPGGGGSGGGGSDIQMTQSPSTLSASVGDRTVITCQASQSISSHLNHYQKPGKAPKLLIYKASTLASGVPSR
FSGSGSGTEFTLTISLQPDFFATYYCQQGYSWGNVDNVFGGGTQKTVLGGGSGGGGSGGGGSGGGGSEVQLLESGLLVQPGGS
LSLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAICAAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAF
SFDYAMD LWGQGLTVTVSS

>Sequence ID 176: SI-49PM1 Chain B Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGGTGACCAATTCATTTCCGGCAGGGGACAAAAGTACCGTCTTAGCGGTGGCGGTGGCGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAAGCAGGACAGACCC
TTAGCCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTCCGGCTGGATTCCGCAGCCTCCCGGCAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAATCAAGTGTACTTGAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGACGGGACTCTCGTCACGGTCTCGAGCGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC

GTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
 TTGGTTAGCCTGTGATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGGCATCTGGGGTCCCAT
 CAAGGTTACAGCGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGC
 CAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
 ACCATCTGTCTTATCTTCCCCTCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCCTGCTGAATAACTTCTATC
 CCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
 GACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCCAAGTACCCCA
 TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCCACCGTGCCAG
 CACCTGAAGCCGCGGGGGGACCGTCAGTCTTCCCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC
 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA
 GACAAAGCCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCA
 AGGAGTACAAGTCCGCGGCTTCCAAACAAAGCCCTCCAGCCCCCTCGAGAAAAACCATCTCCAAAGCCAAAGGCGACCCCGAGAA
 CCACAGGTGTACACCCTGCCCCAAGCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCC
 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCT
 CCTTCTTCCCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCACAACAGATTACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGACATTCAGAT
 GACACAGTCACCGTCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTATAAGTTACACC
 TCAACTGGTATCAACAGAAACCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCTCAGGTGTGCCTAGTCGC
 TTCTCCGGGAGCGCTCCGGTACTGAGTTTACTTTGACGATATCTTCCCTCCAACCCGACGACTTCGCCACATACACTATTGTTCAGCA
 GGGTTATAGTTGGGGAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGAAGTGTGTTGGGAGGGGAGGAAGTGGCGCGGGCG
 GAAGCGGAGGTGGTGGCTCCGGCGGGGGTGAAGCGAAGTGAATGCTCGAAAGTGGTGGCGGACTGTGCAACCTGGTGAAGC
 CTCTCACTCTCTTGC CGCGGAGTGGTTTTAGCTTCAGTAGCGGTACGATATGTGCTGGGTAAGACAGGCTCCTGGTAAAGGCCCT
 TGAGTGGATTGCGTGTATCGCCGCCGGGTCTGCTGGTATAACATACGATGCAACTGGGCGAAAGGCGCTTCACAACTCCAGGG
 ACAACTCAAAAATACATTGTACCTCCAGATGAATAGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTGAGCATTT
 AGCTTCGATTATGCAATGGATCTTTGGGGCCAGGGGACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 177: SI-49P9 Chain A Amino Acid

EIVMTQSPSTLSASVGDRIITCQASESISSWLAWYQQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISSLQPDFFATY
 YCQGYFYFISRTYVNSFGCGTKLTVLGGTSGSGSKYEGSTKGEVQLVESGGGLVQPGGSLRLSCTASGFTISTNAMSWSVRQAPG
 KCLEWVGVITGRDITYYASWAKGRFTISRDTSKNTPYGLQMNLSRAEDTAVYYCARDGGSSAITSNNIWGGQTLTVSTGGGSGGG
 GSFLNSLNFNEVQIPLTESYCGCPKPNWIKYKNNCYQFFDESKNYESQACMSQNASLLKVSKEQDILLKLVKSYHWMGLVHI P
 TNGSQWEDGSI LSPNLLTI IEMQKGDALYASSFKGYIENCSTPNTYICMQRTVASTKGPSVFPLAPSSKSTSGGTAAALGCLVKD
 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTHTCPCPAPEA
 AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
 CAVSNKALPAPIEKTI SKAKGQPREPQVCTLPPSRDELTKNQVLSLCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL
 VSKLTVDKSRWQQGNVFSFCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGP
 LSWYSDPGLAGVSLTGGLSYKEDTKELVVAAGVYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPASSEA
 RNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPEI PAGLGSTGSGSKPGSGEGSTKREGPELSPDDPA
 GLLDLRQGMFAQLVAQNVLIDGP LSWYSDPGLAGVSLTGGLSYKEDTKELVVAAGVYVFFQLELRRVVAGEGSGSVSLALHLQ
 PLRSAAGAAALALTVDLPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPEI PAGLGGGGSG
 GGGSGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGP LSWYSDPGLAGVSLTGGLSYKEDTKELVVAAGVYVFFQLELRRV
 VAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLF
 RVTPEI PAGL

>Sequence ID 178: SI-49P9 Chain A Nucleotide Sequence

GAGATCGTGATGACACAATCTCCATCTACGCTCTCCGCTCAGTGGGCGATAGAGTAATTATTACTTGTCAAGCCTCAGAGAGCAT
 TTCATCATGGCTCGCCTGGTATCAGCAAAAGCCTGGGAAGGCCCCAACTTCTCATCTATGAAGCATCAAAGCTGGCCTCTGGGG
 TTCCGTCTCGCTTCTCCGGGTCCGGCAGTGGTGCAGAGTTTACGTTGACTATATCTTCTTTGCAACCTGACGATTTTCGCAACATAT
 TATTGCCAGGGATACTTTTATTTTATTTCCGAACATATGTTAACTCTTTTGGGTGCGGGACCAAACCTCACTGTGCTGGGGTCTAC
 CGGTAGTGGTTCTAAGCCTGGTTCAGGCGAAGGCAGTACGAAAGGGGAAGTGCAACTGGTTCGAAAGCGGTGGAGGGCTTGTTC AAC
 CTGGAGGAAGCCTCCGCTTGTCTGCACGGCTAGCGGCTTTACAATAAGTACGAACGCCATGAGCTGGGTCCGGCAGGCTCCAGGT
 AAGTGTCTCGAATGGGTGGGGGTATAACAGGCAGGGACATTACCTACTACGCCAGTTGGGCCAAGGGTCGATTTTACCATTTCTAG
 AGATACATCCAAGAACACGGTGTACCTCCAGATGAATTCTCTTAGGGCGGAAGACACAGCAGTATACTACTGCGCGCGAGATGGCG
 GGAGCAGTGCATCACATCCAACAACATCTGGGGTCAGGGCACTCTGTACGGTGTGCACTGGCGGTGGAGGGTCCGGCGGTGGT
 GGATCATTTCTTAATTCCCTTTTCAACCAAGAGGTTAGATCCCCTGACTGAAAGCTATTGCGGCCCTTGTCCGAAAACTGGAT
 ATGTTACAAGAAATAATTGTTACCAATTCTTCGACGAAAGCAAGAAGCTGGTATGAGAGTCAGGCGCTTGTATGAGTCAGAATGCCA
 GCCTGCTTAAGGTTTATTCAAAGAAGACCAGGATCTGCTTAAGTTGGTAAAGAGCTACCACTGGATGGGGCTGGTACATATCCCA
 ACGAATGGGTGATGCGAGTGGGAGGACGGTCTTATTCTGAGTCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGC
 CCTGTATGCATCATCTTCAAGGGGTACATCGAGAACTGCAGTACCCCAATACCTACATTTGTATGCAAGAAGCGGTTGCTAGCA
 CCAAGGGGCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
 TACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGGTGCACACCTTCCGGGTGTCTACAGTCTCT

AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 CCAGCAACACCAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCC
 GCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
 GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC
 GGGAGGAGCAGTACGCCAGCAGTACCGTGTGGTCAGCGTCTCACCGCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAG
 TCGCGCGTCTCCAAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTG
 TACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCGTCAAAGGCTTCTATCCAGCGACATCG
 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTC
 GTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCGAGAGGGCCCCGAGCTGTCTC
 CTGATGACCCAGCAGGCTCTTGGACTTGGCGCAGGGTATGTTCTGCTCAACTTGTGGCTCAGAATGTTCTGCTCATTGATGGACCA
 CTCTCTTGGTATAGTACCGCGGTCTGGCGGGGTGAGTCTGACCGCGGGCTCTCTTATAAAGAGGATACTAAGGAACTGGTCTG
 AGCAAAAGCGGGCGTTTATTACGTTTTTTTTTTCAGCTGGAGCTCAGCGCGTGGTGGCGGGCAGGGCAGTGGCTCTGTCTCCCTGG
 CCCTGCACTTACAGCCCTTGAGAAGCGCTGCAGGTGCTGCCGCACTGGCTTTAACTGTTGACCTCCCTCCGGCTCTTCTGAAGCT
 AGAAACAGCGCTTTCGGCTTCCAAAGGCGCCTGCTGCACCTGAGCGCAGGCCAGCGCTTAGGTGTGACCTTCATACAGAGGCCAG
 GGCCCGACACGCTTGGCAGCTCACACAGGGTGGCAGGTTCTCGGACTTTTCCGCGTTACTCCCGAGATCCCGCTGGCCTCGGAA
 GTACTGGTCTGGGTCTAAACCCGGTTCGGCGAAGGTAGTACTAAAGGACGAGAAGGGCCAGAGTTAAGTCCAGATGACCCTGCT
 GGGCTTTGGACCTGCGGCAGGGCATGTTCTGCTCAACTGCTGCTCAGAACGTGCTGCTGATCGATGGCCCCCTGAGTTGGTACAG
 CGATCCCGGGTGGCAGGCGTGTCACTTACAGGGGCTCTCTTACAAGGAAGACACCAAGGAGTTAGTGGTGGTAAAGCTGGCG
 TGTATTACGTGTTCTTCCAACCTGGAGCTGAGAAGGGTGTGGCAGGAGAGGGTAGCGGCAGCGTGTCTTACGCCCTTCACTTGCAG
 CCCCTGAGGTCTGCTGCAGGTGCAGCGCTCTCGCGCTCACCGTGGATCTCCCCCAGCCTCATCTGAAGCTAGGAACAGTGCATT
 TGCTTTTACGGGACGCTTGGTGCACCTCTCCGCTGGACAGAGGCTGGCGTGCACCTTCACACAGAGGCCCGTGGCAGGCATGCAT
 GGCAGCTCACTCAGGGGGCAACAGTGCTGGGTCTCTTCCGCGTGACTCCTGAAATACCAGCTGGACTTGGCGGTGGAGGCAGCGGC
 GGAGGAGGATCTCGTAGGGGGCAGAAGTGTCCCCGATGACCCAGCCGGACTGCTCGATCTCAGACAGGGCATGTTCTGCTCAGCT
 TGTAGCCCCAAATGTCCTCTGATTGACGGCCCTTGGAGCTGGTATAGTGATCCCGGCTTGGCGGGGTATCTCTGACCGGAGGCC
 TCTCTACAAGGAAGACACCAAGAGCTGGTGGTGGCAAAAGCGGGGTGTATTATGTTCTTTTTCAGCTCGAGCTGCGGAGAGTT
 GTGGCCGGGAAGGGTCTGGGAGCGTATCTCTTGCACCTTCACTGCAGCCCCCTGCGCAGCGCGCTGGAGCCGCCGCCCTTGTCTCT
 TACTGTGGATCTGCCTCTGCTTCTCAGAAGCAGCAACAGCGCTTTCGGCTTTCAAGGACGTCTCTGCACTTGTCCGAGGAC
 AGAGGTTGGGCGTCCATTTACACACTGAGGCACGGGCACGGCAGCTTGGCAGCTTACCCAGGGAGCCACCGTGTGGGACTCTTT
 AGAGTGACACCCGAGATCCCCGCTGGCTTGTA

>Sequence ID 179: SI-49P9 Chain B Amino Acid Sequence

ENVLTSQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTIISSMEPEDFATYY
 CFQGSVYPFTFGQGTKEIKGSTSGSKPGSGEGSTKGQVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTGMGVGWIQPPGKGLE
 WLAHIWDDDKRNPALKSRLTISKDTSKNQVYLQMSLDAEDTAVYYCARMELWSYFDYWGQGLTVTVSTGGGSGGGGSFLNS
 LFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNYESQASCMSONASLLKVYSKEDQDLLKLKVSYHWMGLVHIPTNGSWQ
 WEDGSILSPNLLTIEMQKGDALYASSFKGYIENCSTPNYICMQRTVRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREA
 KVQWKVDNALQSGNSQESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEA
 AGGFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYK
 CAVSNKALPAPIEKTIKAKGQPREPQVYTLPPCRDELTKNQVSLVCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL
 YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFSSSGYDMC
 WVRQAPGKCLEWIIACIAAGSAGITYDANWAKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCARSASFSDYAMDLDWGQGLTVTVSS
 GGGSGGGSGGGSGGGSGGSDIQMTQSPSTLSASVGRVITITCASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFSGSG
 SGTFTLTIISSLQPDFFATYYCQQGYSGWNVNDFGCGTKVEIK

>Sequence ID 180: SI-49P9 Chain B Nucleotide Sequence

GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTCCGGCTCAGGCAACGATCACACCTTACGATTTCAGTATGGAACCCGAAGATTTGCAACTTATTAT
 TGTTTCCAGGGGAGCGTGATCCCATTCATTTCCGGCAGGGGACAAATTGGAGATAAAGGGAAGTACTGGTCTGGGTCTAAACC
 CGGTTCCGGCGAAGGTAGTACTAAAGGACAGGTACATTGAAGGAATCTGGCCCCGCTTGTTCAGCCAGGACAGACCCTTAGGC
 TCACCTGTGCCTTCACTGGTTTTTCTCTTAGCACTAGCGGTATGGGGTCCGGTGGATTCCGGCAGCCTCCCGCAAAGGTCTTGAG
 TGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCTGCTTGAAGTCCGGCTGACCATTAGTAAGGATACCTCAA
 AATCAAGTGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGTCTTACT
 ACTTTGATTATTGGGGGACGGGACTCTCGTCAGGTGTGCACTGGCGGTGGAGGTCCGGCGGTGGTGGATCATTCCTAAACTCA
 TTATTCAACCAAGAAGTTCAAATTCCTTGACCGAAAGTTACTGTGGCCCATGCTCTAAAACTGGATATGTTACAAAATAACTG
 CTACCAATTTTTTGTATGAGAGTAAAACTGGTATGAGAGCCAGGCTTCTGTATGTCTCAAATGCCAGCCTTCTGAAAGTATACA
 GCAAAGAGGACCAGGATTTACTTAACTGGTGAAGTCATATCATTGGATGGGACTAGTACACATTCACAAATGGATCTTGGCAG
 TGGGAAGATGGTCCATTCTCTACCCAACCTACTAACAATAATTGAAATGCAGAAGGGAGACTGTGCACTCTATGCCTCGAGCTT
 TAAAGGCTATATAGAAAAGTGTCAACTCCAAATACGTACATCTGCATGCAAAGGACTGTGCGTACGGTGGCTGCACCATCTGTCT
 TCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCC

AAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACACAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA
GCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCC
GCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTGCATGCATGCGTGGT
GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGCTGGACGGCTGGAGGTGCATAATGCCAAGACAAGAGCCG
GGGAGGAGCATACGCCAGCAGCTACCGTGTGGTCAGCGTCTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAG
TGC GCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAGGGCAGCCCCGAGAACCACAGGTGTA
CACCTGCCCCCATGTGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATACAAGACCAGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTC
TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA
CTACACGCAGAAGACGCTCTCCCTGTCTCCGGTGGCGGTGGAGGCTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTG
GGGAGGCTTGGTACAGCTGGGGGTCCTGAGACTCTCTGTCAGCTCTGGATTCTCCTTCACTAGCGGGTACGACATGTGC
TGGTCCCGCAGGCTCCAGGGAAGTGCTGGAGTGATCGCATGCAATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAAGT
GGCGAAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGATCGGCGTTTTCTGTTGCACTACGCCATGGACCTCTGGGGCCAGGGAACCTGGTCACCGTCTCGTCT
GGTGGAGGCGGTTCAAGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGACATCCAGATGACCCAGTCTCCTTC
CACCTGTCTGCATCTGTAGGAGACAGAGTCAACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGC
AGAAACCAAGGGAAGCCCTAAGCTCTGATCTATAAGGCATCACTCTGGCATCTGGGGTCCCATCAAGGTTCAAGCGGAGTGGTA
CTGGGACAGAATTTACTCTCACCATCAGCAGCCTAGCAGCTGATGATTTTGAACCTATTACTGCCAACAGGGTTATAGTTGGG
TAATGTTGATAATGTTTTCGGCTGCGGGACCAAGGTGGAGATCAAATAG

>Sequence ID 181: SI-1C3 Heavy Chain Amino Acid Sequence

QVQLQESGPGLVKPKSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTNYPNPSLKSRLTISIDTSKTFSLKLSS
YTAADTAIYYCVRDRVTAQFDIWGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCTPPCPAPELLGGPSVFLFPPKPKDTLMISRT
PEVTVCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQ
PREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGYTQNNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTM
HEALHNHYTQKSLSLSPGK

>Sequence ID 182: SI-1C3 Heavy Chain Nucleotide Sequence

CAGGTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCGT
CAGCAGTGGTGATTACTACTTGGACCTGGATCCGGCAGTCCCAGGGAAGGGACTGGAGTGGATTGGACACATCTATTACAGTGGGA
ACACCAATTATAACCCCTCCCTCAAGAGCCGACTCACCATATCAATTGACACCTCCAAGACTCAGTTCTCCCTGAAGCTGAGTTCT
GTGACCGCTCGGCAAGGCCATTATTACTGTGTGCGAGATCGAGTGACTGGTGTCTTTGATATCTGGGGCCAAGGGACATGGT
CACCCTCTCGAGCGCTAGACCAAGGGCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACTCTGGGGGCAAGCGGCC
TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGGCTGCACACCTTC
CCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCCAATCTTGTGACAAAACCTCACACATGCCAC
CGTGCCCGAGCACCTGAACTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACC
CCTGAGGCACATGCGTGGTGCTGGACGTGAGCCACGAAGACCTGAGTCAAGTTCACTGGTACGTGGACGGCTGGAGGTGCA
TAATGCCAAGACAAGCCGCGGGGAGGAGCACTACAACGACACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCTGACCTGCTGGTCAAAGG
CTTCTATCCAGCTGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGACAACACTACAAGACCACGCCTCCCGTGTCTGGACT
CCGACGGCTCCTTCTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA

>Sequence ID 183: SI-1C3 Light Chain Amino Acid Sequence

DIQMTQSPSSLSASVGDRVITITCQASQDISNYLWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATY
FCQHFDHFLPLAFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSST
YSLSTLTLSKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC

>Sequence ID 184: SI-1C3 Light Chain Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACAT
CAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTACGATGCATCCAATTTGGAACAGGGG
TCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACTTTACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
TTCTGTCAACACTTTTGATCATCTCCCGCTCGCTTTCGGCGGAGGGACCAAGGTGGAATAATTAACGTACGGTGGCTGCACCATCTGT
CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGCTCTGAATACTTCTATCCAGAGAGG
CCAAAGTACAGTGGAAAGTTGGATAACGCCCTCCAATCGGGTAACTCCGAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAC

>Sequence ID 189: SI-9C21 Light Chain Amino Acid Sequence

EIVMTQSPSTLSASVGRVITTCQASESISSWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
YQQGYFYFISRTYVNSFGQGTCLTVLRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 190: SI-9C21 Light Chain Nucleotide Sequence

GAAATCGTTATGACGCAGAGTCCCTCCACGCTCTCCGCTAGTGTGCGGGATCGCGTCATTATCACATGCCAGGCCTCCGAGTCAAT
CAGCAGCTGGCTTGCATGGTATCAACAGAAGCCGGGAAAAGCTCCTAAATTGCTGATCTATGAAGCGTCAAATTGGCGTCTGGTG
TCCCATCTAGGTTCTCCGGCTCTGGGTCTGGTGCGGAATTTACTTTGACAATCTCCAGTCTTCAACCAGACGATTTTCGTACCTAC
TACTGCCAAGGGTATTTCTATTTTATAAGCCGGACATATGTAACTCCTTCGGCCAAGGAACAAAGTTGACTGTTCTTCGTACGGT
GGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACT
TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT
CACCCATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG

>Sequence ID 191: SI-35FS11 Amino Acid Sequence

EPKSSDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVELTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGGGGSGGGGSRSLVESGGGLVQPGGSL
RLSCTASGFTISSYHMQWVRQAPGKGLIYIGTISGGNVYYASSARGRFTISRPSKNTVDLQMNLSRAEDTAVYYCARD SGYSDF
MWQGTLLTVTVSSGGGGSGGGGSGGGGSDVMTQSPSSVSASVGRVITTCQASQNI RTYLSWYQQKPKAPKLLIYAAANL
ASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTYLGTDYVGGAFGGGTKEIK

>Sequence ID 192: SI-35FS11 Nucleotide Sequence

GAGCCCAAATCTTCCGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCC
CCCAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
GTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCCAGC
CCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCGAGAACACAGGTGTACACCCTGCCCCATCCCGGGATGAGTGA
CCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG
GAGAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAG
GTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTC
CGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCGGTGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTG
AGACTCTCCTGTACTGCCTCTGGATTCAACATCAGTAGCTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGTGGAGTA
CATCGGAACCATTAGTAGTGGTGGTAATGTATACTACGCGAGCTCCGCGAGAGGCAGATTACCATCTCCAGACCCTCGTCCAAGA
ACACGGTGGATCTTCAAATGAACAGCCTGAGAGCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCCT
ATGTGGGGCCAGGGAACCCCTGGTCACCGTCTCTTCAGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGG
TGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTCCGTGTCTGCATCTGTAGGAGACAGAGTCAACATCACCTGTCAGGCCA
GTGAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTG
GCATCTGGGGTCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCGACCTGGAGCCTGGCGATGC
TGCAACTTACTATTGTGAGTCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAAT
GA

>Sequence ID 193: SI-3FS11 Amino Acid Sequence

EPKSSDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVELTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGGGGSGGGGSEVQLLES GGGLVQPGGS
LRLSCAASGFSFSSGYDMCWVRQAPGKGLIWIACIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARSAF
SFDYAMD LWGQTLTVTVSSGGGGSGGGGSGGGGSGGGSDIQMTQSPSTLSASVGRVITTCQASQSISSHLN WYQQKPKAPKLL
IYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQGYSGWGNVDNVFGGGTKEIK

>Sequence ID 194: SI-3FS11 Nucleotide Sequence

GAGCCCAAATCTTCCGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCC
CCCAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
GTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCCAGC
CCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCATCCCGGGATGAGCTGA
CCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG
GAGAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAG

GTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTC
 CGGGTGGCGGTGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC
 CTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCT
 GGAGTGGATCGCATGCATTGCTGCTGGTAGTGTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGTTACCATCTCCAGAG
 ACAATTCGAAGAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCCTTT
 TCGTTGCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTC
 CGGCGGTGGCGGTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAG
 TCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCCTTAACTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTG
 ATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAG
 CAGCCTGCAGCCTGATGATTTTGCACCTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGA
 CCAAGGTGGAGATCAATAA

>Sequence ID 195: SI-68X1 Chain A Amino Acid Sequence

DIQMTQSPSTLSASVGDRTITCQASENIYSNLAWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
 YCQSTYYNNIIYGAAFGCGTKVEIKGGGSGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFSFSGTQYVQWVRQA
 PGKCLEWIGICIYVDVANTYYATSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCASHDTVCAGCGLDLWGQGLTVTVSTGGGGS
 GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSQVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQ
 MNSLRAEDTAVYYCARDGGSSAITSNNIWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT
 SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDT
 LMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVSVLTVLHQDWLNGKEYKCAVSNKALPAPI EKT
 ISKAKGQPREPQVCTLPSPRDELTKNQVLSLCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNV
 FSCSVMEALHNHYTQKSLSLSPGK

>Sequence ID 196: SI-68X1 Chain A Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTGAGAACAT
 TTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGATGCTTCCACTCTGGCATCTGGGG
 TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCACCTTAT
 TACTGCCAATCTACTTATTATAATAATATCATTATTGGGGTCTTTCGGCTGTGGGACCAAGGTGGAGATCAAAGCGGCTGGCGG
 TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCC
 AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTGGCACCCAGTACGTGTGCTGGGTCCGCCAGGCT
 CCAGGGAAGTGCCTGGAGTGGATCGGATGCATTTATGTGGATGTGGCTAACACTTACTACGCGACCTCCGTGAAGGGCAGATTAC
 CATCTCCAGAGACAATTCGAAGAACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGA
 GTCATGATACTGTTGTGCTGGTGTGGTTTGGACTTGTGGGGCCAGGGAACCCTGGTCACCGTGTGACAGGCGGTGGAGGGTCC
 GCGGCTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC
 CTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTG
 TCGTGATATCACATACTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATTCGAAGAACGCTGTATCTTCAA
 ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGCTGGTTCTTCTGCTATTACTAGTAACAACATTTG
 GGGCCAGGGAACCCTGGTACCGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACCT
 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCAGGTGACGGTGTCTGGAAGTCAAGGCGCCCTGACC
 AGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTT
 GGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACA
 AAATCACACATGCCCCACCTGCCCCAGCACCTGAAGCCGCGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACC
 CTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCTGAGGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
 GGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTGCAGCTCCTCACCG
 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAAACCATC
 TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTGTACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCT
 GTCCTGCGCGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACTACAAGACCA
 CGCCTCCCCTGCTGGACTCCGACGGCTCCTTCTTCTCTGAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
 TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA

>Sequence ID 197: SI-68X1 Chain B Amino Acid Sequence

DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISLQPDPIATY
 FCQHFHDLPLAFGCGTKVEIKGGGSGGGSGGGSGGGSGGGSSVQLQESGPGLVKPSSETLSLTCTVSGGVSVDYWTWIRQSPGK
 CLEWIGHIYYSGNTNYPNLSRLTISIDTSKQFSLKLSVTAADTAIYYCVRDRVTGAFDIWGQGMVTVSTGGGSGGGGSDV
 VMTQSPSTLSASVGDRTITCQASESISWLAWYQQKPGKAPKLLIYASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYC
 QGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
 DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEV
 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVSVLTVLHQDWLNGKEYKCAVSNKALPAPI EKTISKAKGQPRE
 PQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNV FSCSVMEAL
 LHNHYTQKSLSLSPGK

>Sequence ID 198: SI-68X1 Chain B Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACAT
 CAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAACTCCTGATCTACGATGCATCCAATTTGGAAACAGGGG
 TCCCATCAAGGTTTCAGTGGAAGTGGATCTGGGACAGATTTTACTTTACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
 TTCTGTCAACACTTTGATCATCTCCCGCTCGCTTTTCGGCTGTGGGACCAAGGTGGAAATTAAAGGCGGTGGCGGTAGTGGGGGAGG
 CGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGTGCAGCTGCAGGAGTCCGGGCCAGGACTGGTGAAGCCTTCGGAGA
 CCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCGTGAGCAGTGGTGATTACTACTGGACCTGGATCCGGCAGTCCCCAGGGAAG
 TGCTTGGAGTGGATTGGACACATCTATTACAGTGGGAACACCAATTATAACCCCTCCCTCAAGAGCCGACTCACCATATCAATTGA
 CACGTCCAAGACTCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCGGACACGGCCATTTATTACTGTGTGCGAGATCGAGTGA
 CTGGTGCTTTTATATCTGGGGCCCAAGGGACAATGTCTACCGTGTGCAGAGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
 GTGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGACTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
 TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAAACTGGCATCTGGGGTCCCAT
 CAAGGTTTCAGCGGAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCACTTATTACTGC
 CAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAAATTCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGCTGGCTGC
 ACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCCTCTGTTGTGTGCTGCTGAATAACTTCTATC
 CCAGAGAGGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
 GACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTTGCAGAGTCAACCA
 TCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGTGGCCAG
 CACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC
 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA
 GACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAAGCTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCA
 AGGAGTACAAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAA
 CCACAGGTGTACACCTTGGCCCATGTGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTTCTATCC
 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGAGAGCAACTACAAGACCACGCTCCGCTGCTGGACTCCGACCGCT
 CCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCT
 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA

>Sequence ID 199: SI-68X3 Chain A Amino Acid Sequence

DIQMTQSPSSLSASVGRVITITCRASQDVNTAVAWYQQKPKGAPKLLIYSASFLYSVPSRFSGRSGTDFTLTISLQPEDFATY
 YCQQHYTTPTTFQGTKEIKGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGL
 EWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLVTVSTGGGSGGGGSE
 VQLVESGGGLVQPGGSLRLSCAASGFITISNAMSWVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMNSLRA
 EDTAVYYCARDGSSAITSNNIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAAIGCLVKDYFPEPVTVSWNSGALTSGVHTF
 PAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRT
 PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQ
 PREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSQSV
 MHEALHNHYTQKSLSLSPGK

>Sequence ID 200: SI-68X3 Chain A Nucleotide Sequence

GACATCCAAATGACGCAGTCTCCCTCCAGTTTGTAGTGCAAGTGTGGGAGACAGAGTTACGATCACATGTAGGGCAAGTCAGGACGT
 CAATACAGCCGTGCGATGGTACCAGCAGAAGCCTGGAAGGCCCCGAAACTTCTGATTTACTCTGCAAGTTTCTCTACAGTGGTG
 TTCTAGTCGCTTCAGTGGGTCTCGGTGAGGCACCGATTTTACCCTGACAATTAGCAGCTTGCAACCGGAAGATTTTGCACCTAT
 TATTGCCAGCAACATTATACCACCCCTCCACATTTGGACAAGGCACGAAGGTAGAGATTAAAGGCGGTGGAGGGAGCGGTGGAGG
 CGGTTCCGGTGGAGGTGGTTCTGGTGGAGGTGGCAGTGAAGTACAGCTTGTTGAGAGTGGTGGTGGACTTGTCCAACCAGGGGGAA
 GTCTGCGGCTGTCTGCGCAGCCTCTGGCTTCAACATTAAGGACACCTACATTCACTGGGTTCCGGCAGCGCCGGGGAGGGGCTG
 GAATGGGTGCGCAGGATATACCTACCAACGGGTACACAGGTATGCGATAGCGTTAAGGGTAGATTCACTATTTCACTGACAC
 TAGCAAGAACACCGCGTATCTCCAGATGAACTCCCTTCGCGCCGAGGATACGGCTGTGTACTACTGCTCTAGGTGGGAGGAGATG
 GGTTTTACGCAATGGATTACTGGGGACAGGGAACACTCGTTACGGTGTGCGACAGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAG
 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAACATCAG
 TACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCTGTATATCACATACT
 ACGCGAGCTGGGGCAAAGGCAGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
 GAGGACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAAACCTGGT
 CACCGTGTCTCTAGCTAGCACCAAGGGCCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCC
 TGGGCTGCCTGGTCAAGGACTACTTCCCGAACCCTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGGCTGCACACCTTC
 CCGGCTGTCTCAGTCTCCTCAGTCTCCTCCTCAGCAGCTGGTGGTACCGTGCCTCCCTCCAGCAGCTTGGGACCCAGACATCAT
 CTGCAACGTGAATCAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCAC
 CGTGCCAGCACCTGAAGCCGCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCCCTCATGATCTCCGGACC
 CTTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
 TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAAGCTCCTCACCCTCCTGCACCAGGACTGGC
 TGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG

CCCCGAGAACCACAGGTGTGTACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTCTGCGCCGTCAAAGG
CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGTGGACT
CCGACGGCTCCTTCTTCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA

>Sequence ID 201: SI-68X3 Chain B Amino Acid Sequence

DVMTQSPSTLSASVGDRTINCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDDEFATY
YQGGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTF
EVTQVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQP
REPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMH
EALHNHYTQKSLSLSPGK

>Sequence ID 202: SI-68X3 Chain B Nucleotide Sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
TAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATGAAGCATCCAAACTGGCATCTGGGG
TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTAT
TACTGCCAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGT
GGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAATAACT
TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT
CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGAGGCGACAAAACCTCACACATGCCACCGT
GCCCAGCACCTGAAGCCGCGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCTCATGATCTCCCGGACCCCT
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA
TGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCCTGTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGA
ATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCC
CGAGAACCACAGGTGTACACCTGCCCCCATGTCTGGGATGAGCTGACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTCAAAGGCTT
CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCG
ACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA

>Sequence ID 203: αEGFR VH Amino Acid Sequence

QVQLQQSGPGLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKLEWLGLVIWSSGNTDYNTPFTSRFTITKDNSKNQVYFKLRVSR
ADDTAIYYCARALTYDYEFAYWGQGLTVTVSS

>Sequence ID 204: αEGFR VH Nucleotide Sequence

CAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCT
TACGAACTATGGAGTTCACTGGATTCCGGCAGGCACCCGGCAAAGGTTTGAATGGCTGGGTGTTATTTGGTCAGGTGGAATAACAG
ACTATAACACCCCTTTACAAGTCGGTTCACAATTACGAAAGATAAATCCAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCCGC
GCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACGATTACGAATTTGCGTATTGGGGGCAAGGACTCTTGT
AACAGTCTCGAGC

>Sequence ID 205: αEGFR VL Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPGKPPRLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
YCQQNNNWPTTFGPGTKLTVL

>Sequence ID 206: αEGFR VL Nucleotide Sequence

GAAATCGTCCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAAGCGCGACTTTCTCTTGCAGGGCAAGTCAATCCAT
AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAAGTATGCAAGTGAGTCTATTTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCAGAGTTTCACTCACCATATCTAGTGTGCAATCAGAGGACTTCGCCGTGTAT
TACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGACCCGGTACAAAGCTGACCGTTTTA

>Sequence ID 207: αEGFR* VH Amino Acid Sequence

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYIYWTWIRQSPGKLEWIGHIYYSGNTNYPNPSLKSRLTISIDTSKQFSLKLSS
VTAADTAIYYCVRDRVTGAFDIWGQGTMTVTVSS

>Sequence ID 208: αEGFR* VH Nucleotide Sequence

CAAGTGCAACTCCAGGAGAGTGGGCCGGGATTGGTTAAACCGAGCGAGACCCTGAGTCTCACGTGTACAGTTTCAGGCGGGAGCGT
GAGCTCAGGCGACTATTACTGGACATGGATAAGACAGAGTCTTGAAAGGGCCTGGAGTGGATCGGTCATATTTATTATTCAGGGA
ACACTAACTATAATCCATCTTTGAAATCCCGATTGACAATCTCTATCGATACCAGTAAAACCCAGTTAGCCTCAAGCTGTCCAGC
GTTACTGCTGCAGACACAGCCATATACTATTGCGTACGCGATCGCGTGAAGCCTTCGACATATGGGGGCAGGGAACGATGGT
AACAGTCTCGAGC

>Sequence ID 209: αEGFR* VL Amino Acid Sequence

DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLPEDIATY
FCQHFDFHLPALFAGGGTKVEIK

>Sequence ID 210: αEGFR* VL Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACAT
CAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAACTCCTGATCTACGATGCATCCAATTTGGAAACAGGGG
TCCCATCAAGGTTCAAGTGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
TTCTGTCAACACTTTGATCATCTCCCGCTCGCTTTCGGCGGAGGGACCAAGGTGGAAATTAA

>Sequence ID 211: αEGFR* VH Stapled Amino Acid Sequence

QVQLQESGPGLVKPSSETLSLTCTVSGGSVSSGDIYWTWIRQSPGKCLEWIGHIYSGNTNYPNLSKRLTISIDTSKTQFSLKLSS
VTAADTAIYYCVRDRVTGAFDIWGGQTMVTVST

>Sequence ID 212: αEGFR* VH Stapled Nucleotide Sequence

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCGT
CAGCAGTGGTGATTACTACTGGACCTGGATCCGGCAGTCCCCAGGGAAGTGCCTGGAGTGGATTGGACACATCTATTACAGTGGGA
ACACCAATTATAACCCCTCCCTCAAGAGCCGACTCACCATATCAATTGACACGTCCAAGACTCAGTTCTCCCTGAAGCTGAGTTCT
GTGACCGCTGCGGACACGCCATTATTACTGTGTGCGAGATCGAGTGAAGTGGTGTCTTTGATATCTGGGGCCAAGGGACAATGGT
CACCGTGTGACA

>Sequence ID 213: αEGFR* VL Stapled Amino Acid Sequence

DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLPEDIATY
FCQHFDFHLPALFAGCGTKVEIK

>Sequence ID 214: αEGFR* VL Stapled Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACAT
CAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAACTCCTGATCTACGATGCATCCAATTTGGAAACAGGGG
TCCCATCAAGGTTCAAGTGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATAT
TTCTGTCAACACTTTGATCATCTCCCGCTCGCTTTCGGCTGTGGGACCAAGGTGGAAATTAA

>Sequence ID 215: αCD19 VH Amino Acid Sequence

QVTLLKESGPGLVQPGQTLSTLCAFSGFSLSSTSGMGVWIRQPPGKGLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMN
LDAEDTAVGYCCARMELWSYFDYWGGQTLTVSS

>Sequence ID 216: αCD19 VH Nucleotide Sequence

CAGGTACACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCCTTAGCCTCACCTGTGCCTTCAGTGGTCTTTCTCT
TAGCACTAGCGGTATGGGGGTGGCTGGATTGGGACGCTCCCGGCAAAGGTCTTGAGTGGTTGGCTCACATTTGGTGGGACGACG
ACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAAAAATCAAGTGTACTTGCAATGAATAGC
CTTGACGCCGAGGATACGGCTGTATATTATTCGCGCGGATGGAACCTCTGGTCTTACTACTTTGATTATTGGGGGCAGGGGACTCT
CGTCACGGTCTCGAGC

>Sequence ID 217: αCD19 VL Amino Acid Sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKLGSGVPSRFSGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPTFTFGQTKVTVL

>Sequence ID 218: αCD19 VL Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTCCGGCTCAGGCAACGATCACACCCTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGTAACCCATTCACTTTCGGGCAGGGGACAAAAGTGACCGTCCTA

>Sequence ID 219: αCD3 VH Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNSLR
AEDTAVYYCARDGGSSAITSNNIWQGTLVTVSS

>Sequence ID 220: αCD3 VH Nucleotide Sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCAT
CAGTACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACAT
ACTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCT
GGTCACCGTGTCTCA

>Sequence ID 221: αCD3 VL Amino Acid Sequence

DVVMTQSPSTLSASVGDRVTINCQASESISWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
YCQGYFYFISRTYVNSFGGGTKVEIK

>Sequence ID 222: αCD3 VL Nucleotide Sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
TAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGG
TCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTAT
TACTGCCAAGGCTATTTTATTTATTAGTCGTACTTATGTAAATCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>Sequence ID 223: αCD3 VH stapled Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKCLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNSLR
AEDTAVYYCARDGGSSAITSNNIWQGTLVTVSS

>Sequence ID 224: αCD3 VH stapled Nucleotide Sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCAT
CAGTACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACAT
ACTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTTCTTCTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCCCT
GGTCACCGTGTCTCA

>Sequence ID 225: αCD3 VL stapled Amino Acid Sequence

DVVMTQSPSTLSASVGDRVTINCQASESISWLAWYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
YCQGYFYFISRTYVNSFGGGTKVEIK

>Sequence ID 226: αCD3 VL stapled Nucleotide Sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
TAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGG
TCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTAT
TACTGCCAAGGCTATTTTATTTATTAGTCGTACTTATGTAAATCTTTTCGGCTGTGGGACCAAGGTGGAGATCAAA

>Sequence ID 227: αCD3* VH Amino Acid Sequence

QVQLQESGGRLVQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKLEWIGVIFGSGNTYYASWAKGRFTISRSTSTVYLKMNLSLRSE
DTAIYYCARGGYSSDIWQGTLVTVSS

>Sequence ID 228: αCD3* VH Nucleotide Sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCCTTGCTACTGACGTGTAAAAACAAGCGGCATTGATCT
GTCTCTTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAAGGCGGATTTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGCGAGGTACACTGGTTACAGTTTCATCC

>Sequence ID 229: αCD3* VL Amino Acid Sequence

DPQLTQSPSSLSATVGQRTVINCQSSQSVAKNNNLAWFQQKPGKPKLLIYSASTLAAGVPSRFSGSGSGTQFTLLITRVQSEDF
TYYCSARDSGNIQSFGGGTRVEIK

>Sequence ID 230: αCD3* VL Nucleotide Sequence

GATCCTCAATTGACCCAGTCCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTCCGT
AGCGAAGAATAATAATTTGGCATGGTTCCAACAAAACCGGGTAAACCTCCTAAACTCCTTATCTACTCAGCTTCAACCCTTGCCG
CGGTGTGCCAGCCGGTTCTCAGGCTCAGGTTCCGGGACTCAATTTACACTTACCATCACTCGCGTCCAAAGTGAGGATTTTGCA
ACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCCTTTGGGGGTGGAACCTCGGGTGGAGATAAAA

>Sequence ID 231: αCD3** VH Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKGLEWVGIVITGRDITYYASWAKGRFTISRDTSKNTVYLQMNSLR
AEDTAVYYCARDGGSSAITSNNIWGGTLVTVSS

>Sequence ID 232: αCD3** VH Nucleotide Sequence

GAAGTCCAATTGGTAGAAAGTGGCGGTGGTCTGGTGCAACCTGGTGGATCTCTTCGCCTCTCATGCGCCGCTAGTGGCTTTACTAT
TTCAACTAATGCGATGAGCTGGGTTCGCCAGGCCCCCGGCAAAGGACTTGAGTGGGTGCGCGTCATCACCGGCAGGGACATTACAT
ACTATGCGAGTTGGGCAAAGGGCAGGTTACGATTAGCCGCGATACTTCAAAGAATACCGTTTACCTTCAAATGAATAGCTTGAGG
GCGGAAGACACAGCTGTGTATTACTGCGCGAGGGATGGAGGTAGTTCCGCCATAACTTCCAACAACATATGGGGACAAGGCACGCT
GGTTACTGTCTCGAGT

>Sequence ID 233: αCD3** VL Amino Acid Sequence

EIVMTQSPSTLSASVGRVITCQASESISWLAHYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
YCGYFYFISRTYVNSFQGTLTVL

>Sequence ID 234: αCD3** VL Nucleotide Sequence

GAAATCGTTATGACGCAGAGTCCCTCCACGCTCTCCGCTAGTGTGGGGATCGCGTCATTATCACATGCCAGGCCTCCGAGTCAAT
CAGCAGCTGGCTTGCATGGTATCAACAGAAGCCGGGAAAAGCTCCTAAATTGCTGATCTATGAAGCGTCAAATTTGGCGTCTGGT
TCCCATCTAGGTTCTCCGGCTCTGGGTCTGGTGCGGAATTTACTTTGACAATCTCCAGTCTTCAACAGACGATTTTCGTACCTAC
TACTGCCAAGGTATTTCTATTTTATAAGCCGGACATATGTAACTCCTTCGGCCAGGAACAAAGTTGACTGTTCTT

>Sequence ID 235: αCD3*** VH Amino Acid Sequence

QQLLESGRRLIKPGATLRLTCKTSGFTISTNAMSWVRQPPGKLEWIGVITGRDITYYASWAKGRFTISKTSINTVFLQMRLRAE
DTAVYYCARDGGSSAITSNNIWGRGTLVTVSS

>Sequence ID 236: αCD3*** VH Nucleotide Sequence

CAGCAGCTGCTGAAAGCGGCGGCCGCTGATTAAACCGGGCGCGACCCTGCGCCTGACCTGCAAAACCAGCGGCTTTACCATTAG
CACCAACGCGATGAGCTGGGTGCGCCAGCCGCGGGCAAAGGCCTGGAATGGATTGGCGTGATTACCGGCCGCGATATTACCTATT
ATGCGAGCTGGGCGAAAGGCCGCTTTACCATTAGCAAAACCAGCATTAACACCGTGTTTCTGCAGATGCGCAGCCTGCGCGCGGAA
GATACCGCGGTGATTATTGCGCGCGCGATGGCGGCAGCAGCGGATTACCAGCAACAACATTTGGGGCCGCGGCACCTGGTGAC
CGTGAGCAGC

>Sequence ID 237: αCD3*** VL Amino Acid Sequence

DVQMTQSPSTLSATVGQRTVINCQASESISWLAHYQQKPGQPPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQSDDFATY
YCGYFYFISRTYVNSFGGGTRVEIK

>Sequence ID 238: αCD3*** VL Nucleotide Sequence

GATGTGCAGATGACCCAGAGCCCGAGCACCCCTGAGCGCGACCGTGGGCCAGCGCGTGACCATTAACTGCCAGGCGAGCGAAAGCAT
TAGCAGCTGGCTGGCGTGGTATCAGCAGAAACCGGGCCAGCCGCCGAAACTGCTGATTTATGAAGCGAGCAAACCTGGCGAGCGGCG
TGCCGAGCCGCTTTAGCGGCGAGCGGCAGCGGCACCGAATTTACCCCTGACCATTAGCAGCCTGCAGAGCGATGATTTTGGCAGCCTAT
TATTGCCAGGGCTATTTTATTTTATTAGCCGCACCTATGTGAACAGCTTTGGCGGGCGGCACCCGCGTGGAATTAAA

>Sequence ID 239: αCD3**** VH Amino Acid Sequence

QQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSQVRQAPGKLEWVGVTGRDITYYASWAKGRFTISKTSKNTVYLQMNSLRAE
DTAVYYCARDGSSSAITSNNIWGQGLVTVSS

>Sequence ID 240: αCD3**** VH Nucleotide Sequence

CAGCAGCTGGTGGAAAGCGGGCGGGCCTGGTGAACCGGGCGGCAGCCTGCGCCTGAGCTGCGCGGCGAGCGGCTTTACCATTAG
CACCAACGCGATGAGCTGGGTGCGCCAGGCGCCGGGCAAAGGCCTGGAATGGGTGGCGTGATTACCGGCCGCGATATTACCTATT
ATGCGAGCTGGGCGAAAGGCCGCTTTACCATTAGCAAAACAGCAAAAACACCGTGTATCTGCAGATGAACAGCCTGCGCGCGGAA
GATACCGCGGTGTATTATTGCGCGCGCGATGGCGGCAGCAGCGGATTACCAGCAACAACATTTGGGGCCAGGCGACCCCTGGTGAC
CGTGAGCAGC

>Sequence ID 241: αCD3**** VL Amino Acid Sequence

DVVMTQSPSSLSASVGRVTISCQASESISSWLAWYQQKPGQAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLLEPEDFATY
YCGGYFYFISRTYVNSFGGGTKVEIK

>Sequence ID 242: αCD3**** VL Nucleotide Sequence

GATGTGGTGATGACCCAGAGCCCGAGCAGCCTGAGCGCGAGCGTGGGCGATCGCGTGACCATTAGCTGCCAGGCGAGCGAAAGCAT
TAGCAGCTGGCTGGCGTGGTATCAGCAGAAACCGGGCCAGGCGCCGAAACTGCTGATTTATGAAGCGAGCAAACCTGGCGAGCGGCG
TGCCGAGCCGCTTTAGCGGCGAGCGGCAGCGGCACCGAATTTACCCCTGACCATTAGCAGCCTGGAACCGGAAGATTTTGGCAGCCTAT
TATTGCCAGGGCTATTTTATTTTATTAGCCGCACCTATGTGAACAGCTTTGGCGGGCGGCACCAAAGTGGAATTAAA

>Sequence ID 243: αPD-L1 VH Amino Acid Sequence

EVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWVIAAGSAGITYDANWAKGRFTISRDNKNTLYLQMN
SLRAEDTAVYYCARSAFSDYAMDLDWGQGLVTVSS

>Sequence ID 244: αPD-L1 VH Nucleotide Sequence

GAAGTGCAATTGCTCGAAAGTGGTGGCGGACTTGTGCAACCTGGTGAAGCCTCTCACTCTCTTGC CGCGGAGTGTTTGTAGCTT
CAGTAGCGGCTACGATATGTGCTGGGTAAAGACAGGCTCCTGGTAAAGGCCTTGAGTGGATTGCGTGTATCGCCGCCGGGTCTGCTG
GTATAACATACGATGCAAACTGGGCGAAAGGGCGCTTACAATCTCCAGGGACAACCTCAAAAAATACATTGTACCTCCAGATGAAT
AGCCTGAGAGCCGAAGACACCGCAGTCTACTATTGCGCAAGGTCAGCATTTAGCTTCGATTATGCAATGGATCTTTGGGGCCAGGG
GACGCTCGTCACCGTCTCATCTTGA

>Sequence ID 245: αPD-L1 VL Amino Acid Sequence

DIQMTQSPSTLSASVGRVTITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
YCGQGYSWGNVDFGGGTKVTVL

>Sequence ID 246: αPD-L1 VL Nucleotide Sequence

GACATTGAGATGACACAGTCACCGTCTACGCTCTCAGCCTCAGTAGGCGATAGGGTGACTATCACCTGCCAAGCCTCCCAATCTAT
AAGTTCACACCTCAACTGGTATCAACAGAAACCGGTAAAGCACCGAAGCTGCTCATCTACAAGGCATCAACTCTTGCCTCAGGTG
TGCTTAGTCGCTTCTCCGGGAGCGGCTCCGGTACTGAGTTTACTTTGACGATATCTCCCTCCAACCCGACGACTTCGCCACATAC
TATTGTGACAGGGTTATAGTTGGGGAAATGTTGACAATGTGTTTGGAGGGGGAACGAAAGTGAAGTGTGTTG

>Sequence ID 247: α4-1BB VH Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGGNVYASSARGRFTISRPSKNTVDLQMNSLR
AEDTAVYYCARDSGYSDPMWGQGLVTVSS

>Sequence ID 248: α4-1BB VH Nucleotide Sequence

GAGGTT CAGTTGGTTGAAAGTGGGGGGGACTCGTT CAGCCTGGAGGCTCTTTGCGACTTTCTTG TACCGCTTCTGGGTTCACTAT
AAGTT CATATCATATGCAATGGGTAAGACAGGCGCCTGGTAAGGGACTTGAATACATAGGAACAATAAGCTCTGGTGGTAACGTCT
ATTACGCCCTCATCCGCGCGGGGGAGGTTTACAATTTCCAGGCCTTCTAGCAAAAACACGGTAGATCTGCAAATGAACTCTCTTCGC
GTGAAGATACAGCAGTCTACTACTGCGCCAGGGATT CAGGGTATTCTGACCCCATGTGGGGGCAGGCACATTGGTTACCGTGTC
CTCT

>Sequence ID 249: α4-1BB VL Amino Acid Sequence

DVVMTQSPSSVSASVGDVRTITCQASQNIRTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATY
YCQSTYLGTDYVGGAFGGGKTLTVL

>Sequence ID 250: α4-1BB VL Nucleotide Sequence

GACGTTGTGATGACGCAGTCTCCTAGTTCAGTATCAGCGTCTGTTGGGGATCGAGTCACGATTACATGCCAGGCGAGCCAAAATAT
TAGGACGTATCTGTCTTGGTATCAACAAAAGCCTGGTAAGGCTCCAAAACCTCTCATTTACGCCGCTGCCAACTTGGCTAGTGGAG
TACCTTCACGCTTTAGTGGGTCAAGTTCGGAACAGATTTACGTTGACGATCTCCGATTTGGAACAGGGGACGTGCCACGTAT
TATTGCCAGTCCACCTACCTCGGGACTGACTACGTTGGTGGGGCGTTTGGCGGAGGAACAAAACCTACTGTACTT

>Sequence ID 251: 41BBL Amino Acid Sequence

REGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKELVVAKAGVYVFFQLELRRVVAGE
GSGSVSLALHLQPLRSAAGAAALALTVDLPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTE
EIPAGLGSTGSGSKPGSGEGSTKGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKE
LVVAKAGVYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPASSEARNSAFGFQGRLLHLSAGQRLGVHLHT
EARARHAWQLTQGATVLGLFRVTEPEIPAGLGGGGSGGGSGREGPELSPDDPAGLLDLRQGMFAQLVAQNVLIDGPLSWYSDPGLA
GVSLTGGLSYKEDTKELVVAKAGVYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPASSEARNSAFGFQGR
LLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTEPEIPAGL

>Sequence ID 252: 41BBL Nucleotide Sequence

CGAGAGGGCCCCGAGCTGTCTCCTGATGACCCAGCAGGCCCTCTTGGACTTGCGGCAGGGTATGTTTCGCTCAACTTGTGGCTCAGAA
TGTTCTGCTCATTGATGGACCACTCTCTTGGTATAGTGACCCCGGTCTGGCCGGGGTGAGTCTGACCGCGGGCTCTCTTATAAAG
AGGATACTAAGGAACTGGTCGTAGCAAAAGCGGGCGTTTATTACGTTTTTTTTTCAGCTGGAGCTCAGGCGCGTGGTGGCCGGCGAG
GGCAGTGGCTCTGTGTCCCTGGCCCTGCACTTACAGCCCTTGAGAAGCGCTGCAGGTGCTGCCGCACTGGCTTTAACTGTTGACCT
CCCTCCGGCCTCTTCTGAAGCTAGAAACAGCGCTTTTGGCTTCCAAGGGCGCTCTGCACCTGAGCGCAGGCCAGCGCTTAGGTG
TGCACCTTTCATACAGAGGCCAGGGCCCGACAGCTTTCGGAGCTCACACAGGGTGCCACGGTTCTCGGACTTTTCCGGTTACTCCC
GAGATCCCCGCTGGCCTCGGAAGTACTGTTCTGGGTCTAAACCCGGTTCCGGCGAAGGTAGTACTAAAGGACGAGAAGGGCCAGA
GTTAAGTCCAGATGACCCGTCTGGGCTTTTGGACCTGCGGCAGGGCATGTTTCGCTCAACTGGTGGCTCAGAACGTGCTGCTGATCG
ATGGCCCCCTGAGTTGGTACAGCGATCCCGGGCTGGCAGGCGTGTCACTTACAGGGGGCTCTCTTACAAGGAAGACCAAGGAG
TTAGTGGTCGCTAAGGCTGCGGTGTATTACGTGTTCTTCCAACCTGGAGCTGAGAAGGGTTGTGGCAGGAGAGGGTAGCGGCAGCGT
GTCTTTAGCCCTTCACTTGCAGCCCCCTGAGGTCTGCTGCAGGTGCAGCCGCTCTCGCGCTCACCGTGGATCTCCCCCAGCCTCAT
CTGAAGCTAGGAACAGTGCATTTGGCTTTACGGACGCTTGTCTGCACCTCTCCGCTGGACAGGGCTGGGCGTGCACCTTACACA
GAGGCCGCTGCCAGGCATGCATGGCAGCTCACTCAGGGGGCAACAGTGTCTGGGTCTCTCCGCGTGACTCTGAAATACCAAGCTGG
ACTTGGCGGTGGAGGCAGCGGCGGAGGAGGATCTCGTGAGGGGCCAGAACTGTCCCCCGATGACCCAGCCGGACTGCTCGATCTCA
GACAGGGCATGTTTCGCTCAGCTTGTAGCCCAAATGTCCTCCTGATTGACGGCCCTTTGAGCTGGTATAGTGATCCCGGCTTGGCC
GGGGTATCTCTGACCGGAGGCCCTCTCCTACAAGGAAGACACCAAAGAGCTGGTGGTGGCAAAGCGGGGGTGTATTATGTGTTCTT
TCAGCTCGAGCTGCGGAGAGTGTGTGGCCGGGGAAGGGTCTGGGAGCGTATCTCTTGCACTTCACTGCAAGCCCTGCGCAGCGCCG
CTGGAGCGCCGCCCTTGCTCTTACTGTGGATCTGCCTCCTGCTTCTCAGAAGCAGCAACAGCGCCTTGGCTTTCAAGGACGT
CTCCTGCACCTGTCCGACGAGCAGAGGTTGGGCGTCCATTACACACTGAGGCAGGGCACGGCACGCTTGGCAGCTTACCCAGGG
AGCCACCGTGTCTGGGACTCTTTAGAGTGACACCCGAGATCCCCGCTGGCTTGTGA

>Sequence ID 253: NKG2D dimer Amino Acid Sequence

FLNSLFNQEVQIPLTESYCGPCPNWICYKNNCYQFFDESKNWYESQASCSMQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIPTN
GSWQWEDGSILSPNLLTIIEMQKGDALYASSFKGYIENCSTPNTYICMORTVGGGGSGGGSGGGSGGGGSFLNSLFNQEVQIP
LTESYCGPCPNWICYKNNCYQFFDESKNWYESQASCSMQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIPTN GSWQWEDGSILSP
NLLTIIEMQKGDALYASSFKGYIENCSTPNTYICMORTV

>Sequence ID 254: NKG2D dimer Nucleotide Sequence

TTTCTTAATTCCCTTTTCAACCAAGAGGTTGAGATCCCTTGACTGAAAGCTATTGCGGCCCTTGTCGAAAACTGGATATGTTA
CAAGAATAATTGTTACCAATTCTTCGACGAAAGCAAGAAGCTGGTATGAGAGTCAGGCGTCTTGATGAGTCAGAATGCCAGCCTGC
TTAAGGTTTATTCAAAGAAGACCAGGATCTGCTTAAGTTGGTAAAGAGCTACCACTGGATGGGGCTGGTACATATCCCAACGAAT

GGGTCATGGCAGTGGGAGGACGGTTCATTCTGAGTCCAAATCTCCTGACGATCATCGAAATGCAGAAAGGGGACTGTGCCCTGTA
TGCATCATCCTTCAAGGGGTACATCGAGAACTGCAGTACCCCAAATACCTACATTTGTATGCAAAGAACGGTTGGAGGCGGTGGCT
CAGGCGGAGGCGGCTCAGGAGGTGGCGGTTTCAAGGAGGCGGCGGATCTTTCTAAACTCATTATTCAACCAAGAAGTTCAAATTCCC
TTGACCGAAAGTTACTGTGGCCCATGTCCTAAAACTGGATATGTTACAAAAATAACTGCTACCAATTTTTTGTATGAGAGTAAAAA
CTGGTATGAGAGCCAGGCTTCTTGTATGTCTCAAAATGCCAGCCTTCTGAAAGTATACAGCAAAGAGGACCAGGATTTACTTAAAC
TGGTGAAGTCATATCATTGGATGGGACTAGTACACATTCCAACAAATGGATCTTGGCAGTGGGAAGATGGCTCCATTCTCTCACC
AACCTACTAACAATAATTGAAATGCAGAAGGGAGACTGTGCACTCTATGCCTCGAGCTTTAAAGGCTATATAGAAAAGTGTTCAC
TCCAATACGTACATCTGCATGCAAAGGACTGTG

>Sequence ID 255: αHER3 VH Amino Acid Sequence

QVQLQESGGGLVLPKGGSLSLSCAASGFTFSSYWMSWVRQAPGKGLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSL
RAEDTAVYYCARDRGVGYFDLWGRGLVTVSS

>Sequence ID 256: αHER3 VH Nucleotide Sequence

CAGGTGCAATTGCAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTT
TAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAACATAAACCGCGATGGAAGTGCGA
GTTACTATGTGGACTCTGTGAAGGCGGATTACCATCTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTG
AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGTGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAC
CGTCTCGAGT

>Sequence ID 257: αHER3 VL Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGINFVSWYQQHPGKAPKLMYIDVSDRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYCCSSYGSSSTHVIFGGGTKVTVL

>Sequence ID 258: αHER3 VL Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTGCATCACCATCTCCTGCACTGGAACAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCAAACTCATGATCTATGATGTGAGTGATCGGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCCTA

>Sequence ID 259: αCD20 VH Amino Acid Sequence

QVQLQPPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPNGDTSYNQKFKGKATLTADKSSSTAYMQLSL
TSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVSS

>Sequence ID 260: αCD20 VH Nucleotide Sequence

CAGGTGCAGCTGCAGCAGCCCCGGCGCCGAGCTGGTGAAGCCCGGCGCCAGCGTGAAGATGAGCTGCAAGGCCAGCGGCTACACCTT
CACCAGCTACAACATGCACTGGGTGAAGCAGACCCCCGGCGCGGCTGGAGTGGATCGGCGCCATCTACCCCGGCAACGGCGACA
CCAGCTACAACCAGAAGTTCAAGGGCAAGGCCACCTGACCGCCGACAAGAGCAGCAGCACCGCTACATGCAGCTGAGCAGCCTG
ACCAGCGAGGACAGCGCCGTGTACTACTGCGCCCGGAGCACCTACTACGGCGGCGACTGGTACTTCAACGTGTGGGGCGCCGGCAC
CACCGTGACCGTCTCGAGC

>Sequence ID 261: αCD20 VL Amino Acid Sequence

QIVLSQSPAILASPGKEVTMTCRASSSVSYIHWFQKPGSSPKPWYATSNLASGVFVRFSGSGSGTSYSLTISRVEAEDAATYY
CQQTWSNPPTFGGGTKLTVL

>Sequence ID 262: αCD20 VL Nucleotide Sequence

CAGATCGTGCTGAGCCAGAGCCCCGCCATCCTGAGCGCCAGCCCCGGCGAGAAGGTGACCATGACCTGCCGGGCCAGCAGCAGCGT
GAGCTACATCCACTGGTTCCAGCAGAAGCCCCGGCAGCAGCCCCAAGCCCTGGATCTACGCCACCAGCAACCTGGCCAGCGGCGTGC
CCGTGCGGTTACGCGGACGCGGACCGGCACCAGCTACAGCCTGACCATCAGCCGGGTGGAGGCCGAGACGCGGCCACCTACTAC
TGCCAGCAGTGGACCAGCAACCCCCACCTTCGGCGGCGGCACCAAGCTGACCGTGCTG

>Sequence ID 263: EGFR VHH Amino Acid Sequence

EVQLQESGGGLVQAGDSLSSLCLVSGRFSNYSYTMGWFRQAPGKEREFVAAILWSGPTTYADSVKGRFTISRDNAKNTVYLQMNSL
KPEDTAVYYCAAALGVLVLPAGNVYSYWGQGTQVTVSS

>Sequence ID 264: EGFR VHH Nucleotide Sequence

GAGGTGCAGCTGCAGGAGTCTGGCGGCGGCCTGGTGCAGGCTGGGGACAGCCTGAGCCTGTCCTGCCTGGTGTCTGGCCGCTCCTT
CAACTCCTACACCATGGGCTGGTTCCGCCAGGCCCCCTGGGAAGGAGCGGGAGTTTGTGGCTGCCATCCTGTGGAGTGGCCCCACCA
CCTACTATGCTGACTCTGTGAAGGCGCGCTTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTGTACCTGCAGATGAACAGCCTG
AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGCCCTGGGAGTGCTGGTGTGGCCCTGGCAATGTGTACAGCTACTGGGG
CCAGGGCACCCAGGTGACTGTCTCGAGC

>Sequence ID 265: HER3 VHH Amino Acid Sequence

QVQLVQSGGGLVQAGGSLSLSCAFSGRTFSMYTMGWFRQAPGKEREFVAANRGRGLSPDIADSVNGRFTISRDNKNTLYLQMDSL
KPEDTAVYYCAADLQYGSWPQRS SAEYDYWGQGTITVTVSS

>Sequence ID 266: HER3 VHH Nucleotide Sequence

CAGGTGCAGCTGGTGCAGTCTGGCGGAGGCCTGGTGCAGGCTGGGGGACAGCCTGAGCCTGAGCTGTGCCTTCTCTGGCCGCACCTT
CTCCATGTACACCATGGGCTGGTTCCGCCAGGCCCCAGGGAAGGAGAGAGAGTTTGTGGCTGCCAAGAGGAGAGGCTGAGCC
CAGACATTGCTGACTCTGTGAATGGCGCGCTTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTACCTGCAGATGGACAGCCTG
AAGCCAGAGGACACAGCTGTGTACTACTGTGCTGCTGACCTGCAGTATGGCAGCAGCTGGCCTCAGAGGAGCTCTGCTGAGTATGA
CTACTGGGGCCAGGGCACCACTGTGACTGTCTCGAGC

>Sequence ID 267: αPD-L1 Stapled VH Amino Acid Sequence

EVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKCLEWIAICIAAGSAGITYDANWAKGRFTISRDNKNTLYLQMN
SLRAEDTAVYYCARSAFSDYAMDLDWGQGTITVTVSS

>Sequence ID 268: αPD-L1 Stapled VH Nucleotide Sequence

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTT
CAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGTGCCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTG
GTATCACTTACGACGCGGAACCTGGGCGAAAGGCCGTTTCACCATCTCCAGAGACAATCCAAGAACAACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTTTTCGTTCGACTACGCCATGGACCTCTGGGGCCAGGG
AACCCTGGTCACCGTCTCGTCT

>Sequence ID 269: αPD-L1 Stapled VL Amino Acid Sequence

DIQMTQSPSTLSASVGRVITITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISSLQPDFFATY
YCQQGYSWGNDVNFVGCSTKVEIK

>Sequence ID 270: αPD-L1 Stapled VL Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCAT
TAGTTCCTCACTTAACTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGG
TCCCATCAAGGTTACGCGGAGTGGATCTGGGACAGAAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCACCTTAT
TACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTTCGGCTGCGGGACCAAGGTGGAGATCAAATAG

>Sequence ID 271: α4-1BB VH Stapled Amino Acid Sequence

RSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQVVRQAPGKCLEYIGTISGGNVYYASSARGRFTISRPSKNTVDLQMNSLRA
EDTAVYYCARDGYS DPMWGQGTITVTVSS

>Sequence ID 272: α4-1BB VH Stapled Nucleotide Sequence

CGGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACTGCCTCTGGATTACCATCAG
TAGCTACCACATGCGAGTGGGTCCGGCAGGCACCTGGGAAGTGCTGGAGTACATCGGAACCATAGTAGTGGTGGTAATGTATACT
ACGCAAGCTCCGCTAGAGGAGATTCACCATCTCCAGACCCTCGTCCAAGAACAACGCTGGATCTTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCCTATGTGGGGCCAGGGAACCTGGTCACCGTCTCTTC
A

>Sequence ID 273: α4-1BB VL Stapled Amino Acid Sequence

DVVMTQSPSSVSASVGRVITITCQASQNIPTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEFGDAATY
YCQSTYLGTDYVGGAFGCGTKVEIK

>Sequence ID 274: α4-1BB VL Stapled Nucleotide Sequence

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCAGTCAGAACAT
TAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGG
TCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGACTTGGAACCTGGCGATGCTGCAACTTAC
TATTGTCACTTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCTGTGGGACCAAGGTGGAGATCAAATGA

>Sequence ID 275: αHer3 VH Stapled Amino Acid Sequence

QVQLQESGGGLVKPGGSLRLSCAASGFTFSSYWMSWVRQAPGKCLEWVANINRDGSASYVDSVKGRFTISRDDAKNSLYLQMNSL
RAEDTAVYYCARDRGVGYFDLWGRGTLVTVST

>Sequence ID 276: αHer3 VH Stapled Nucleotide Sequence

CAGGTGCAATTGCAGGAGTCGGGGGGAGGCCTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTT
TAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGTGCCTGGAGTGGGTGGCCAACATAAACCGCGATGGAAGTGCGA
GTTACTATGTGGACTCTGTGAAGGGCCGATTACCATCTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTG
AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGTGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCTGGTCAC
CGTGTGACAA

>Sequence ID 277: αHer3 VL Stapled Amino Acid Sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNFVSWYQQHPGKAPKLMYIDVSDRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYCSSYSSSTHVIFGCGTKVTVL

>Sequence ID 278: αHer3 VL Stapled Nucleotide Sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCAAACCTCATGATCTATGATGTCACTGATCGGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCTGTGGGACCAAGGTGACCGTCCTA

>Sequence ID 279: αCEA 656E11 VH Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFSFSGTQYVCWVRQAPGKLEWIGCIYVDVANTYYATSVKGRFTISRDN SKNTLYLQMNS
LRAEDTAVYYCASHDTVACGGLDLWGQGT LTVVSS

>Sequence ID 280: αCEA 656E11 VH Nucleotide Sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTT
CAGTGGCACCCAGTACGTGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTTATGTGGATGTGGCTA
ACACTTACTACGCGACCTCCGTGAAGGGCAGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGC
CTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGTCATGATACTGTTTGTGCTGTTGTGGTTTGGACTTGTGGGGCCAGGG
AACCCTGGTCACCGTCTCGAGC

>Sequence ID 281: αCEA 656E11 VL Amino Acid Sequence

DIQMTQSPSTLSASVGRVTITCQASENIYNSLAWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTEFTLTISSLQPDFFATY
YCQSTYYNNIIYGAAFGGKVEIK

>Sequence ID 282: αCEA 656E11 VL Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTGAGAACAT
TTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCTATGATGCTTCCACTCTGGCATCTGGGG
TCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTAT
TACTGCCAATCTACTTATTATAATAATATCATTATGGGGCTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>Sequence ID 283: αHER2 VH Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSL
RAEDTAVYYCSRWGGDGYAMDYWGQGT LTVTVST

>Sequence ID 284: αHER2 VH Nucleotide Sequence

GAAGTACAGCTTGTGAGAGTGGTGGTGGACTTGTCCAACCAGGGGGAAGTCTGCGGCTGTCATGCGCAGCCTCTGGCTTCAACAT
TAAGGACACCTACATTCACTGGGTTCGGCAAGCGCCGGGGAAGGGGCTGGAATGGGTGCGCCAGGATATACCCTACCAACGGGTACA
CCAGGTATGCAGATAGCGTTAAGGGTAGATTCACTATTTTCACTGACACTAGCAAGAACACCGCGTATCTCCAGATGAACCTCCCTT
CGCGCCGAGGATACGGCTGTGTACTACTGCTCTAGGTGGGGAGGAGATGGGTTTTACGCAATGGATTACTGGGGACAGGGAACACT
CGTTACGGTGTGACA

>Sequence ID 285: αHER2 VL Amino Acid Sequence

DIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFVLYSGVPSRFSGSRSGTDFTLTISLQPEDFATY
YCQQHYTTPPTFGQGTKVEIK

>Sequence ID 286: αHER2 VL Nucleotide Sequence

GACATCCAAATGACGCGAGTCTCCCTCCAGTTTGTAGTGCAAGTGTGGGAGACAGAGTTACGATCACATGTAGGGCAAGTCAGGACGT
CAATACAGCCGTCGCATGGTACCAGCAGAAGCCTGGAAAGGCCCGGAACTTCTGATTTACTCTGCAAGTTTCTCTACAGTGGTG
TTCTTAGTCGCTTCAGTGGGTCTCGGTCAAGCACCGATTTTACCCTGACAATTAGCAGCTTGCAACCGGAAGATTTTGCACCTAT
TATTGCCAGCAACATTATACACCCCTCCCACATTTGGACAAGGCACGAAGGTAGAGATTAA

>Sequence ID 287: SI-20C14 (anti-CEA 656E11) Heavy Chain Amino Acid Sequence

EVQLVESGGGLVQPGGSLRLSCAASGFSFSGTQYVWVRQAPGKGLEWIGCIYVDVANTYYATSVKGRFTISRDNSKNTLYLQMNS
LRAEDTAVYYCASHDTVCAGCGLDLWQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI
SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CVMHEALHNHYTQKSLSLSPG

>Sequence ID 288: SI-20C14 (anti-CEA 656E11) Heavy Chain Nucleotide Sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTT
CAGTGGCACCCAGTACGTGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTTATGTGGATGTGGCTA
ACACTTACTACGCGACCTCCGTGAAGGGCAGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAATGAACAGC
CTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGTCATGATACTGTTTGTGCTGGTGTGGTTTGGACTTGTGGGGCCAGGG
AACCTTGGTCAACGCTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA
CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCGGCGTG
CACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
GACCTACATCTGCAACGTGAATCACAAGCCAGCAGCAACCAAGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTCACA
CATGCCACCGTGCACGACCTGAAGCGCGGGGCAACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATC
TCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACC
AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCT
GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACTACAAGACCACGCTCCCG
TGCTGGACTCCGACGGCTCCTTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA

>Sequence ID 289: SI-20C14 (anti-CEA 656E11) Light Chain Amino Acid Sequence

DIQMTQSPSTLSASVGDRTITCQASENIYSNLAWYQQKPGKAPKLLIYDASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATY
YCQSTYYNNIIYGAAFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
KDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 290: SI-20C14 (anti-CEA 656E11) Light Chain Nucleotide Sequence

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTGAGAACAT
TTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATGATGCTTCCACTCTGGCATCTGGGG
TCCCATCAAGTTTCAAGCGGAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCTTAT
TACTGCCAATCTACTTATTATAATAATATCATTTATGGGGCTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGC
TGCACCATCTGTCTTCTATCTTCCCGCATCTGATGAGCAGTTGAACTCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCT
ATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAATCCAGGAGAGTGTACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

>Sequence ID 291: αCD3***** VH Amino Acid Sequence

QQLVESGGGLVKPGGSLRLSCAASGIDLSSNAIGWVRQAPGKGLEWVGVI FGSGNTYYASWAKGRFTISRKNTVYLQMNSLRAED
TAVYYCARGGYSSDIWGQGLTVTVSS

>Sequence ID 292: αCD3***** VH Nucleotide Sequence

CAACAGTTGGTTGAGTCTGGTGGCGGTCTCGTTAAGCCTGGAGGGTCCCTTCGGCTTAGTTGTGCGGCCTCTGGGATCGACCTGTC
TAGCAACGCTATAGGATGGGTACGGCAAGCTCCGGGCAAAGGCCTTGAGTGGGTGGCGCTTATTTTGGGAGCGGTAATACGTACT
ACGCCAGCTGGGCAAAGGTAGGTTCACTATCAGTCGATCAAAGAACACGGTATATCTTCAGATGAACAGTCTCCGGGCGGAGGAC
ACCGCGGTTTATTATTGCGCAAGGGGGGGATACTCCTCAGACATATGGGGCCAAGGTACTTTGGTGACGGTCTCGAGC

>Sequence ID 293: αCD3***** VL Amino Acid Sequence

DPVLTQSPSSLSASVGDRTVISCQSSQSVAKNNNLAWFQQKPGQAPKLLIYASTLAAGVPSRFSGSGSGTDFTLTISVQPEDFA
TYYCSARDSGNIQSFGGGTKVEIK

>Sequence ID 294: αCD3***** VL Nucleotide Sequence

GATCCAGTTCTGACACAAAGTCCATCCAGCCTGTCTGCCTCAGTCGGCGACAGAGTGACCATCAGTTGCCAGAGCTCACAGTCTGT
GGCTAAGAACAACAACCTTGGCGTGGTTCCAACAGAAACCTGGACAGGCTCCGAAATGCTGATCTATCTGCTTCCACGCTTGCTG
CTGGTGTTCCTTCCCCTTTTTCAGGTAGTGGTAGCGGGACAGACTTCACTTTGACTATAAGCAGCGTGCAGCCTGAAGATTTTGC
ACCTACTATTGTTCTGCTAGAGACAGTGGAAATATTAGTCTTTGGGGGGGGAACGAAGGTGAAATAAAG

>Sequence ID 295: NKG2D Monomer Amino Acid Sequence

FLNSLFNQEVQIPLTESYCGPCPKNWICYKNNCYQFFDESKNWEYESQASCMSQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIPTN
GSWQWEDGSILSPNLLTIEMQKGDICALYASSFKGYIENCSTPNTYICMQRTV

>Sequence ID 296: NKG2D Monomer Nucleotide Sequence

TTTCTGAATAGCCTGTTCAACCAGGAGGTGCAGATCCCACTGACCGAGAGCTATTGTGGACCTTGTCTAAGAACTGGATCTGTTA
CAAGAACAACCTGCTACCACTTCTTCGACGAGAGCAAGAATTGGTATGAAAGCCAGGCCAGCTGCATGAGCCAAAACGCTCTCTGC
TGAAGGTGTACTCCAAAGAAGATCAGGACCTGCTGAAGCTGGTGAAGTCTTACCCTGGATGGGCCTGGTGCACATCCCAACCAAC
GGCAGCTGGCAGTGGGAAGACGGCAGCATCCTGAGCCCTAACCTGCTGACAATCATTGAGATGCAGAAAGGCGACTGCGCCCTGTA
CGCCAGTTCTTTTAAGGGCTACATCGAAAACCTGTAGCACCCCTAACACCTACATCTGCATGCAGAGAACAGTG

>Sequence ID 297: SI-75XM9 chain A amino acid sequence

QVQLQESGGRLVQPGPEPLSLTCKTSGIDLSSNAIGWVRQAPGKGLEWVGVI FGSGNTYYASWAKGRFTISRSTSTVYLMNSLRSE
DTAIYYCARGGYSSDIWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVTVTPSSSLGKTYTCNVNHNKPSNTKVDKRVESKYGPPCPPEAAGGFSVFLFPPKPKDTLMI SRTPEVTCVVVD
VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHLQDNLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTL
PPSQEEMTKNQVSLTSCAVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSRITVDKSRWQEGNVFSCSVMHEALHNYT
QKSLSLSLG

>Sequence ID 298: SI-75XM9 chain A nucleotide sequence

CAAGTGCAGTTGCAAGAAAGTGGTGGTAGACTGGTTCAGCCTGGTGAACCCTTGTCAGTGCAGTGTAAAAACAAGCGGCATTGATCT
GTCTCTAACGCCATCGGATGGGTCCGACAGGCCCCAGGAAAAGGTCTGGAGTGGATCGGAGTTATCTTCGGGAGCGGCAATACAT
ACTACGCAAGCTGGGCAAAGGGCGATTACGATATCACGGAGCACCTCTACAGTTTATTTGAAAATGAACTCCCTCCGGTCCGAG
GATACCGCGATATATTACTGTGCCAGAGGGGGTACTCCTCTGATATCTGGGGGCAGGGTACACTGGTTACAGTTTCATCCGCTAG
CACCAAGGGACCTCTGTGTTTCTCTGGCTCCTTGCTCCAGATCCACCTCCGAGTCTACAGCTGCTCTGGGCTGCCTGGTCAAGG
ACTACTTTCTGAGCCTGTGACCGTGTCTGGAACCTCTGGCGCTCTGACATCTGGCGTGCACACCTTTCAGCTGTGCTGCAGTCC
TCCGGCCTGTACTCTCTGTCTCTGTCTGTGACCGTGCCTTCTCTAGCCTGGGCACCAAGACCTACACCTGTAATGTGGACCACAA
GCCTTCCAACACCAAGGTGGACAAGCGCGTGAATCTAAGTACGGCCCTCCTTGCTCCTCCATGTCTGCTCCAGAAGCTGCTGGCG
GCCCATCCGTGTTCTGTTCCCTCCAAAGCCTAAGGACACCTGATGATCTCTCGGACCCCTGAAGTGACCTGCGTGGTGGTGGAT
GTGTCCAAGAGGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGA
ACAGTTCAACTCCACCTACAGAGTGGTGTCCGTGCTGACCGTGTGACCAAGGATTGGCTGAACGGCAAAGAGTACAAGTGCAAGG
TGTCCAACAAGGGCCTGCCTTCCAGCATCGAAAAGACCATCTCCAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTACACCCTG
CCTCCAAGCCAAGAGGAAATGACCAAGAACCAGGTGTCCCTGTCTGCGCCGTGAAGGGCTTCTACCTTCCGATATCGCCGTGGA
ATGGGAGAGCAATGGCCAGCCTGAGAACAACTACAAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCCTTCTCTGGTGTCCC

GCCTGACCGTGGACAAGTCCAGATGGCAAGAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACC
CAGAAGTCCCTGTCTCTGTCCCTGGGATGA

>Sequence ID 299: SI-75XM9 chain B amino acid sequence

QSALTQPASVSGSPGQSITISCTGTSSDVGGINFVSWYQQHPGKAPKLMYDVS DRPSGVSDRFSGSKSGNTASLIISGLQADDEA
DYICSSYSSSTHVFIFGGGKT VTLGGGGSGGGSGGGSGGGSGVQLQESGGGLVKPGGSLSLSCAASGFTFSSYMSWVRQAP
GKGLEWVANINRDGSASYVD SVKGRFTISRDDAKNSLYLQMNLSLAEDTAVYYCARDRGVGYFDLWGRGTLVTVSSGGGGSGGGG
SDPQLTQSPSSLATVGQRTINCQSSQSVAKNNNLAWFQQKPGKPKLLIYSASTLAAGVPSRFSGSGSGTQFTLLITRVQSEDF
ATYYCSARDSGNIQSFGGGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
KDYSLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSLVTLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREP
QVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEAL
HNRFTQKSLSLSLG

>Sequence ID 300: SI-75XM9 chain B nucleotide sequence

CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGT
TGGTGGTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCAAACCTCATGATCTATGATGTGAGTATCGGCCCT
CAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCCAGGCTGACGACGAGGCT
GATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTTAGGCGGTGGCGG
TAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTGCAATTGCAGGAGTCGGGGGGAGGCTTGGTCA
AGCCTGGAGGGTCCCTGAGCCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA
GGGAAGGGGCTGGAGTGGGTGGCAACATAAACCGCGATGGAAGTGCGAGTTACTATGTGGACTCTGTGAAGGGCCGATTACCAT
CTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAG
ATCGTGGGGTGGGCTACTTCGATCTCTGGGGCCGTGGCACCCCTGGTCACCGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGA
TCAGATCCTCAATTGACCCAGTCCCTAGTAGCCTTTCTGCAACCGTGGGCCAGAGGGTAACAATCAATTGCCAGTCAAGCCAGTC
CGTAGCGAAGAATAATAATTTGGCATGGTTCCAACAAAAACCGGTAAACCTCCTAACTCCTTATCTACTCAGCTTCAACCCTTG
CCGCGGGTGTGCCAGCCGGTTCTCAGGCTCAGGTTCCGGGACTCAATTTACCTTACCATCACTCGCGTCCAAAGTGAGGATTTT
GCAACCTACTATTGTTCTGCACGGGATTCCGGGAACATACAGTCCTTTGGGGGTGGAACCTCGGGTGAGATAAAACGTACGGTGGC
TGCAACATGTGCTTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATAACTTCT
ATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGCGGCGGACCTCCTTGTCTCCATGTCTGCTC
CAGAAGCTGCTGGCGGCCCATCCGTGTTTCTGTTCCCTCCAAGCCTAAGGACACCCCTGATGATCTCTCGGACCCCTGAAGTGACC
TGCGTGGTGGTGGATGTGTCCCAAGAGGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAAGTGACAACGCCAAGAC
CAAGCCTAGAGAGGAACAGTTCAACTCCACCTACAGAGTGGTGTCCGTGCTGACCGTGTGTCACCAAGGATTGGCTGAACGGCAAAG
AGTACCAATGTGCTTTCATCTTCCAGCAAGGGCCTGCCTGAGCATCGAAAAGACCATCTCCAAGGCCAAGGGCCAGCCTAGGGAAACC
CAGGTTTACACCTTGCCTCCAAGCCAAGAGGAAATGACCAAGAACCAGGTGTCCCTGTGGTGCCTCGTGAAGGGCTTCTACCCCTC
CGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCTGAGAACAACCTACAAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCCT
TCTTCTGTATTCCCGCCTGACCGTGGACAAGTCCAGATGGCAAGAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGAGGCCCTG
CACAATCGCTTCAACCAGAAGTCCCTGTCTCTGTCCCTGGGATGA

>Sequence ID 301: anti-CEA 656E11 CDR-H1 amino acid sequence

GTQYVC

>Sequence ID 302: anti-CEA 656E11 CDR-H2 amino acid sequence

CIYVDVANTYYATSVKG

>Sequence ID 303: anti-CEA 656E11 CDR-H3 amino acid sequence

HDTVCAAGCLDL

>Sequence ID 304: anti-CEA 656E11 CDR-L1 amino acid sequence

QASENIYSNLA

>Sequence ID 305: anti-CEA 656E11 CDR-L2 amino acid sequence

DASTLAS

>Sequence ID 306: anti-CEA 656E11 CDR-L3 amino acid sequence

QSTYYNNIIYGAA

>Sequence ID 307: anti-CD3 283E3 (BSM/FRS) CDR-H1 amino acid sequence

SNAIG>Sequence ID 308: anti-CD3 283E3 (BSM/FRS) CDR-H2 amino acid sequence

VIFGSGNTYYASWAKG

>Sequence ID 309: anti-CD3 283E3 (BSM/FRS) CDR-H3 amino acid sequence

GGYSSDI

>Sequence ID 310: anti-CD3 283E3 (BSM/FRS) CDR-L1 amino acid sequence

QSSQSVAKNNNLA

>Sequence ID 311: anti-CD3 283E3 (BSM/FRS) CDR-L2 amino acid sequence

SASTLAA

>Sequence ID 312: anti-CD3 283E3 (BSM/FRS) CDR-L3 amino acid sequence

SARDSGNIQS

>Sequence ID 313: human IgG1 amino acid sequence

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVN
HKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

>Sequence ID 314: human IgG4 amino acid sequence

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTYTCNVN
HKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPR
EEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFCFSVMHEALHNHYTQKSLSLSLG

CLAIMS

What is claimed is:

1. A multi-specific antibody-like protein having a N-terminus and a C-terminus, comprising,
a first monomer, comprising, from the N-terminus to the C-terminus, a first binding monomer, a CH1 domain, a first hinge, a first CH2 domain, and a first CH3 domain, wherein the first monomer comprises optionally a first binding domain (D1) linked to the N-terminus, a fourth binding domain (D4) linked to the C-terminus, or both,

a second monomer, comprising, from the N-terminus to the C-terminus, a second binding monomer, a CL domain, a second hinge, a second CH2 domain, and a second CH3 domain, wherein the second monomer comprises optionally a second binding domain (D2) linked to the N-terminus, a fifth binding domain (D5) linked to the C-terminus, or both,

wherein the first binding monomer and a second binding monomer are configured to form a dimer,

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.
2. The multi-specific antibody-like protein of Claim 1, wherein the first binding monomer comprises a VH domain, a second binding monomer comprises a VL domain, and wherein the VH, CH1, VL, CL domains form a Fab region as a third binding domain (D3).
3. The multi-specific antibody-like protein of Claim 1, wherein the first binding monomer and the second binding monomer form a NKG2D receptor as a third binding domain (D3).
4. The multi-specific antibody-like protein of Claim 1, wherein the first CH3 domain is configured to form a hole structure, wherein the second CH3 domain is configured to form a knob structure, and wherein the first CH2 and CH3 domains and the second CH2 and CH3 domains are configured to heterodimerize to form a complementary Fc domain.
5. The multi-specific antibody-like protein of Claim 1, wherein the D1, D2, D4, and D5 is independently a scFv domain, a VHH domain, a receptor, or a ligand.
6. The multi-specific antibody-like protein of Claim 1, wherein the D1, D2, D3, D4, and D5 each independently has a binding specificity against an antigen selected, EGFR, HER2, HER3, EGFRvIII, ROR1, CD3, CD28, CEA, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypican-3, gpA33,

GD2, TROP2, NKG2D, NKG2D ligand, BCMA, CD19, CD20, CD33, CD123, CD22, CD30, PD-L1, PD1, OX40, 4-1BB, GITR, TIGIT, TIM-3, LAG-3, CTLA4, CD40, CD40L, VISTA, ICOS, BTLA, LIGHT, HVEM, CSF1R, CD73, CD39, CLDN18.2, DLL3, HLA-G, FcRH5, GPRC5D, LIV-1, MUC1, CD138, CD70, CD16, uPAR, Siglec-15, CD47, CD38, , NKp46, PD-L2, CD160, LOX-1, SIRP α , CD27 and wherein the Fc domain comprises a human IgG Fc domain.

7. The multi-specific antibody-like protein of Claim 1, wherein D1 has a binding specificity to CD3, CD20, CEA, HER2, EGFR, or NKG2D ligand.

8. The multi-specific antibody-like protein of Claim 1, wherein D2 has a binding specificity to HER3, EGFR, CD3, or CD19.

9. The multi-specific antibody-like protein of Claim 1, wherein D3 has a binding specificity to HER3, EGFR, CD3, or NKG2D ligands.

10. The multi-specific antibody-like protein of Claim 1, wherein D4 has a binding specificity to 4-1BB, or EGFR.

11. The multi-specific antibody-like protein of Claim 1, wherein D5 has a binding specificity to PD-L1 or HER3.

12. The multi-specific antibody-like protein of Claim 1, wherein the antibody is a tri-specific antibody having the binding specificity to EGFR, HER3, and CD3.

13. The multi-specific antibody-like protein of Claim 1, wherein the antibody is a tetra-specific antibody having the binding specificity to EGFR, HER3, CD3, and 4-1BB.

14. The multi-specific antibody-like protein of Claim 1, wherein the antibody is a tetra-specific antibody having the binding specificity to EGFR, HER3, CD3, and PD-L1.

15. The multi-specific antibody-like protein of Claim 1, wherein the antibody is a penta-specific antibody having the binding specificity to EGFR, HER3, CD3, 4-1BB and PD-L1.

16. A complimentary determining region (CDR) having an affinity to CEA, comprising an amino acid sequence having at least 80% sequence identity to SEQ ID NO. 301, 302, 303, 304, 305, or 306.

17. A protein having an affinity to CEA, comprising the CDR of Claim 16.

18. A multi-specific antibody-like protein having a binding affinity to CEA, wherein the antibody-like protein comprises an amino acid sequence having at least 98% sequence identity to an amino acid sequence selected from SEQ ID NO. 279, 280, 281 or 282.

19. A complimentary determining region (CDR) having a binding affinity to CD3, comprising an amino acid sequence having at least 80% sequence identity to SEQ ID NO. 307, 308, 309, 310, 311 or 312.
20. A protein having an affinity to CD3, comprising CDR of Claim 19.
21. A multi-specific antibody-like protein having a binding affinity to CD3, wherein the antibody-like protein comprises an amino acid sequence having at least 98% sequence identity to an amino acid sequence selected from SEQ ID NO. 227-230, 231-234, 235-238, 239-242 and 291-294.
22. An isolated nucleic acid sequence encoding the multi-specific antibody-like protein of Claim 1.
23. An expression vector comprising the isolated nucleic acid sequences of Claim 22.
24. A host cell comprising the isolated nucleic acid sequence of Claim 22.
25. An immunoconjugate comprising the multi-specific antibody-like protein of Claim 1 and a cytotoxic agent.
26. A pharmaceutical composition, comprising the multi-specific antibody-like protein of Claim 1 and a pharmaceutically acceptable carrier.
27. A pharmaceutical composition, comprising the immunoconjugate of Claim 25 and a pharmaceutically acceptable carrier.
28. 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 multi-specific antibody-like protein of Claim 1.
29. A method for producing the multi-specific antibody-like protein of Claim 1, comprising
culturing a host cell such that the DNA sequence encoding the multi-specific antibody-like protein of Claim 1 is expressed, and
purifying said multi-specific antibody-like protein.
30. A solution comprising an effective concentration of the multi-specific antibody-like protein of Claim 1, wherein the solution is blood plasma in a subject.

Figure 1

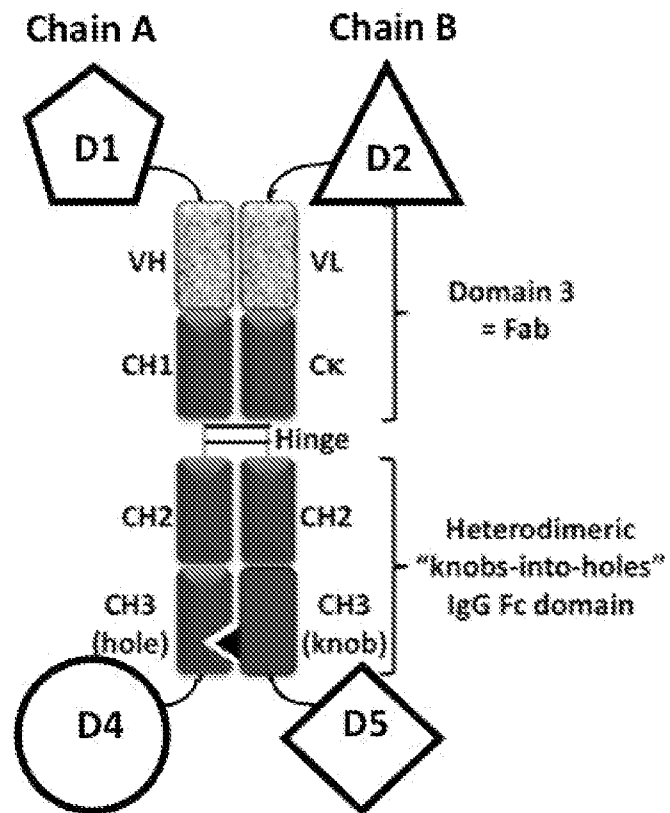


Figure 2

Fig. 2A

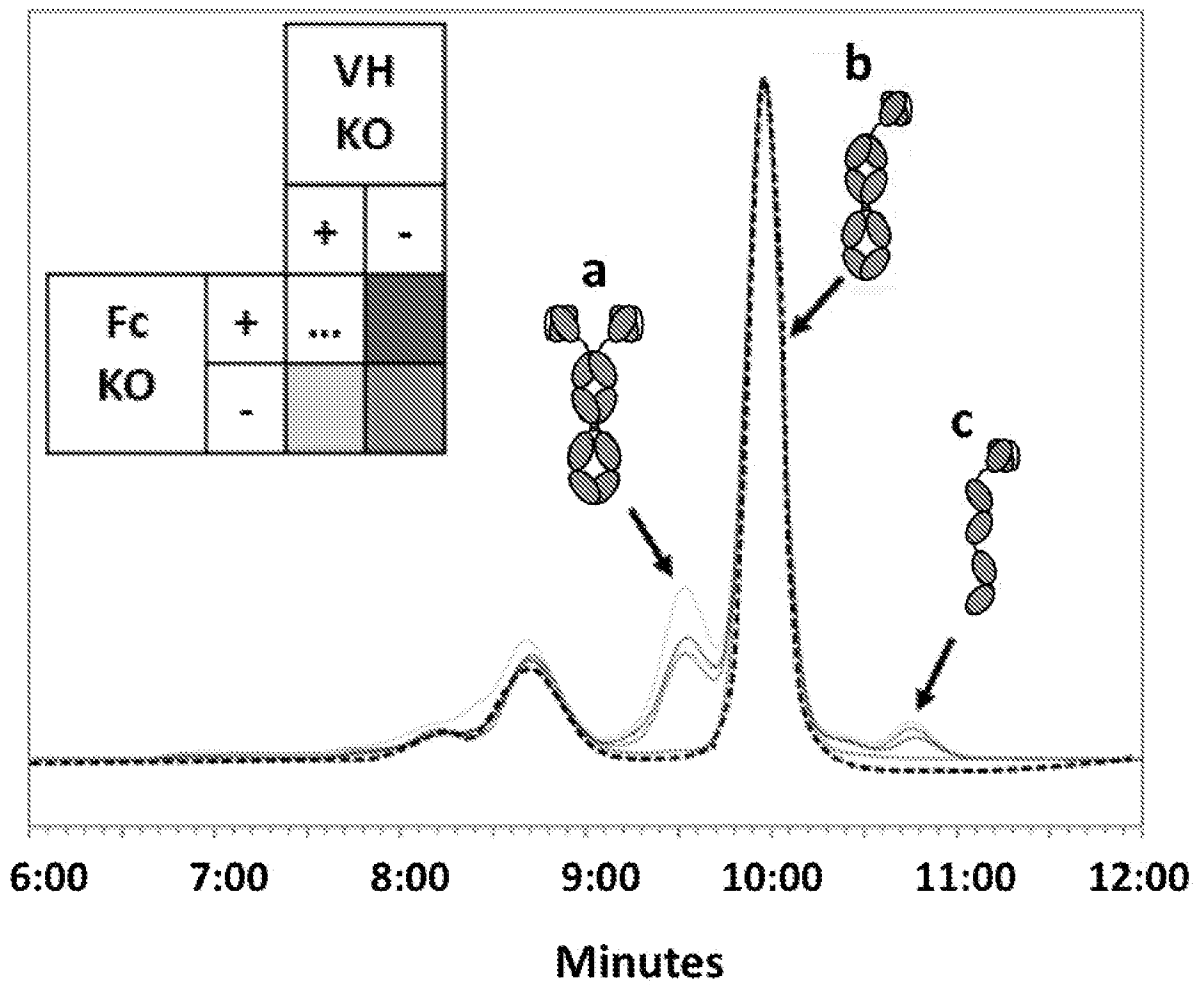


Fig. 2B

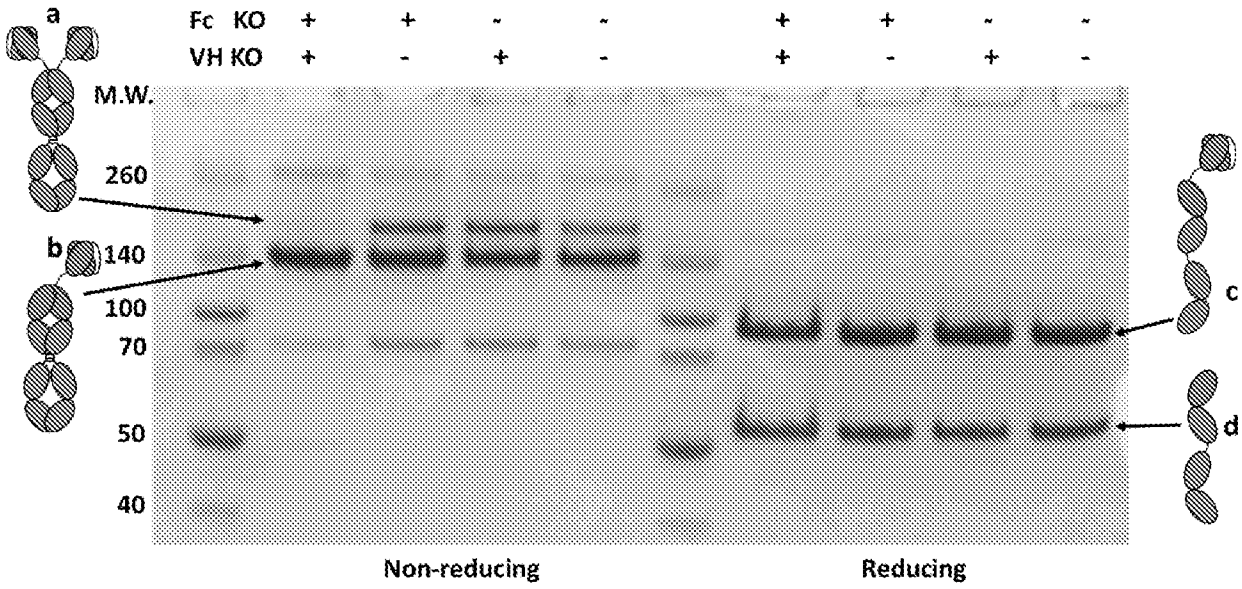


Figure 3

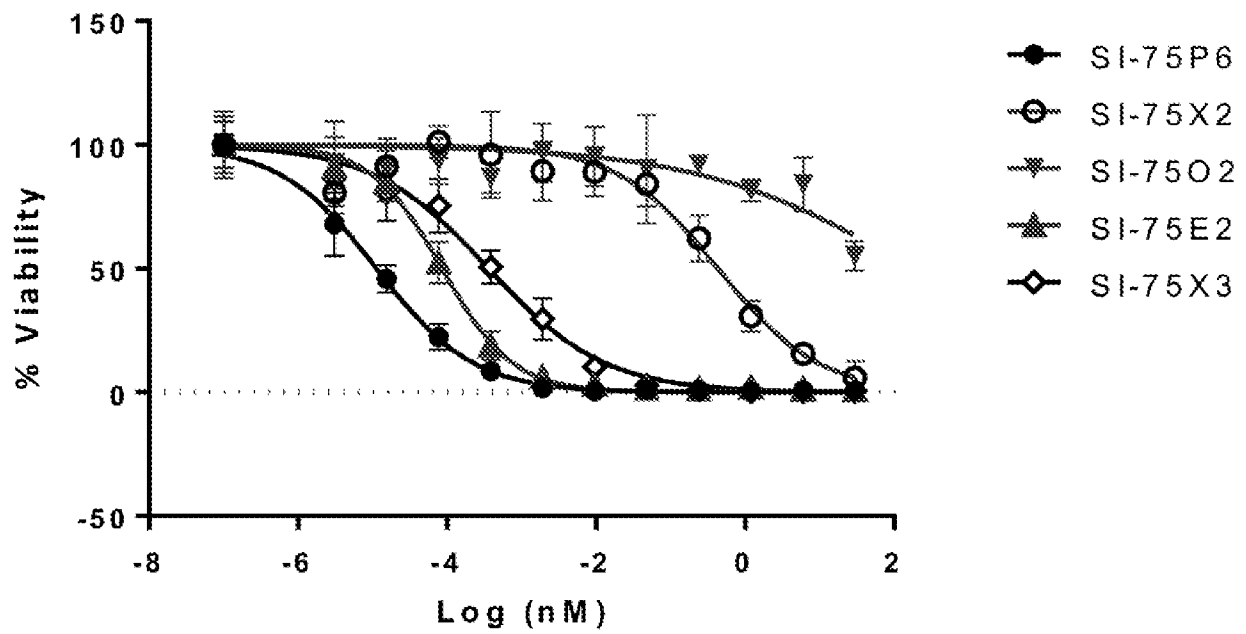


Figure 4

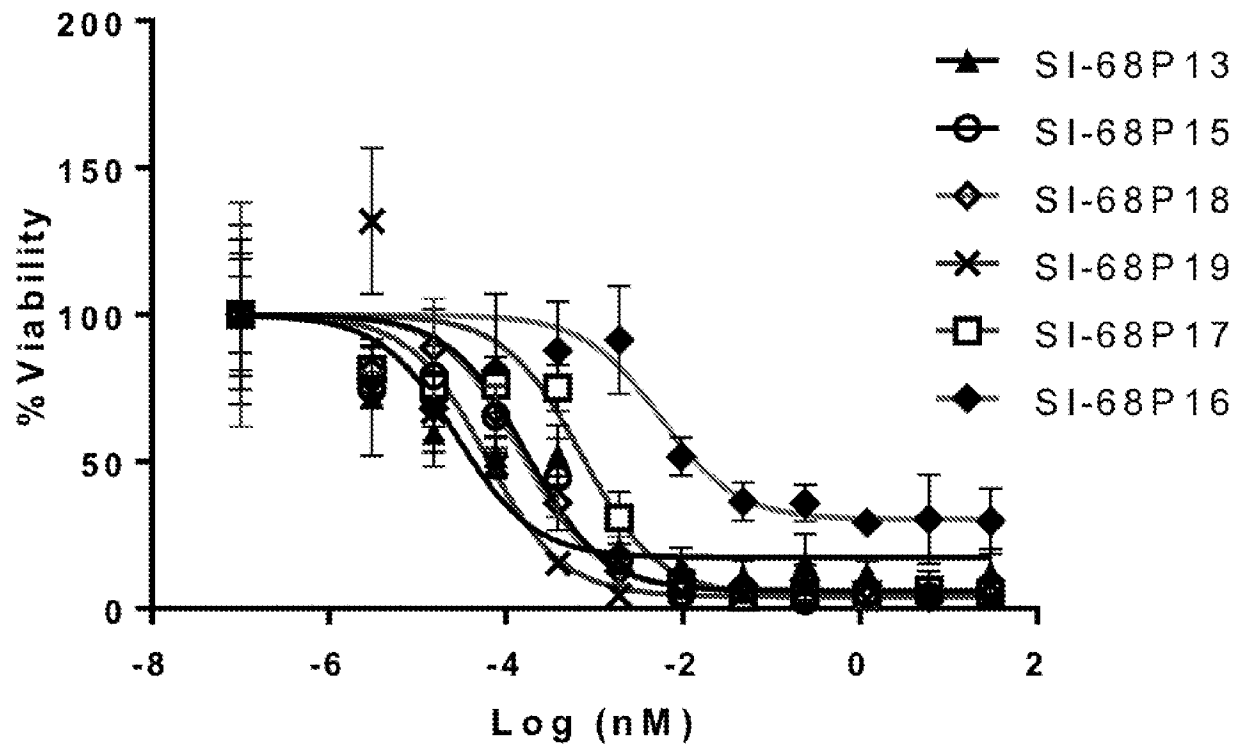


FIGURE 5

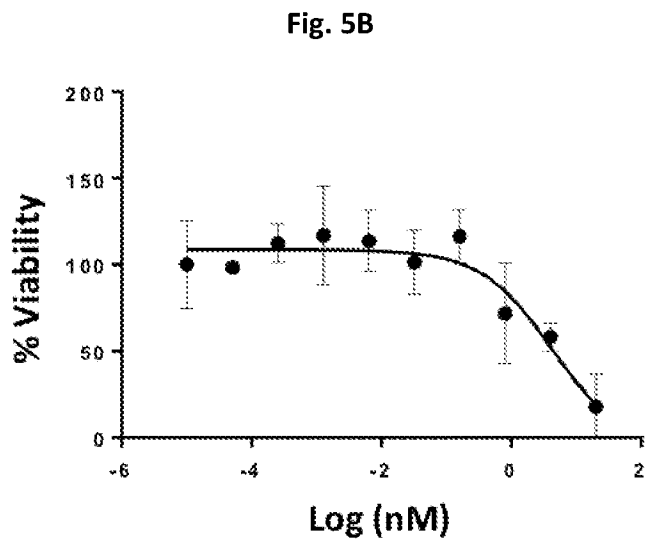
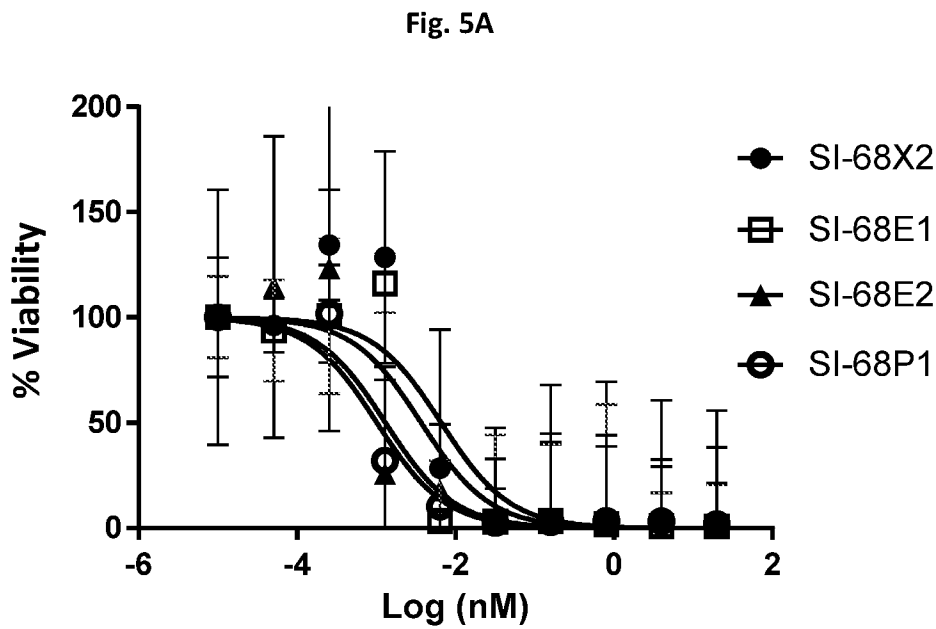
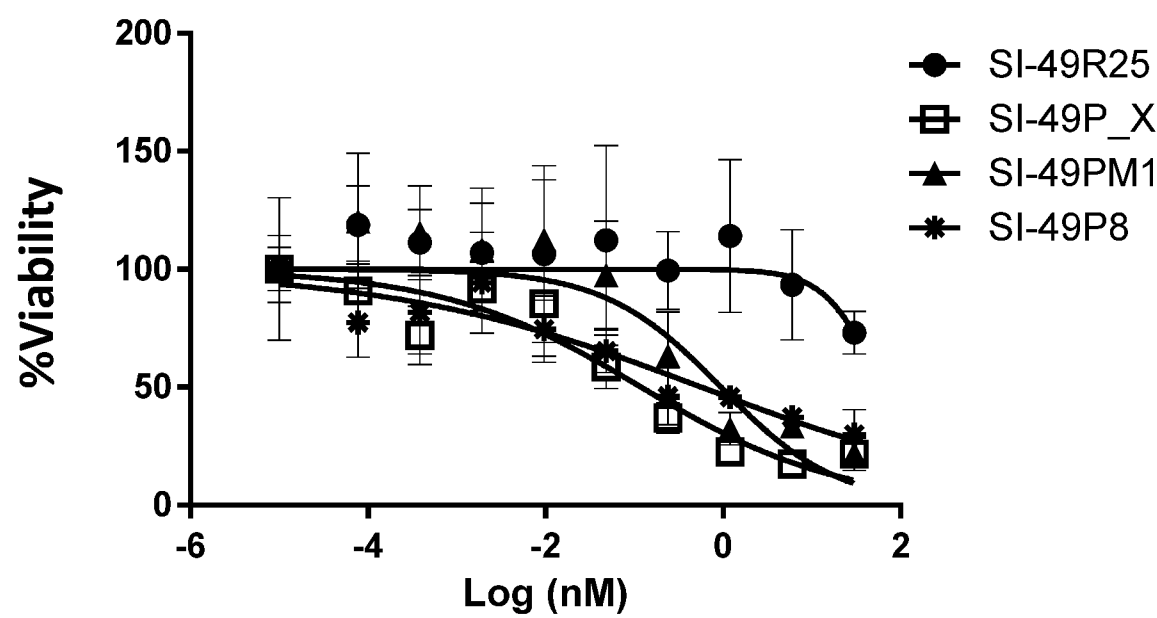


Figure 6



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/22847

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C07K 16/28, C07K 16/30, A61K 39/395 (2021.01)

CPC - C07K 16/2803, C07K 16/2809, C07K 16/2863, C07K 2317/31, C07K 2317/55, C07K 2317/56, C07K 2317/565, C07K 2317/569, C07K 16/3007

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X -- Y --- A	WO 2019/005640 A2 (SYSTIMMUNE, INC.) 03 January 2019 (03.01.2019). pg 2 para 3-pg 2 para 4, pg 3 para 2, pg 4 para 3, pg 4 para 7-pg 4 para 8, pg 5 para 2-pg 5 para 7, pg 6 para 2-pg 6 para 4, pg 8 para 3-pg 8 para 3, pg 10 para 4, pg 11 para 4, pg 12 para 1, pg 12 para 7, pg 13 para 1-pg 13 para 3, pg 14 para 2, Claim 2, Claim 26, Abstract	1-3, 5-11, 22-30 ----- 4 ----- 19-21
Y	US 2015/0315296 A1 (HOFFMANN-LA ROCHE INC.) 05 November 2015 (05.11.2015). para [0010], [0137], [0151], Claim 1, Abstract	4
A	WO 2019/136309 A1 (ICONIC THERAPEUTICS, INC.) 11 July 2019 (11.07.2019) SEQ ID NO:387	19-20
A	WO 2009/040562 A1 (UCB PHARMA S.A.) 02 April 2009 (02.04.2009) p18, ln 25-27; SEQ ID NO:52	21

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"D" document cited by the applicant in the international application

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

21 July 2021

Date of mailing of the international search report

AUG 16 2021

Name and mailing address of the ISA/US

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Authorized officer

Lee Young

Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/22847

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

a. ☒ forming part of the international application as filed:

☒ in the form of an Annex C/ST.25 text file.

☐ on paper or in the form of an image file.

b. ☐ furnished together with the international application under PCT Rule 13ter.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

c. ☐ furnished subsequent to the international filing date for the purposes of international search only:

☐ in the form of an Annex C/ST.25 text file (Rule 13ter.1(a)).

☐ on paper or in the form of an image file (Rule 13ter.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/22847

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

-----Please see continuation in first extra sheet-----

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11, 19-30, limited to a bispecific protein as noted in extra sheet

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/22847

Continuation of Box No. III. Observations where unity of invention is lacking

Group I+, Claims 1-30, directed to a multi-specific antibody-like protein and complementary determining region (CDR) having an affinity to an antigen. The multi-specific antibody-like protein and CDR will be searched to the extent that the multi-specific antibody-like protein and CDR encompasses a bi-specific antibody-like protein further wherein D1 has a binding specificity to CD3 comprising a CDR of SEQ ID NO:307, D2 has a binding specificity to HER3, wherein the first binding monomer and the second binding monomer form a NKG2D receptor as a third binding domain (D3), wherein D4 has a binding specificity to 4-1BB, wherein D5 has a binding specificity to PD-L1, further wherein the antibody-like protein comprises an amino acid sequence having at least 100% sequence identity to an amino acid sequence of SEQ ID NO: 22 (note, these are the first claimed sequences for the inventive multi-specific antibody-like protein and CDR embodiment). It is believed that claims 1-11, 19-30 encompass this first named invention, and thus these claims will be searched without fee to the extent that the multi-specific antibody-like protein and CDR encompasses a bi-specific antibody-like protein further wherein D1 has a binding specificity to CD3 comprising a CDR of SEQ ID NO:307, D2 has a binding specificity to HER3, wherein the first binding monomer and the second binding monomer form a NKG2D receptor as a third binding domain (D3), wherein D4 has a binding specificity to 4-1BB, wherein D5 has a binding specificity to PD-L1, further wherein the antibody-like protein comprises an amino acid sequence having at least 100% sequence identity to an amino acid sequence of SEQ ID NO: 22. Additional multi-specific antibody-like protein(s) and CDR polypeptide(s) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected multi-specific antibody-like protein(s) and CDR polypeptide(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be a multi-specific antibody-like protein and CDR comprising a bi-specific antibody-like protein further wherein D1 has a binding specificity to CD3 comprising a CDR of SEQ ID NO:308, D2 has a binding specificity to HER3, wherein the first binding monomer and the second binding monomer form a NKG2D receptor as a third binding domain (D3), wherein D4 has a binding specificity to 4-1BB, wherein D5 has a binding specificity to PD-L1, further wherein the antibody-like protein comprises an amino acid sequence having at least 100% sequence identity to an amino acid sequence of SEQ ID NO: 22 (claims 1-11, 19-30).

The inventions listed as Group I+ do not relate to a single special technical feature under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special technical features

The inventions of Group I+ each include the special technical feature of a unique amino acid sequence. Each amino acid sequence encodes a unique peptide, and is considered a distinct technical feature.

Common technical features

No technical features are shared between the polypeptide amino acid sequences of Group I+ and, accordingly, these groups lack unity a priori.

Additionally, even if Group I+ were considered to share the technical features of including:

a multi-specific antibody-like protein having a N-terminus and a C-terminus, comprising, a first monomer, comprising, from the N-terminus to the C-terminus, a first binding monomer, a CH1 domain, a first hinge, a first CH2 domain, and a first CH3 domain, wherein the first monomer comprises optionally a first binding domain (D1) linked to the N-terminus, a fourth binding domain (D4) linked to the C-terminus, or both, a second monomer, comprising, from the N-terminus to the C-terminus, a second binding monomer, a CL domain, a second hinge, a second CH2 domain, and a second CH3 domain, wherein the second monomer comprises optionally a second binding domain (D2) linked to the N-terminus, a fifth binding domain (D5) linked to the C-terminus, or both, wherein the first binding monomer and a second binding monomer are configured to form a dimer, 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 a complementary determining region (CDR) and multi-specific antibody-like protein having an affinity to CEA, a complementary determining region (CDR) and multi-specific antibody-like protein having a binding affinity to CD3; these shared technical features are previously disclosed by WO 2019/005640 A2 to Systimmune, Inc. (hereinafter 'Systimmune').

-----please see continuation on next extra sheet -----

Continuation of Box No. III. Observations where unity of invention is lacking

-----continued from previous sheet -----

Systimmune discloses a multi-specific antibody-like protein having a N-terminus and a C-terminus (Abstract - "The disclosure provides a tetra-specific antibody monomer having a N-terminal and a C-terminal"), comprising, a first monomer, comprising, from the N-terminus to the C-terminus, a first binding monomer, a CH1 domain, a first hinge, a first CH2 domain, and a first CH3 domain (pg 13 para 2 - "The remaining position in the tetra-specific protein, Domain 3 (D3), consists of an IgG1 heavy chain, VH-CH1-Hinge- CH2-CH3... D1 and D2 are genetically linked through a 10 amino acid (G4S) x 2 linker, as are D2, D3 and D4 resulting in a contiguous ~150 kDa heavy chain monomer peptide."; pg 14 para 2 - "the application provides pharmaceutical compositions including the multi-specific antibody monomers, the multi-specific antibodies"), wherein the first monomer comprises optionally a first binding domain (D1) linked to the N-terminus, a fourth binding domain (D4) linked to the C-terminus, or both (pg 13 para 2 - "D1 and D2 are genetically linked through a 10 amino acid (G4S) x 2 linker, as are D2, D3 and D4 resulting in a contiguous ~150 kDa heavy chain monomer peptide."; pg 12 para 1 - "The tetra-specific molecule binding domains are arrayed such that the binding domain placement proceeds from the N-terminus to D1, scFv VLVH, followed by D2, scFv VLVH, D3 which is in the Fab position in this class of tetra-specific proteins, followed by the human IgG1 Fc and an scFv, VHVL, in D4."), a second monomer, comprising, from the N-terminus to the C-terminus, a second binding monomer, a CL domain, a second hinge, a second CH2 domain, and a second CH3 domain (pg 12 para 7 - "the disclosure provides an engineered antibody with 4 different binding domains or a "tetra-specific antibody"; pg 2 para 3 - "tetra-specific antibody monomers, antibodies containing tetra-specific monomers"; pg 14 para 2 - "the application provides pharmaceutical compositions including the multi-specific antibody monomers"; pg 13 para 2 - "tetra-specific protein...is composed of an anti-human CD19 21D4 scFv, anti-human CD3 284A10 scFv, anti-human CD137 (Fab) and anti-human PD-L1 clone PL221G5 scFv occupying positions D1, D2, D3 and D4, respectively ... VL, regardless of the V-region orientation (LH or HL). The remaining position in the tetra-specific protein, Domain 3 (D3), consists of an IgG1 heavy chain, VH-CH1-Hinge- CH2-CH3, and its corresponding light chain, VL-CL, which can be either a kappa or lambda chain."), wherein the first binding monomer and a second binding monomer are configured to form a dimer (pg 4 para 7 - "the multi-specific antibody includes a dimer of a tetra-specific antibody monomer therefor providing a tetra-specific antibody."), 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 (pg 13 para 2 - "When co-transfected with the appropriate light chain, the final symmetric tetra-specific peptide can be purified through the IgG1 Fc (Protein A/Protein G) and assayed to assess functional activity."; pg 10 para 4 - "Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')2 antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them."), and wherein the multi-specific antibody-like protein is at least bi-specific (pg 2 para 3 - "tetra-specific antibody monomers, antibodies containing tetra-specific monomers"; pg 4 para 7 - "the multi-specific antibody includes a dimer of a tetra-specific antibody monomer therefor providing a tetra-specific antibody."; pg 8 para 3 - "the antibody may be...bispecific").

Systimmune further discloses a complementary determining region (CDR) having an affinity to CEA (pg 8 para 3 - "The VH and VL regions can be further subdivided into domains of hypervariable complementarity determining regions (CDR)"; pg 12 para 7 - "the disclosure provides an engineered antibody with 4 different binding domains or a "tetra-specific antibody"...a second binding domain is specific for a tumor associated antigen including but not limited to...CEA"; pg 3 para 2 - "the scFv domain, the second scFv domain, the Fab domain, and the third scFv domain each independently has a binding specificity against tumor specific antigens including, but not limited to...CEA"; Claim 2), and a multi-specific antibody-like protein having a binding affinity to CEA (pg 12 para 7 - "the disclosure provides an engineered antibody with 4 different binding domains or a "tetra-specific antibody"...a second binding domain is specific for a tumor associated antigen including but not limited to...CEA"; pg 3 para 2 - "the scFv domain, the second scFv domain, the Fab domain, and the third scFv domain each independently has a binding specificity against tumor specific antigens including, but not limited to...CEA"; Claim 2).

Systimmune additionally discloses a complementary determining region (CDR) having a binding affinity to CD3 (pg 8 para 3 - "The VH and VL regions can be further subdivided into domains of hypervariable complementarity determining regions (CDR)"; pg 12 para 7 - "One binding domain is specific for CD3") and a multi-specific antibody-like protein having a binding affinity to CD3 (pg 13 para 1 - "these targeted tetra-specific proteins carry...an anti-human CD3 binding domain"; pg 3 para 2 - "The scFv specific to CD3 component"; pg 12 para 7 - "One binding domain is specific for CD3").

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the groups.

Therefore, Group I+ inventions lack unity under PCT Rule 13 because they do not share the same or corresponding special technical feature.