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(54) Title: VARIANT NUCLEIC ACID LIBRARIES FOR MAST CELLS

(57) Abstract: Provided herein are antibodies and antibody fragments relating to SIGLEC-8 and CD117. Provided herein are methods and compositions relating to SIGLEC-8 and/or CD117 libraries having nucleic acids encoding for a scaffold comprising a SIGLEC-8 and/or CD117 domain. SIGLEC-8 and/or CD117 libraries described herein encode for immunoglobulins such as antibodies.



WO 2024/178392 A2

VARIANT NUCLEIC ACID LIBRARIES FOR MAST CELLS

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/486,754 filed on February 24, 2023, which is incorporated herein by reference in its entirety.

BACKGROUND

[0002] Mast cells, also known as mastocytes or labrocytes, are connective tissue cells that are a part of the immune system. Mast cells are involved in wound healing, angiogenesis, immune tolerance, defense against pathogens, and vascular permeability. Salic acid-binding Ig-like lectin 8 (SIGLEC-8) is a protein expressed by mast cells involved in asthma and allergies. Cluster of differentiation 117 (CD117), also known as tyrosine-protein kinase KIT and mast/stem cell growth factor receptor (SCFR), is a receptor tyrosine kinase that can be used in the diagnosis of mast cell and other tumors.

[0003] Both SIGLEC-8 and CD117 play an important role in various diseases and conditions related to mast cells including cancer and immune diseases (e.g., asthma, allergies), and therapeutic antibodies targeting mast cells, SIGLEC-8 and/or CD117 have clinical significance. Antibodies possess the capability to bind with high specificity and affinity to biological targets. However, the design of therapeutic antibodies is challenging due to balancing of immunological effects with efficacy. Thus, there is a need to develop compositions and methods for generation of antibodies for use in therapeutics.

INCORPORATION BY REFERENCE

[0004] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF SUMMARY

[0005] Provided herein are antibodies and antibody fragments comprising an amino acid sequence at least about 90% identical to that set forth in any one of SEQ ID NOs: 1-450. In some embodiments, the antibody or antibody fragment comprises an amino acid sequence at least about 95% identical to that set forth in any one of SEQ ID NOs: 1-450. In some embodiments, the antibody or antibody fragment comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 1-450. In some embodiments, the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized

antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 75 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 50 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 25 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 10 nM.

[0006] Provided herein are antibodies or antibody fragments that binds SIGLEC, comprising an immunoglobulin heavy chain comprising an amino acid sequence at least about 90% identical to that set forth in any one of SEQ ID NOs: 151-200. In some embodiments, the immunoglobulin heavy chain comprises an amino acid sequence at least about 95% identical to that set forth in any one of SEQ ID NOs: 151-200. In some embodiments, the immunoglobulin heavy chain comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 151-200. In some embodiments, the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some embodiments, the antibody or antibody fragment thereof is chimeric or humanized. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 75 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 50 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 25 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 10 nM.

[0007] Provided herein are antibodies or antibody fragments that binds SIGLEC, comprising an immunoglobulin light chain comprising an amino acid sequence at least about 90% identical to that set forth in any one of SEQ ID NOs: 351-400. In some embodiments, the immunoglobulin light chain comprises an amino acid sequence at least about 95% identical to that set forth in any one of SEQ ID NOs: 351-400. In some embodiments, the immunoglobulin light chain comprises an amino

acid sequence as set forth in any one of SEQ ID NOs: 351-400. In some embodiments, the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some embodiments, the antibody or antibody fragment thereof is chimeric or humanized. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 75 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 50 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 25 nM. In some embodiments, the antibody or antibody fragment binds to SIGLEC with a K_D of less than 10 nM.

[0008] Provided herein are antibodies and antibody fragments comprising an amino acid sequence at least about 90% identical to that set forth in any one of SEQ ID NOs: 451-639. In some embodiments, the antibody or antibody fragment comprises an amino acid sequence at least about 95% identical to that set forth in any one of SEQ ID NOs: 451-639. In some embodiments, the antibody or antibody fragment comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 451-639. In some embodiments, the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 75 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 50 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 25 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 10 nM.

[0009] Provided herein are antibodies and antibody fragments that binds CD117, comprising an immunoglobulin heavy chain comprising an amino acid sequence at least about 90% identical to that set forth in any one of SEQ ID NOs: 514-534. In some embodiments, the immunoglobulin heavy chain comprises an amino acid sequence at least about 95% identical to that set forth in any

one of SEQ ID NOs: 514-534. In some embodiments, the immunoglobulin heavy chain comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 514-534. In some embodiments, the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some embodiments, the antibody or antibody fragment thereof is chimeric or humanized. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 75 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 50 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 25 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 10 nM.

[0010] Provided herein are antibodies and antibody fragments that binds CD117, comprising an immunoglobulin light chain comprising an amino acid sequence at least about 90% identical to that set forth in any one of SEQ ID NOs: 598-618. In some embodiments, the immunoglobulin light chain comprises an amino acid sequence at least about 95% identical to that set forth in any one of SEQ ID NOs: 598-618. In some embodiments, the immunoglobulin light chain comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 598-618. In some embodiments, the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some embodiments, the antibody or antibody fragment thereof is chimeric or humanized. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 75 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 50 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 25 nM. In some embodiments, the antibody or antibody fragment binds to CD117 with a K_D of less than 10 nM.

[0011] Provided herein are methods of treating a disease or disorder comprising administering any one of the antibodies or antibody fragments as disclosed herein. In some embodiments, the disease is a mast cell disease. In some embodiments, the disease is cancer. In some embodiments, the disease is an immune disease. In some embodiments, the disease is allergies. In some embodiments, the disease is asthma.

[0012] Certain nonlimiting embodiments are provided below.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013] **Figure 1** presents a diagram of steps demonstrating an exemplary process workflow for gene synthesis as disclosed herein.

[0014] **Figure 2** illustrates an example of a computer system.

[0015] **Figure 3** is a block diagram illustrating an architecture of a computer system.

[0016] **Figure 4** is a diagram demonstrating a network configured to incorporate a plurality of computer systems, a plurality of cell phones and personal data assistants, and Network Attached Storage (NAS).

[0017] **Figure 5** is a block diagram of a multiprocessor computer system using a shared virtual address memory space.

[0018] **Figure 6A** depicts SIGLEC-8 cassette pTT5-SIGLEC-8 P2A mVenus. **Figure 6B** depicts SIGLEC-8 cassette pTT5-SIGLEC-8 mVenus. **Figure 6C** depicts a cartoon of both SIGLEC-8 and CD117 localization. **Figure 6D** shows fluorescence of cassette pTT5-SIGLEC-8 mVenus. **Figure 6E** shows fluorescence of cassette pTT5-SIGLEC-8 P2A mVenus. **Figure 6F** shows the results of SIGLEC-8 titrations. **Figure 6G** shows the transient expression of increasing amounts of SIGLEC-8 during titration.

[0019] **Figure 7A** depicts a panning strategy for SIGLEC-8 antibodies. **Figure 7B** shows phage recovery after each panning round.

[0020] **Figure 8A** depicts the results of a clonal ELISA screen after round 3 panning. **Figure 8B** depicts the results of a clonal ELISA screen after round 4 panning. **Figure 8C** summarizes the results of clonal ELISA screening across panning rounds 3 and 4.

[0021] **Figure 9A** depicts expression yield of SIGLEC-8 antibodies. **Figure 9B** depicts a gel showing relative expression of purified SIGLEC-8 antibodies. **Figure 9C** depicts an additional gel showing relative expression of purified SIGLEC-8 antibodies.

[0022] **Figure 10A** depicts Carterra kinetics data for each SIGLEC-8 clone. **Figure 10B** summarizes the Cartera kinetics data.

[0023] **Figures 11A-11O** show titration assay data for SIGLEC-8 antibodies SIGLEC-8-48 (**Figure 11A**), SIGLEC-8-49 (**Figure 11B**), SIGLEC-8-50 (**Figure 11C**), SIGLEC-8-51 (**Figure 11D**), SIGLEC-8-52 (**Figure 11E**), SIGLEC-8-53 (**Figure 11F**), SIGLEC-8-54 (**Figure 11G**), SIGLEC-8-55 (**Figure 11H**), SIGLEC-8-56 (**Figure 11I**), SIGLEC-8-57 (**Figure 11J**), SIGLEC-8-58 (**Figure 11K**), SIGLEC-8-59 (**Figure 11L**), SIGLEC-8-60 (**Figure 11M**), and SIGLEC-8-61 (**Figure 11N**). **Figure 11O** depicts a summary of K_D vs EC_{50} regression data for the SIGLEC-8 antibodies.

[0024] **Figure 12A** depicts SIGLEC genes which are related to SIGLEC-8. **Figure 12B** depicts a comparison of different SIGLEC sequences (SEQ ID NOs: 644-649).

[0025] **Figure 13A** shows kinetics data for sub-nanomolar clones. **Figure 13B** summarizes the kinetics data for sub-nanomolar clones. **Figure 13C** depicts cross-reactivity profiles of SIGLEC-8 mAbs with closely related SIGLEC proteins.

[0026] **Figure 14A** depicts binning leads for SIGLEC-8. **Figure 14B** shows the relatedness of various SIGLEC-8 antibodies.

[0027] **Figure 15A** depicts results from investigating immobilized lirentelimab, an antibody known to bind SIGLEC-8. **Figure 15B** depicts immobilized SIGLEC-8-40 antibody results.

[0028] **Figure 16A** depicts CD117 cassette pTT5-CD117 P2A mVenus. **Figure 16B** depicts CD117 cassette pTT5-CD117 mVenus. **Figure 16C** shows fluorescence of cassette pTT5- CD117 mVenus. **Figure 16D** shows fluorescence of cassette pTT5- CD117 P2A mVenus.

[0029] **Figures 17A-17E** show the results of transient expression of CD117 antibodies CD117-1 (**Figure 17A**), CD117-2 (**Figure 17B**), CD117-3 (**Figure 17C**), and CD117-4 (**Figure 17D**). **Figure 17E** shows the specific binding to CD117 transient cells by FACS.

[0030] **Figure 18A** depicts a panning strategy for CD117 antibodies. **Figure 18B** shows phage recovery after each panning round.

[0031] **Figures 19A-19B** show cluster enrichment in panning round 4 (**Figure 19A**) and panning round 5 (**Figure 19B**). **Figures 19C-19E** show CDR3 enrichment between panning rounds 2 and 3 (**Figure 19C**), between panning rounds 3 and 4 (**Figure 19D**), and between panning rounds 4 and 5 (**Figure 19E**).

[0032] **Figure 20A** shows binding of transient cell lines by FACS. **Figure 20B** shows additional binding of transient cell lines by FACS. **Figure 20C** summarizes top CD117 antibodies identified through FACS.

[0033] **Figures 21A-21X** show specific binding by FACS of antibodies CD117-2 (**Figure 21A**), CD117-9 (**Figure 21B**), CD117-1 (**Figure 21C**), CD117-7 (**Figure 21D**), CD117-3 (**Figure 21E**), CD117-5 (**Figure 21F**), CD117-21 (**Figure 21G**), CD117-10 (**Figure 21H**), CD117-17

(**Figure 21I**), CD117-15 (**Figure 21J**), CD117-13 (**Figure 21K**), CD117-11 (**Figure 21L**), CD117-18 (**Figure 21M**), CD117-20 (**Figure 21N**), CD117-19 (**Figure 21O**), CD117-14 (**Figure 21P**), CD117-12 (**Figure 21Q**), CD117-4 (**Figure 21R**), CD117-16 (**Figure 21S**), CD117-8 (**Figure 21T**), CD117-6 (**Figure 21U**), control 1 (**Figure 21V**), control 2 (**Figure 21W**), and control 4 (**Figure 21X**). Outlined graphs indicate functional screen leads.

[0034] **Figures 22A-22D** show the EC50 results for CD117-2 (**Figure 22A**), CD117-14 (**Figure 22B**), CD117-6 (**Figure 22C**), and CD117-9 (**Figure 22D**). **Figure 22E** summarizes the EC50 top results.

[0035] **Figure 23** shows a titration curve for Stem Cell Factor (also known as SCF or c-KIT ligand).

[0036] **Figure 24A** shows titration of control antibodies against the standard 585 pM concentration of SCF. **Figure 24B** shows the results of a control in which CD117 and SIGLEC antibodies were tested for effects on EGF signaling.

[0037] **Figure 25A** shows ERK activation, highlighting top hits. **Figure 25B** shows a graph of concentration screens for top hits. **Figure 25C** shows MFI binding screen results for top hits.

[0038] **Figure 26A** shows the control titrations for ERK activation. **Figure 26B** shows the control titrations for serum factor response (SRF) signal.

[0039] **Figures 27A-27C** show the SFR signal results for top antagonists CD117-6 (**Figure 27A**), CD117-14 (**Figure 27B**), and CD117-7 (**Figure 27C**). **Figure 27D** summarizes the IC50 data of the top antagonists.

[0040] **Figures 28A-28H** show additional titrations for CD117-131 (**Figure 28A**), CD117-10 (**Figure 28B**), CD117-79 (**Figure 28C**), CD117-125 (**Figure 28D**), CD117-11 (**Figure 28E**), CD117-17 (**Figure 28F**), CD117-18 (**Figure 28G**), and CD117-150 (**Figure 28H**).

[0041] **Figure 29A-29B** show binding kinetics of anti-CD117 antibodies for human, cynomolgus monkey, and mouse CD117.

[0042] **Figure 30** shows the frequency of mCD45+ cells in live cells (A) and the number of mCD45+ cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0043] **Figure 31** shows the frequency of mCD3+ cells in mCD45+ (A) and the number of mCD3+ cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0044] **Figure 32** shows the frequency of mCD3- cells in mCD45+ (A) and the number of mCD3- cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0045] **Figure 33** shows the frequency of NK cells in mCD3- (A) and the number of NK cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0046] **Figure 34** shows the frequency of Siglec-F+ cells in mCD3- (A) and the number of Siglec-F+ cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0047] **Figure 35** shows serum IgE (ng/mL) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0048] **Figure 36** shows the frequency of mCD19+ cells in mCD3- (A) and the number of mCD19+ cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0049] **Figure 37** shows the frequency of mCD11b+ cells in CD3- cells (A) and the number of mCD11b+ cells (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0050] **Figure 38** shows the frequency of macrophage in mCD11b+ cells (A) and the number of macrophage mCD11b+ cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0051] **Figure 39** shows the frequency of mCD11c+ cells in mCD45+ cells (A) and the number of mCD11c+ cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

[0052] **Figure 40** shows the frequency of macrophages in mCD11c+ cells (A) and the number of macrophage mCD11c+ cells per milliliter BALF (B) in mice administered SIGLEC-8 antibodies or controls. The groups listed from top to bottom in the legend are shown in the bar graphs from left to right, respectively.

DETAILED DESCRIPTION

[0053] The present disclosure employs, unless otherwise indicated, conventional molecular biology techniques, which are within the skill of the art. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of ordinary skill in the art.

[0054] Overview

[0055] Disclosed herein are antibodies or antigen-binding fragments thereof that bind an antigen of interest (e.g., salic acid-binding Ig-like lectin 8 (SIGLEC-8) and cluster of differentiation 117 (CD117). The antibodies or antigen-binding fragments thereof as described herein can be used to treat diseases or conditions described herein. In some cases, the antibodies or antigen-binding fragments thereof as described herein can be used to treat diseases or conditions associated with mast cells or eosinophils.

[0056] Mast cells (MCs) and eosinophils are important cells of the immune system. MCs may be associated with allergic inflammation, during which MC activation may play a role in driving type-2 inflammatory diseases, such as eosinophilic asthma, atopic dermatitis, and eosinophilic gastrointestinal diseases. They may also be implicated in non-allergic diseases, such as inflammatory bowel diseases, irritable bowel syndrome, functional dyspepsia, idiopathic pulmonary fibrosis, and chronic obstructive pulmonary disease. In these diseases, mast cells and eosinophils may be activated by inflammatory mediators, such as cytokines, toll-like receptor ligands, and neuropeptides. Upon activation, mast cells and eosinophils release mediators that can attract or activate other immune cells and mediate acute and chronic inflammatory responses, such as vasodilation, vasculitis, cardiovascular diseases, angiogenesis plasma extravasation, smooth muscle contraction, stimulation of sensory nerves, tissue eosinophilia, epithelial barrier destruction as well as cancer (solid and hematologic tumors).

[0057] MCs are distributed throughout all normal human tissues, whereas eosinophils are generally present in gastrointestinal tract, secondary lymphoid tissues, and adipose tissue, thymus, mammary gland, and uterus. Despite having distinct myeloid progenitors, MCs and eosinophils present common surface markers such as salic acid-binding Ig-like lectin 8 (SIGLEC-8) and cluster of differentiation 117 (CD117), also known as tyrosine-protein kinase KIT and mast/stem cell growth factor receptor (SCFR), is a receptor tyrosine kinase. The present application demonstrates that modulation of Siglec-8 and CD117 function using antibodies or antigen-binding fragments thereof as targeted therapies allow for treatment various immune-related conditions, including cancer. Thus, the current application solves a clear unmet medical need associated with disease related to mast cell and eosinophil biology and their respective surface markers.

[0058] Definitions

[0059] Throughout this disclosure, various embodiments are presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of any embodiments. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range to the tenth of the unit of the lower limit unless the context clearly dictates otherwise. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual values within that range, for example, 1.1, 2, 2.3, 5, and 5.9. This applies regardless of the breadth of the range. The upper and lower limits of these intervening ranges may independently be included in the smaller ranges, and are also encompassed within the disclosure, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the disclosure, unless the context clearly dictates otherwise.

[0060] The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting of any embodiment. As used herein, the singular forms “a,” “an” and “the” are intended to include the plural forms as well, unless the context clearly indicates otherwise. It will be further understood that the terms “comprises” and/or “comprising,” when used in this specification, specify the presence of stated features, integers, steps, operations, elements, and/or components, but do not preclude the presence or addition of one or more other features, integers, steps, operations, elements, components, and/or groups thereof. As used herein, the term “and/or” includes any and all combinations of one or more of the associated listed items.

[0061] Unless specifically stated or obvious from context, as used herein, the term “about” in reference to a number or range of numbers is understood to mean the stated number and numbers +/- 10% thereof, or 10% below the lower listed limit and 10% above the higher listed limit for the values listed for a range.

[0062] Unless specifically stated, as used herein, the term “nucleic acid” encompasses double- or triple-stranded nucleic acids, as well as single-stranded molecules. In double- or triple-stranded nucleic acids, the nucleic acid strands need not be coextensive (i.e., a double-stranded nucleic acid need not be double-stranded along the entire length of both strands). Nucleic acid sequences, when provided, are listed in the 5' to 3' direction, unless stated otherwise. Methods described herein provide for the generation of isolated nucleic acids. Methods described herein additionally provide for the generation of isolated and purified nucleic acids. A “nucleic acid” as referred to herein can

comprise at least 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, or more bases in length. Moreover, provided herein are methods for the synthesis of any number of polypeptide-segments encoding nucleotide sequences, including sequences encoding non-ribosomal peptides (NRPs), sequences encoding non-ribosomal peptide-synthetase (NRPS) modules and synthetic variants, polypeptide segments of other modular proteins, such as antibodies, polypeptide segments from other protein families, including non-coding DNA or RNA, such as regulatory sequences e.g. promoters, transcription factors, enhancers, siRNA, shRNA, RNAi, miRNA, small nucleolar RNA derived from microRNA, or any functional or structural DNA or RNA unit of interest. The following are non-limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, intergenic DNA, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), small nucleolar RNA, ribozymes, complementary DNA (cDNA), which is a DNA representation of mRNA, usually obtained by reverse transcription of messenger RNA (mRNA) or by amplification; DNA molecules produced synthetically or by amplification, genomic DNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. cDNA encoding for a gene or gene fragment referred herein may comprise at least one region encoding for exon sequences without an intervening intron sequence in the genomic equivalent sequence.

[0063] Antibody Libraries

[0064] Provided herein are methods, compositions, and systems for generation of antibodies. Methods, compositions, and systems described herein for the optimization of antibodies comprise a ratio-variant approach that mirror the natural diversity of antibody sequences. In some instances, libraries of optimized antibodies comprise variant antibody sequences. In some instances, the variant antibody sequences are designed comprising variant CDR regions. In some instances, the variant antibody sequences comprising variant CDR regions are generated by shuffling the natural CDR sequences in a llama, humanized, or chimeric framework. In some instances, such libraries are synthesized, cloned into expression vectors, and translation products (antibodies) evaluated for activity. In some instances, fragments of sequences are synthesized and subsequently assembled. In some instances, expression vectors are used to display and enrich desired antibodies, such as phage display. In some instances, the phage vector is a Fab phagemid vector. Selection pressures used during enrichment in some instances includes binding affinity, toxicity, immunological tolerance, stability, or other factor. Such expression vectors allow antibodies with specific properties to be

selected (“panning”), and subsequent propagation or amplification of such sequences enriches the library with these sequences. Panning rounds can be repeated any number of times, such as 1, 2, 3, 4, 5, 6, 7, or more than 7 rounds. In some instances, each round of panning involves a number of washes. In some instances, each round of panning involves at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 washes.

[0065] Described herein are methods and systems of in-silico library design. Libraries as described herein, in some instances, are designed based on a database comprising a variety of antibody sequences. In some instances, the database comprises a plurality of variant antibody sequences against various targets. In some instances, the database comprises at least 100, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 antibody sequences. An exemplary database is an iCAN database. In some instances, the database comprises naïve and memory B-cell receptor sequences. In some instances, the naïve and memory B-cell receptor sequences are human, mouse, or primate sequences. In some instances, the naïve and memory B-cell receptor sequences are human sequences. In some instances, the database is analyzed for position specific variation. In some instances, antibodies described herein comprise position specific variations in CDR regions. In some instances, the CDR regions comprise multiple sites for variation.

[0066] Described herein are libraries comprising variation in a CDR region. In some instances, the CDR is CDR1, CDR2, or CDR3 of a variable heavy chain. In some instances, the CDR is CDR1, CDR2, or CDR3 of a variable light chain. In some instances, the libraries comprise multiple variants encoding for CDR1, CDR2, or CDR3. In some instances, the libraries as described herein encode for at least 50, 100, 200, 300, 400, 500, 1000, 1200, 1500, 1700, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 CDR1 sequences. In some instances, the libraries as described herein encode for at least 50, 100, 200, 300, 400, 500, 1000, 1200, 1500, 1700, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 CDR2 sequences. In some instances, the libraries as described herein encode for at least 50, 100, 200, 300, 400, 500, 1000, 1200, 1500, 1700, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 CDR3 sequences. In-silico antibodies libraries are in some instances synthesized, assembled, and enriched for desired sequences.

[0067] Following synthesis of CDR1 variants, CDR2 variants, and CDR3 variants, in some instances, the CDR1 variants, the CDR2 variants, and the CDR3 variants are shuffled to generate a diverse library. In some instances, the diversity of the libraries generated by methods described herein have a theoretical diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences. In some instances, the library has a final library

diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences.

[0068] The germline sequences corresponding to a variant sequence may also be modified to generate sequences in a library. For example, sequences generated by methods described herein comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 mutations from the germline sequence. In some instances, sequences generated comprise no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or no more than 18 mutations from the germline sequence. In some instances, sequences generated comprise about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or about 18 mutations relative to the germline sequence.

[0069] *Antibody Libraries*

[0070] Provided herein are libraries generated from methods described herein. Antibodies described herein result in improved functional activity, structural stability, expression, specificity, or a combination thereof. In some instances, the antibody is a single domain antibody. In some instances, the single domain antibody comprises one heavy chain variable domain. In some instances, the single domain antibody is a VHH antibody.

[0071] As used herein, the term antibody will be understood to include proteins having the characteristic two-armed, Y-shape of a typical antibody molecule as well as one or more fragments of an antibody that retain the ability to specifically bind to an antigen. Exemplary antibodies include, but are not limited to, a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv) (including fragments in which the VL and VH are joined using recombinant methods by a synthetic or natural linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules, including single chain Fab and scFab), a single chain antibody, a Fab fragment (including monovalent fragments comprising the VL, VH, CL, and CH1 domains), a F(ab')₂ fragment (including bivalent fragments comprising two Fab fragments linked by a disulfide bridge at the hinge region), a Fd fragment (including fragments comprising the VH and CH1 fragment), a Fv fragment (including fragments comprising the VL and VH domains of a single arm of an antibody), a single-domain antibody (dAb or sdAb) (including fragments comprising a VH domain), an isolated complementarity determining region (CDR), a diabody (including fragments comprising bivalent dimers such as two VL and VH domains bound to each other and recognizing two different antigens), a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some instances, the libraries disclosed herein comprise nucleic acids encoding

for an antibody, wherein the antibody is a Fv antibody, including Fv antibodies comprised of the minimum antibody fragment which contains a complete antigen-recognition and antigen-binding site. In some embodiments, the Fv antibody consists of a dimer of one heavy chain and one light chain variable domain in tight, non-covalent association, and the three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. In some embodiments, the six hypervariable regions confer antigen-binding specificity to the antibody. In some embodiments, a single variable domain (or half of an Fv comprising only three hypervariable regions specific for an antigen, including single domain antibodies isolated from camelid animals comprising one heavy chain variable domain such as VHH antibodies or nanobodies) has the ability to recognize and bind antigen. In some instances, the libraries disclosed herein comprise nucleic acids encoding for an antibody, wherein the antibody is a single-chain Fv or scFv, including antibody fragments comprising a VH, a VL, or both a VH and VL domain, wherein both domains are present in a single polypeptide chain. In some embodiments, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains allowing the scFv to form the desired structure for antigen binding. In some instances, a scFv is linked to the Fc fragment or a VHH is linked to the Fc fragment (including minibodies). In some instances, the antibody comprises immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, e.g., molecules that contain an antigen binding site. Immunoglobulin molecules are of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG 1, IgG 2, IgG 3, IgG 4, IgA 1 and IgA 2) or subclass.

[0072] In some embodiments, libraries comprise immunoglobulins that are adapted to the species of an intended therapeutic target. Generally, these methods include “mammalization” and comprises methods for transferring donor antigen-binding information to a less immunogenic mammal antibody acceptor to generate useful therapeutic treatments. In some instances, the mammal is mouse, rat, equine, sheep, cow, primate (e.g., chimpanzee, baboon, gorilla, orangutan, monkey), dog, cat, pig, donkey, rabbit, and human. In some instances, provided herein are libraries and methods for felinization and caninization of antibodies.

[0073] “Humanized” forms of non-human antibodies can be chimeric antibodies that contain minimal sequence derived from the non-human antibody. A humanized antibody is generally a human antibody (recipient antibody) in which residues from one or more CDRs are replaced by residues from one or more CDRs of a non-human antibody (donor antibody). The donor antibody can be any suitable non-human antibody, such as a mouse, rat, rabbit, chicken, or non-human primate antibody having a desired specificity, affinity, or biological effect. In some instances, selected framework region residues of the recipient antibody are replaced by the corresponding

framework region residues from the donor antibody. Humanized antibodies may also comprise residues that are not found in either the recipient antibody or the donor antibody. In some instances, these modifications are made to further refine antibody performance.

[0074] “Caninization” can comprise a method for transferring non-canine antigen-binding information from a donor antibody to a less immunogenic canine antibody acceptor to generate treatments useful as therapeutics in dogs. In some instances, caninized forms of non-canine antibodies provided herein are chimeric antibodies that contain minimal sequence derived from non-canine antibodies. In some instances, caninized antibodies are canine antibody sequences (“acceptor” or “recipient” antibody) in which hypervariable region residues of the recipient are replaced by hypervariable region residues from a non-canine species (“donor” antibody) such as mouse, rat, rabbit, cat, dogs, goat, chicken, bovine, horse, llama, camel, dromedaries, sharks, non-human primates, human, humanized, recombinant sequence, or an engineered sequence having the desired properties. In some instances, framework region (FR) residues of the canine antibody are replaced by corresponding non-canine FR residues. In some instances, caninized antibodies include residues that are not found in the recipient antibody or in the donor antibody. In some instances, these modifications are made to further refine antibody performance. The caninized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc) of a canine antibody.

[0075] “Felinization” can comprise a method for transferring non-feline antigen-binding information from a donor antibody to a less immunogenic feline antibody acceptor to generate treatments useful as therapeutics in cats. In some instances, felinized forms of non-feline antibodies provided herein are chimeric antibodies that contain minimal sequence derived from non-feline antibodies. In some instances, felinized antibodies are feline antibody sequences (“acceptor” or “recipient” antibody) in which hypervariable region residues of the recipient are replaced by hypervariable region residues from a non-feline species (“donor” antibody) such as mouse, rat, rabbit, cat, dogs, goat, chicken, bovine, horse, llama, camel, dromedaries, sharks, non-human primates, human, humanized, recombinant sequence, or an engineered sequence having the desired properties. In some instances, framework region (FR) residues of the feline antibody are replaced by corresponding non-feline FR residues. In some instances, felinized antibodies include residues that are not found in the recipient antibody or in the donor antibody. In some instances, these modifications are made to further refine antibody performance. The felinized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc) of a felinize antibody.

[0076] Methods as described herein may be used for generation of libraries encoding a non-immunoglobulin. In some instances, the libraries comprise antibody mimetics. Exemplary antibody mimetics include, but are not limited to, anticalins, affilins, affibody molecules, affimers, affitins,

alphabodies, avimers, atrimers, DARPins, fynomers, Kunitz domain-based proteins, monobodies, anticalins, knottins, armadillo repeat protein-based proteins, and bicyclic peptides.

[0077] Libraries described herein comprising nucleic acids encoding for an antibody comprise variations in at least one region of the antibody. Exemplary regions of the antibody for variation include, but are not limited to, a complementarity-determining region (CDR), a variable domain, or a constant domain. In some instances, the CDR is CDR1, CDR2, or CDR3. In some instances, the CDR is a heavy domain including, but not limited to, CDRH1, CDRH2, and CDRH3. In some instances, the CDR is a light domain including, but not limited to, CDRL1, CDRL2, and CDRL3. In some instances, the variable domain is variable domain, light chain (VL) or variable domain, heavy chain (VH). In some instances, the CDR1, CDR2, or CDR3 is of a variable domain, light chain (VL). CDR1, CDR2, or CDR3 of a variable domain, light chain (VL) can be referred to as CDRL1, CDRL2, or CDRL3, respectively. CDR1, CDR2, or CDR3 of a variable domain, heavy chain (VH) can be referred to as CDRH1, CDRH2, or CDRH3, respectively. In some instances, the VL domain comprises kappa or lambda chains. In some instances, the constant domain is constant domain, light chain (CL) or constant domain, heavy chain (CH).

[0078] Provided herein are libraries comprising nucleic acids encoding for an antibody comprising variation in at least one region of the antibody, wherein the region is the CDR region. In some instances, the antibody is a single domain antibody comprising one heavy chain variable domain such as a VHH antibody. In some instances, the VHH antibody comprises variation in one or more CDR regions. In some instances, the VHH libraries described herein comprise at least or about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2400, 2600, 2800, 3000, or more than 3000 sequences of a CDR1, CDR2, or CDR3. For example, the libraries comprise at least 2000 sequences of a CDR1, at least 1200 sequences for CDR2, and at least 1600 sequences for CDR3. In some instances, each sequence is non-identical.

[0079] Libraries as described herein may comprise varying lengths of a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, or combinations thereof of amino acids when translated. In some instances, the length of the CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, or combinations thereof of amino acids when translated is at least or about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more than 30 amino acids.

[0080] Libraries comprising nucleic acids encoding for antibodies having variant CDR sequences as described herein comprise various lengths of amino acids when translated. In some instances, the length of each of the amino acid fragments or average length of the amino acid synthesized may be at least or about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, or more than 150 amino acids. In some

instances, the length of the amino acid is about 15 to 150, 20 to 145, 25 to 140, 30 to 135, 35 to 130, 40 to 125, 45 to 120, 50 to 115, 55 to 110, 60 to 110, 65 to 105, 70 to 100, or 75 to 95 amino acids. In some instances, the length of the amino acid is about 22 amino acids to about 75 amino acids. In some instances, the antibodies comprise at least or about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, or more than 5000 amino acids. In some instances, the library is a VHH library. In some instances, the library is an antibody library.

[0081] Libraries as described herein encoding for a VHH antibody comprise variant CDR sequences that are shuffled to generate a library with a theoretical diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences. In some instances, the library has a final library diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences.

[0082] Libraries as described herein encoding for an antibody or immunoglobulin comprise variant CDR sequences that are shuffled to generate a library with a theoretical diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences. In some instances, the library has a final library diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences.

[0083] Methods described herein provide for synthesis of libraries comprising nucleic acids encoding an antibody or immunoglobulin, wherein each nucleic acid encodes for a predetermined variant of at least one predetermined reference nucleic acid sequence. In some cases, the predetermined reference sequence is a nucleic acid sequence encoding for a protein, and the variant library comprises sequences encoding for variation of at least a single codon such that a plurality of different variants of a single residue in the subsequent protein encoded by the synthesized nucleic acid are generated by standard translation processes. In some instances, the antibody library comprises varied nucleic acids collectively encoding variations at multiple positions. In some instances, the variant library comprises sequences encoding for variation of at least a single codon of a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons of a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons of framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). An exemplary number of codons for variation include, but are not limited to, at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons.

[0084] In some instances, the at least one region of the antibody for variation is from heavy chain V-gene family, heavy chain D-gene family, heavy chain J-gene family, light chain V-gene family, or light chain J-gene family. In some instances, the light chain V-gene family comprises immunoglobulin kappa (IGK) gene or immunoglobulin lambda (IGL). Exemplary regions of the antibody for variation include, but are not limited to, IGHV1-18, IGHV1-69, IGHV1-8, IGHV3-21, IGHV3-23, IGHV3-30/33rn, IGHV3-28, IGHV1-69, IGHV3-74, IGHV4-39, IGHV4-59/61, IGKV1-39, IGKV1-9, IGKV2-28, IGKV3-11, IGKV3-15, IGKV3-20, IGKV4-1, IGLV1-51, IGLV2-14, IGLV1-40, and IGLV3-1. In some instances, the gene is IGHV1-69, IGHV3-30, IGHV3-23, IGHV3, IGHV1-46, IGHV3-7, IGHV1, or IGHV1-8. In some instances, the gene is IGHV1-69 and IGHV3-30. In some instances, the region of the antibody for variation is IGHJ3, IGHJ6, IGHJ, IGHJ4, IGHJ5, IGHJ2, or IGH1. In some instances, the region of the antibody for variation is IGHJ3, IGHJ6, IGHJ, or IGHJ4. In some instances, the at least one region of the antibody for variation is IGHV1-69, IGHV3-23, IGKV3-20, IGKV1-39 or combinations thereof. In some instances, the at least one region of the antibody for variation is IGHV1-69 or IGHV3-23. In some instances, the at least one region of the antibody for variation is IGKV3-20 or IGKV1-39. In some instances, the at least one region of the antibody for variation is IGHV1-69 and IGKV3-20. In some instances, the at least one region of the antibody for variation is IGHV1-69 and IGKV1-39. In some instances, the at least one region of the antibody for variation is IGHV3-23 and IGKV3-20. In some instances, the at least one region of the antibody for variation is IGHV3-23 and IGKV1-39.

[0085] Provided herein are libraries comprising nucleic acids encoding for antibodies, wherein the libraries are synthesized with various numbers of fragments. In some instances, the fragments comprise the CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the fragments comprise framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, the antibody libraries are synthesized with at least or about 2 fragments, 3 fragments, 4 fragments, 5 fragments, or more than 5 fragments. The length of each of the nucleic acid fragments or average length of the nucleic acids synthesized may be at least or about 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, or more than 600 base pairs. In some instances, the length is about 50 to 600, 75 to 575, 100 to 550, 125 to 525, 150 to 500, 175 to 475, 200 to 450, 225 to 425, 250 to 400, 275 to 375, or 300 to 350 base pairs.

[0086] Libraries comprising nucleic acids encoding for antibodies or immunoglobulins as described herein comprise various lengths of amino acids when translated. In some instances, the length of each of the amino acid fragments or average length of the amino acid synthesized may be at least or about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115,

120, 125, 130, 135, 140, 145, 150, or more than 150 amino acids. In some instances, the length of the amino acid is about 15 to 150, 20 to 145, 25 to 140, 30 to 135, 35 to 130, 40 to 125, 45 to 120, 50 to 115, 55 to 110, 60 to 110, 65 to 105, 70 to 100, or 75 to 95 amino acids. In some instances, the length of the amino acid is about 22 amino acids to about 75 amino acids. In some instances, the antibodies comprise at least or about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, or more than 5000 amino acids.

[0087] A number of variant sequences for the at least one region of the antibody for variation are de novo synthesized using methods as described herein. In some instances, a number of variant sequences is de novo synthesized for CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or combinations thereof. In some instances, a number of variant sequences is de novo synthesized for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). The number of variant sequences may be at least or about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, or more than 500 sequences. In some instances, the number of variant sequences is at least or about 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, or more than 8000 sequences. In some instances, the number of variant sequences is about 10 to 500, 25 to 475, 50 to 450, 75 to 425, 100 to 400, 125 to 375, 150 to 350, 175 to 325, 200 to 300, 225 to 375, 250 to 350, or 275 to 325 sequences.

[0088] Variant sequences for the at least one region of the antibody, in some instances, vary in length or sequence. In some instances, the at least one region that is de novo synthesized is for CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or combinations thereof. In some instances, the at least one region that is de novo synthesized is for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, or more than 50 variant nucleotides or amino acids as compared to wild-type. In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, or 50 additional nucleotides or amino acids as compared to wild-type. In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, or 50 less nucleotides or amino acids as compared to wild-type. In some instances, the libraries comprise at least or about 10^1 , 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , or more than 10^{10} variants.

[0089] Following synthesis of antibody libraries, antibody libraries may be used for screening and analysis. For example, antibody libraries are assayed for library displayability and panning. In some instances, displayability is assayed using a selectable tag. Exemplary tags include, but are not

limited to, a radioactive label, a fluorescent label, an enzyme, a chemiluminescent tag, a colorimetric tag, an affinity tag or other labels or tags that are known in the art. In some instances, the tag is histidine, polyhistidine, myc, hemagglutinin (HA), or FLAG. In some instances, antibody libraries are assayed by sequencing using various methods including, but not limited to, single-molecule real-time (SMRT) sequencing, Polony sequencing, sequencing by ligation, reversible terminator sequencing, proton detection sequencing, ion semiconductor sequencing, nanopore sequencing, electronic sequencing, pyrosequencing, Maxam-Gilbert sequencing, chain termination (e.g., Sanger) sequencing, +S sequencing, or sequencing by synthesis. In some instances, antibody libraries are displayed on the surface of a cell or phage. In some instances, antibody libraries are enriched for sequences with a desired activity using phage display.

[0090] In some instances, the antibody libraries are assayed for functional activity, structural stability (e.g., thermal stable or pH stable), expression, specificity, or a combination thereof. In some instances, the antibody libraries are assayed for antibody capable of folding. In some instances, a region of the antibody is assayed for functional activity, structural stability, expression, specificity, folding, or a combination thereof. For example, a VH region or VL region is assayed for functional activity, structural stability, expression, specificity, folding, or a combination thereof.

[0091] Antibodies or IgGs generated by methods as described herein comprise improved binding affinity. In some instances, the antibody comprises a binding affinity (e.g., K_D) of less than 1 nM, less than 1.2 nM, less than 2 nM, less than 5 nM, less than 10 nM, less than 11 nM, less than 13.5 nM, less than 15 nM, less than 20 nM, less than 25 nM, or less than 30 nM. In some instances, the antibody comprises a K_D of less than 400 nM, less than 350 nM, less than 300 nM, less than 250 nM, less than 200 nM, less than 150 nM, less than 100 nM, less than 50 nM, less than 25 nM, less than 15 nM, or less than 10 nM. In some instances, the antibody comprises a K_D of less than 1 nM. In some instances, the antibody comprises a K_D of less than 1.2 nM. In some instances, the antibody comprises a K_D of less than 2 nM. In some instances, the antibody comprises a K_D of less than 5 nM. In some instances, the antibody comprises a K_D of less than 10 nM. In some instances, the antibody comprises a K_D of less than 13.5 nM. In some instances, the antibody comprises a K_D of less than 15 nM. In some instances, the antibody comprises a K_D of less than 20 nM. In some instances, the antibody comprises a K_D of less than 25 nM. In some instances, the antibody comprises a K_D of less than 30 nM.

[0092] In some instances, the affinity of antibodies or IgGs generated by methods as described herein is at least or about 1.5x, 2.0x, 5x, 10x, 20x, 30x, 40x, 50x, 60x, 70x, 80x, 90x, 100x, 200x, or more than 200x improved binding affinity as compared to a comparator antibody. In some instances, the affinity of antibodies or IgGs generated by methods as described herein is at least or

about 1.5x, 2.0x, 5x, 10x, 20x, 30x, 40x, 50x, 60x, 70x, 80x, 90x, 100x, 200x, or more than 200x improved function as compared to a comparator antibody. In some instances, the comparator antibody is an antibody with similar structure, sequence, or antigen target.

[0093] In some embodiments, the variant antibodies or IgGs generated by methods as described herein result in a decreased EC_{50} in a T-cell cytotoxicity assay as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 5X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 8X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 10X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 20X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 25X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 30X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 40X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgG. In some embodiments, the variant antibodies or IgGs have an EC_{50} in a T-cell cytotoxicity assay that is at least 50X decreased as compared to the EC_{50} in a T-cell cytotoxicity assay of a reference antibody or IgGs.

[0094] Methods as described herein, in some instances, result in increased yield of antibodies or IgGs. In some instances, the yield is at least or about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or more than 80 micrograms (ug). In some instances, the yield is in a range of about 5 to about 80, about 10 to about 75, about 15 to about 60, about 20 to about 50, or about 30 to about 40 micrograms (ug).

[0095] *Expression Systems*

[0096] Provided herein are libraries comprising nucleic acids encoding for antibody comprising binding domains, wherein the libraries have improved specificity, stability, expression, folding, or downstream activity. In some instances, libraries described herein are used for screening and analysis.

[0097] Provided herein are libraries comprising nucleic acids encoding for antibody comprising binding domains, wherein the nucleic acid libraries are used for screening and analysis. In some instances, screening and analysis comprises *in vitro*, *in vivo*, or *ex vivo* assays. Cells for screening include primary cells taken from living subjects or cell lines. Cells may be from prokaryotes (e.g., bacteria and fungi) or eukaryotes (e.g., animals and plants). Exemplary animal cells include, without limitation, those from a mouse, rabbit, primate, and insect. In some instances, cells for screening include a cell line including, but not limited to, Chinese Hamster Ovary (CHO) cell line, human embryonic kidney (HEK) cell line, or baby hamster kidney (BHK) cell line. In some instances, nucleic acid libraries described herein may also be delivered to a multicellular organism. Exemplary multicellular organisms include, without limitation, a plant, a mouse, rabbit, primate, and insect.

[0098] Nucleic acid libraries described herein may be screened for various pharmacological or pharmacokinetic properties. In some instances, the libraries are screened using *in vitro* assays, *in vivo* assays, or *ex vivo* assays. For example, *in vitro* pharmacological or pharmacokinetic properties that are screened include, but are not limited to, binding affinity, binding specificity, and binding avidity. Exemplary *in vivo* pharmacological or pharmacokinetic properties of libraries described herein that are screened include, but are not limited to, therapeutic efficacy, activity, preclinical toxicity properties, clinical efficacy properties, clinical toxicity properties, immunogenicity, potency, and clinical safety properties.

[0099] Provided herein are nucleic acid libraries, wherein the nucleic acid libraries may be expressed in a vector. Expression vectors for inserting nucleic acid libraries disclosed herein may comprise eukaryotic or prokaryotic expression vectors. Exemplary expression vectors include, without limitation, mammalian expression vectors: pSF-CMV-NEO-NH2-PPT-3XFLAG, pSF-CMV-NEO-COOH-3XFLAG, pSF-CMV-PURO-NH2-GST-TEV, pSF-OXB20-COOH-TEV-FLAG(R)-6His, pCEP4 pDEST27, pSF-CMV-Ub-KrYFP, pSF-CMV-FMDV-daGFP, pEF1a-mCherry-N1 Vector, pEF1a-tdTomato Vector, pSF-CMV-FMDV-Hygro, pSF-CMV-PGK-Puro, pMCP-tag(m), and pSF-CMV-PURO-NH2-CMYC; bacterial expression vectors: pSF-OXB20-BetaGal, pSF-OXB20-Fluc, pSF-OXB20, and pSF-Tac; plant expression vectors: pRI 101-AN DNA and pCambia2301; and yeast expression vectors: pTYB21 and pKLAC2, and insect vectors: pAc5.1/V5-His A and pDEST8. In some instances, the vector is pcDNA3 or pcDNA3.1.

[00100] Described herein are nucleic acid libraries that are expressed in a vector to generate a construct comprising an antibody. In some instances, a size of the construct varies. In some instances, the construct comprises at least or about 500, 600, 700, 800, 900, 1000, 1100, 1300, 1400, 1500, 1600, 1700, 1800, 2000, 2400, 2600, 2800, 3000, 3200, 3400, 3600, 3800, 4000,

4200, 4400, 4600, 4800, 5000, 6000, 7000, 8000, 9000, 10000, or more than 10000 bases. In some instances, a the construct comprises a range of about 300 to 1,000, 300 to 2,000, 300 to 3,000, 300 to 4,000, 300 to 5,000, 300 to 6,000, 300 to 7,000, 300 to 8,000, 300 to 9,000, 300 to 10,000, 1,000 to 2,000, 1,000 to 3,000, 1,000 to 4,000, 1,000 to 5,000, 1,000 to 6,000, 1,000 to 7,000, 1,000 to 8,000, 1,000 to 9,000, 1,000 to 10,000, 2,000 to 3,000, 2,000 to 4,000, 2,000 to 5,000, 2,000 to 6,000, 2,000 to 7,000, 2,000 to 8,000, 2,000 to 9,000, 2,000 to 10,000, 3,000 to 4,000, 3,000 to 5,000, 3,000 to 6,000, 3,000 to 7,000, 3,000 to 8,000, 3,000 to 9,000, 3,000 to 10,000, 4,000 to 5,000, 4,000 to 6,000, 4,000 to 7,000, 4,000 to 8,000, 4,000 to 9,000, 4,000 to 10,000, 5,000 to 6,000, 5,000 to 7,000, 5,000 to 8,000, 5,000 to 9,000, 5,000 to 10,000, 6,000 to 7,000, 6,000 to 8,000, 6,000 to 9,000, 6,000 to 10,000, 7,000 to 8,000, 7,000 to 9,000, 7,000 to 10,000, 8,000 to 9,000, 8,000 to 10,000, or 9,000 to 10,000 bases.

[00101] Provided herein are libraries comprising nucleic acids encoding for antibodies, wherein the nucleic acid libraries are expressed in a cell. In some instances, the libraries are synthesized to express a reporter gene. Exemplary reporter genes include, but are not limited to, acetohydroxyacid synthase (AHAS), alkaline phosphatase (AP), beta galactosidase (LacZ), beta glucuronidase (GUS), chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), red fluorescent protein (RFP), yellow fluorescent protein (YFP), cyan fluorescent protein (CFP), cerulean fluorescent protein, citrine fluorescent protein, orange fluorescent protein, cherry fluorescent protein, turquoise fluorescent protein, blue fluorescent protein, horseradish peroxidase (HRP), luciferase (Luc), nopaline synthase (NOS), octopine synthase (OCS), luciferase, and derivatives thereof. Methods to determine modulation of a reporter gene are well known in the art, and include, but are not limited to, fluorometric methods (*e.g.* fluorescence spectroscopy, Fluorescence Activated Cell Sorting (FACS), fluorescence microscopy), and antibiotic resistance determination.

[00102] Diseases and Disorders

[00103] Provided herein are libraries comprising nucleic acids encoding for antibodies or immunoglobulins that may have therapeutic effects. In some instances, the antibodies or immunoglobulin result in protein when translated that is used to treat a disease or disorder in a subject. Exemplary diseases include, but are not limited to, cancer, inflammatory diseases or disorders, a metabolic disease or disorder, a cardiovascular disease or disorder, an immunodeficiency disease or disorder, a respiratory disease or disorder, pain, a digestive disease or disorder, a reproductive disease or disorder, an endocrine disease or disorder, an immune disease or disorder, an autoimmune disease or disorder, or a neurological disease or disorder. In some instances, the cancer is a solid cancer or a hematologic cancer. In some instances, the disease or disorder is an immunodeficiency disease. In some instances, the disease or disorder is an

inflammatory disease. In some instances, the disease or disorder is an immune disorder (e.g., allergies or asthma). In some instances, the disease or disorder is a mast cell disease (e.g., systemic mastocytosis, mast cell activation syndrome, or hereditary alpha-tryptasemia). In some instances, the subject is a mammal. In some instances, the subject is a mouse, rabbit, dog, or human. Subjects treated by methods described herein may be infants, adults, or children. Pharmaceutical compositions comprising antibodies or antibody fragments as described herein may be administered intravenously or subcutaneously.

[00104] In some instances, the disease or disorder is associated with SIGLEC-8 dysfunction. In some instances, the disease or disorder is associated with aberrant signaling via SIGLEC-8. In some instances, the disease or disorder is a mast cell disease (e.g., systemic mastocytosis, mast cell activation syndrome, or hereditary alpha-tryptasemia). In some instances, the disease or disorder is an eosinophilic reflux disease (e.g., eosinophilic esophagitis or gastroenteritis). In some instances, the disease or disorder is duodenitis. In some instances, the disease or disorder is cancer. In some instances, the disease or disorder is an immune disease. In some instances, the disease or disorder is an allergy (e.g., a nut allergy or allergic conjunctivitis), chronic urticaria (e.g., hives), atopic dermatitis, or asthma (e.g., allergic asthma).

[00105] For example, SIGLEC-8 is a part of the sialic acid-binding IG-like lectin (siglec) family of transmembrane proteins which are a CD33-related group of receptors. SIGLEC-8 has two splice variants and may function as an inhibitory immunoregulatory receptor. SIGLEC-8 has a finely-tuned specificity toward different sialylated and sulfated carbohydrate ligands. SIGLEC-8 is expressed late in development and is expressed by immune effector cells such as eosinophils, mast cells, and basophils. SIGLEC-8 can be involved in asthma and allergies. SIGLEC-8 can be expressed by eosinophils and/or basophils from subjects with certain cancers (e.g., chronic eosinophilic leukemia, hypereosinophilic syndrome, or chronic myeloid leukemia). SIGLEC-8 can also be expressed by bone marrow mast cells from subjects with mastocytosis and/or aplastic anemia.

[00106] For example, CD117 is a transmembrane tyrosine kinase growth factor receptor that is the product of c-kit gene expression. CD117 is the receptor for stem cell factor (SCF) and can play a role in early hemopoiesis. CD117 is expressed by breast epithelium cells, germ cells, melanocytes, myeloid cells, and mast cells. CD117 can be expressed by certain types of cancer such as but not limited to ovarian carcinoma, seminoma, glioma, glioblastoma, mast cell tumors, melanoma, and gastrointestinal tumors. CD117 can also be related to chronic urticaria (hives), prurigo nodularis, severe combined immunodeficiency, or retinopathies (e.g., diabetic retinopathy, retinopathy of prematurity, or wet macular degeneration).

[00107] *Protein Targets*

[00108] Provided herein are libraries comprising nucleic acids encoding for antibodies or antigen-binding fragments thereof that target SIGLEC-8. SIGLEC-8 is a transmembrane protein and can function as an inhibitory immunoregulatory receptor.

[00109] Provided herein are SIGLEC-8 antibodies or immunoglobulins, wherein the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a sequence at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-450. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 95% sequence identity to any one of SEQ ID NOs: 1-450. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 97% sequence identity to any one of SEQ ID NOs: 1-450. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 99% sequence identity to any one of SEQ ID NOs: 1-450. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 100% sequence identity to any one SEQ ID NOs: 1-450.

[00110] In some embodiments, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-150 and 201-350. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 95% homology to any one of SEQ ID NOs: 1-150 and 201-350. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 97% homology to any one of SEQ ID NOs: 1-150 and 201-350. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 99% homology to any one of SEQ ID NOs: 1-150 and 201-350. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 100% homology to any one of SEQ ID NOs: 1-150 and 201-350. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 17, 18, 19, 20, 21, 22, or more than 22 amino acids of any one of SEQ ID NOs: 1-150 and 201-350.

[00111] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising the amino acid sequence of any one of SEQ ID NOs: 1-150 or 201-350, or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of any one of SEQ ID

NOs: 1-150 or 201-350. A “functional variant” as described herein with respect to a complementarity determining region (CDR) refers to a variant of a CDR having one or more amino acid modification(s) (e.g., amino acid insertions, substitutions, or deletions) with respect to a CDR sequence of a variable domain that binds to a particular antigen, where the one or more amino acid modification(s) to the CDR does not result in ablation of antigen binding of the variable domain to the particular antigen.

[00112] In some embodiments, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain CDR1 (HCDR1) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-50. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 95% homology of any one of SEQ ID NOs: 1-50. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 97% homology to any one of SEQ ID NOs: 1-50. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 99% homology to any one of SEQ ID NOs: 1-50. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 100% homology to any one of SEQ ID NOs: 1-50. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, or more than 8 amino acids of any one of SEQ ID NOs: 1-50.

[00113] In some embodiments, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain CDR2 (HCDR2) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 51-100. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 95% homology to any one of SEQ ID NOs: 51-100. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 97% homology to any one of SEQ ID NOs: 51-100. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 99% homology to any one of SEQ ID NOs: 51-100. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 100% homology to any one of SEQ ID NOs: 51-100. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more than 12 amino acids of any one of SEQ ID NOs: 51-100.

[00114] In some embodiments, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain CDR3 (HCDR3) comprising at least or about 70%, 80%, 85%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 101-150. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 95% homology to any one of SEQ ID NOs: 101-150. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 97% homology to any one of SEQ ID NOs: 101-150. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 99% homology to any one of SEQ ID NOs: 101-150. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 100% homology to any one of SEQ ID NOs: 101-150. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22 or more than 22 amino acids of any one of SEQ ID NOs: 101-150.

[00115] In some embodiments, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain CDR1 (LCDR1) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 201-250. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least or about 95% homology of any one of SEQ ID NOs: 201-250. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least or about 97% homology to any one of SEQ ID NOs: 201-250. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least or about 99% homology to any one of SEQ ID NOs: 201-250. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least or about 100% homology to any one of SEQ ID NOs: 201-250. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, or more than 8 amino acids of any one of SEQ ID NOs: 201-250.

[00116] In some embodiments, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain CDR2 (LCDR2) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 251-300. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 95% homology to any one of SEQ ID NOs: 251-300. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 97% homology to any one of SEQ ID NOs: 251-300. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 99% homology to any one of SEQ ID NOs: 251-300. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 100% homology to any one of SEQ ID

NOs: 251-300. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more than 12 amino acids of any one of SEQ ID NOs: 251-300.

[00117] In some embodiments, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain CDR3 (LCDR3) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 301-350. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 95% homology to any one of SEQ ID NOs: 301-350. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 97% homology to any one of SEQ ID NOs: 301-350. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 99% homology to any one of SEQ ID NOs: 301-350. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 100% homology to any one of SEQ ID NOs: 301-350. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22 or more than 22 amino acids of any one of SEQ ID NOs: 301-350.

[00118] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 1 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 1, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 51 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 51, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 101 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 101, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 201 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 201, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 251 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 251, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 301 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 301.

[00119] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 2 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 2, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 52 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 52, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 102 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 102, an LCDR1

comprising the amino acid sequence of SEQ ID NO: 202 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 202, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 252 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 252, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 302 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 302.

[00120] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 3 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 3, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 53 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 53, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 103 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 103, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 203 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 203, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 253 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 253, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 303 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 303.

[00121] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 4 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 4, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 54 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 54, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 104 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 104, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 204 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 204, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 254 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 254, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 304 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 304.

[00122] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 5 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 5, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 55 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 55, an HCDR3

comprising the amino acid sequence of SEQ ID NO: 105 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 105, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 205 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 205, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 255 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 255, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 305 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 305.

[00123] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 6 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 6, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 56 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 56, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 106 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 106, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 206 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 206, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 256 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 256, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 306 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 306.

[00124] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 7 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 7, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 57 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 57, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 107 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 107, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 207 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 207, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 257 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 257, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 307 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 307.

[00125] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 8 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 8, an

HCDR2 comprising the amino acid sequence of SEQ ID NO: 58 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 58, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 108 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 108, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 208 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 208, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 258 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 258, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 308 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 308.

[00126] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 9 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 9, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 59 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 59, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 109 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 109, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 209 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 209, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 259 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 259, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 309 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 309.

[00127] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 10 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 10, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 60 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 60, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 110 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 110, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 210 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 210, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 260 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 260, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 310 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 310.

[00128] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 11 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 11, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 61 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 61, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 111 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 111, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 211 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 211, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 261 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 261, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 311 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 311.

[00129] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 12 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 12, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 62 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 62, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 112 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 112, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 212 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 212, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 262 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 262, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 312 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 312.

[00130] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 13 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 13, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 63 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 63, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 113 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 113, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 213 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 213, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 263 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 263, and an LCDR3

comprising the amino acid sequence of SEQ ID NO: 313 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 313.

[00131] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 14 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 14, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 64 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 64, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 114 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 114, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 214 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 214, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 264 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 264, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 314 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 314.

[00132] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 15 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 15, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 65 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 65, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 115 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 115, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 215 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 215, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 265 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 265, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 315 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 315.

[00133] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 16 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 16, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 66 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 66, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 116 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 116, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 216 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 216, an LCDR2

comprising the amino acid sequence of SEQ ID NO: 266 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 266, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 316 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 316.

[00134] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 17 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 17, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 67 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 67, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 117 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 117, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 217 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 217, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 267 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 267, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 317 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 317.

[00135] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 18 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 18, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 68 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 68, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 118 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 118, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 218 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 218, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 268 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 268, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 318 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 318.

[00136] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 19 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 19, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 69 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 69, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 119 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 119, an LCDR1

comprising the amino acid sequence of SEQ ID NO: 219 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 219, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 269 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 269, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 319 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 319.

[00137] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 20 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 20, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 70 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 70, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 120 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 120, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 220 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 220, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 270 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 270, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 320 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 320.

[00138] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 21 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 21, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 71 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 71, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 121 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 121, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 221 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 221, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 271 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 271, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 321 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 321.

[00139] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 22 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 22, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 72 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 72, an

HCDR3 comprising the amino acid sequence of SEQ ID NO: 122 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 122, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 222 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 222, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 272 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 272, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 322 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 322.

[00140] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 23 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 23, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 73 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 73, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 123 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 123, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 223 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 223, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 273 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 273, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 323 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 323.

[00141] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 24 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 24, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 74 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 74, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 124 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 124, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 224 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 224, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 274 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 274, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 324 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 324.

[00142] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 25 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO:

25, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 75 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 75, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 125 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 125, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 225 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 225, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 275 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 275, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 325 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 325.

[00143] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 26 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 26, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 76 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 76, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 126 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 126, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 226 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 226, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 276 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 276, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 326 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 326.

[00144] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 27 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 27, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 77 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 77, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 127 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 127, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 227 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 227, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 277 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 277, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 327 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 327.

[00145] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 28 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 28, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 78 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 78, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 128 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 128, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 228 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 228, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 278 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 278, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 328 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 328.

[00146] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 29 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 29, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 79 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 79, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 129 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 129, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 229 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 229, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 279 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 279, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 329 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 329.

[00147] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 30 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 30, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 80 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 80, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 130 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 130, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 230 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 230, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 280 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 280, and an LCDR3

comprising the amino acid sequence of SEQ ID NO: 330 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 330.

[00148] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 31 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 31, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 81 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 81, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 131 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 131, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 231 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 231, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 281 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 281, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 331 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 331.

[00149] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 32 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 32, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 82 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 82, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 132 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 132, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 232 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 232, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 282 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 282, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 332 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 332.

[00150] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 33 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 33, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 83 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 83, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 133 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 133, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 233 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 233, an LCDR2

comprising the amino acid sequence of SEQ ID NO: 283 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 283, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 333 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 333.

[00151] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 34 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 34, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 84 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 84, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 134 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 134, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 234 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 234, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 284 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 284, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 334 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 334.

[00152] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 35 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 35, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 85 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 85, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 135 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 135, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 235 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 235, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 285 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 285, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 335 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 335.

[00153] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 36 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 36, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 86 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 86, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 136 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 136, an LCDR1

comprising the amino acid sequence of SEQ ID NO: 236 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 236, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 286 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 286, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 336 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 336.

[00154] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 37 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 37, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 87 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 87, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 137 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 137, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 237 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 237, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 287 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 287, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 337 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 337.

[00155] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 38 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 38, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 88 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 88, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 138 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 138, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 238 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 238, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 288 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 288, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 338 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 338.

[00156] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 39 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 39, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 89 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 89, an

HCDR3 comprising the amino acid sequence of SEQ ID NO: 139 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 139, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 239 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 239, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 289 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 289, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 339 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 339.

[00157] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 40 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 40, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 90 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 90, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 140 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 140, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 240 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 240, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 290 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 290, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 340 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 340.

[00158] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 41 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 41, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 91 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 91, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 141 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 141, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 241, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 291 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 291, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 341 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 341.

[00159] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 42 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 42, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 92 or a functional variant thereof

having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 92, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 142 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 142, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 242 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 242, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 292 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 292, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 342 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 342.

[00160] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 43 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 43, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 93 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 93, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 143 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 143, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 243 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 243, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 293 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 293, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 343 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 343.

[00161] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 44 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 44, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 94 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 94, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 144 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 144, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 244 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 244, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 294 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 294, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 344 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 344.

[00162] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 45 or a functional variant

thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 45, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 95 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 95, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 145 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 145, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 245 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 245, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 295 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 295, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 345 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 345.

[00163] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 46 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 46, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 96 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 96, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 146 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 146, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 246 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 246, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 296 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 296, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 346 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 346.

[00164] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 47 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 47, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 97 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 97, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 147 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 147, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 247 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 247, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 297 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 297, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 347 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 347.

[00165] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 48 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 48, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 98 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 98, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 148 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 148, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 248 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 248, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 298 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 298, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 348 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 348.

[00166] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 49 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 49, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 99 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 99, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 149 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 149, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 249 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 249, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 299 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 299, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 349 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 349.

[00167] In some embodiments, the SIGLEC-8-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 50 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 50, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 100 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 100, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 150 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 150, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 250 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 250, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 300 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 300, and an LCDR3

comprising the amino acid sequence of SEQ ID NO: 350 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 350.

[00168] In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 151-200. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 95% sequence identity to any one of SEQ ID NOs: 151-200. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 97% sequence identity to any one of SEQ ID NOs: 151-200. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 99% sequence identity to any one of SEQ ID NOs: 151-200. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 100% sequence identity to any one of SEQ ID NOs: 151-200. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least a portion having at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, or more than 150 amino acids of any one of SEQ ID NOs: 151-200.

[00169] In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 351-400. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 95% sequence identity to any one of SEQ ID NOs: 351-400. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 97% sequence identity to any one of SEQ ID NOs: 351-400. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 99% sequence identity to any one of SEQ ID NOs: 351-400. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 100% sequence identity to any one of SEQ ID NOs: 351-400. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least a portion having at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, or more than 150 amino acids of any one of SEQ ID NOs: 351-400.

[00170] In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 401-450. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 95% sequence identity to any one of SEQ ID NOs: 401-450. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 97% sequence identity to any one of SEQ ID NOs: 401-450. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 99% sequence identity to any one of SEQ ID NOs: 401-450. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 100% sequence identity to any one of SEQ ID NOs: 401-450. In some instances, the SIGLEC-8 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least a portion having at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, or more than 250 amino acids of any one of SEQ ID NOs: 401-450.

[00171] Provided herein are libraries comprising nucleic acids encoding for antibodies or immunoglobulins that target CD117, also known as KIT proto-oncogene receptor tyrosine kinase or mast/stem cell growth factor receptor (SCFR). CD117 is a cytokine receptor protein which binds to stem cell factor to form a dimer to activate signal transduction molecules that propagates the SCF signal into the cell. Signaling through CD117 plays a role in cell survival, proliferation, and differentiation.

[00172] Provided herein are CD117 antibodies or immunoglobulins, wherein the CD117 antibody or immunoglobulin comprises a sequence at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 451-639. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 95% sequence identity to any one of SEQ ID NOs: 451-639. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 97% sequence identity to any one of SEQ ID NOs: 451-639. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 99% sequence identity to any one of SEQ ID NOs: 451-639. In some instances, the antibody or antigen-binding fragment thereof comprises at least or about 100% sequence identity to any one SEQ ID NOs: 451-639.

[00173] In some embodiments, the CD117 antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 70%, 80%,

85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 451-513 and 535-597. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 95% homology to any one of SEQ ID NOs: 451-513 and 535-597. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 97% homology to any one of SEQ ID NOs: 451-513 and 535-597. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 99% homology to any one of SEQ ID NOs: 451-513 and 535-597. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least or about 100% homology to any one of SEQ ID NOs: 451-513 and 535-597. In some instances, the antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 17, 18, 19, 20, 21, 22, or more than 22 amino acids of any one of SEQ ID NOs: 451-513 and 535-597.

[00174] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises complementarity determining regions (CDRs) comprising the amino acid sequence of any one of SEQ ID NOs: 1-150 or 201-350, or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of any one of SEQ ID NOs: 1-150 or 201-350. A “functional variant” as described herein with respect to a complementarity determining region (CDR) refers to a variant of a CDR having one or more amino acid modification(s) (e.g., amino acid insertions, substitutions, or deletions) with respect to a CDR sequence of a variable domain that binds to a particular antigen, where the one or more amino acid modification(s) to the CDR does not result in ablation of antigen binding of the variable domain to the particular antigen.

[00175] In some embodiments, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain CDR1 (HCDR1) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 451-471. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 95% homology of any one of SEQ ID NOs: 451-471. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 97% homology to any one of SEQ ID NOs: 451-471. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 99% homology to any one of SEQ ID NOs: 451-471. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 100% homology to any one of SEQ ID NOs: 451-471. In some instances, the antibody or antigen-binding fragment thereof comprises

HCDR1 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, or more than 8 amino acids of any one of SEQ ID NOs: 451-471.

[00176] In some embodiments, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain CDR2 (HCDR2) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 472-492. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 95% homology to any one of SEQ ID NOs: 472-492. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 97% homology to any one of SEQ ID NOs: 472-492. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 99% homology to any one of SEQ ID NOs: 472-492. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least or about 100% homology to any one of SEQ ID NOs: 472-492. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR2 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more than 12 amino acids of any one of SEQ ID NOs: 472-492.

[00177] In some embodiments, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain CDR3 (HCDR3) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 493-513. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 95% homology to any one of SEQ ID NOs: 493-513. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 97% homology to any one of SEQ ID NOs: 493-513. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 99% homology to any one of SEQ ID NOs: 493-513. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least or about 100% homology to any one of SEQ ID NOs: 493-513. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR3 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22 or more than 22 amino acids of any one of SEQ ID NOs: 493-513.

[00178] In some embodiments, the CD117 antibody or antigen-binding fragment thereof comprises a light chain CDR1 (LCDR1) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 535-555. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least or about 95% homology of any one of SEQ ID NOs: 535-555. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least

or about 97% homology to any one of SEQ ID NOs: 535-555. In some instances, the antibody or antigen-binding fragment thereof comprises HCDR1 comprising at least or about 99% homology to any one of SEQ ID NOs: 535-555. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least or about 100% homology to any one of SEQ ID NOs: 535-555. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR1 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, or more than 8 amino acids of any one of SEQ ID NOs: 535-555.

[00179] In some embodiments, the CD117 antibody or antigen-binding fragment thereof comprises a light chain CDR2 (LCDR2) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 556-576. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 95% homology to any one of SEQ ID NOs: 556-576. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 97% homology to any one of SEQ ID NOs: 556-576. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 99% homology to any one of SEQ ID NOs: 556-576. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least or about 100% homology to any one of SEQ ID NOs: 556-576. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR2 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more than 12 amino acids of any one of SEQ ID NOs: 556-576.

[00180] In some embodiments, the CD117 antibody or antigen-binding fragment thereof comprises a light chain CDR3 (LCDR3) comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 577-597. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 95% homology to any one of SEQ ID NOs: 577-597. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 97% homology to any one of SEQ ID NOs: 577-597. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 99% homology to any one of SEQ ID NOs: 577-597. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least or about 100% homology to any one of SEQ ID NOs: 577-597. In some instances, the antibody or antigen-binding fragment thereof comprises LCDR3 comprising at least a portion having at least or about 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22 or more than 22 amino acids of any one of SEQ ID NOs: 577-597.

[00181] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 451 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 451, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 472 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 472, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 493 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 493, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 535 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 535, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 556 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 556, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 577 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 577.

[00182] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 452 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 452, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 473 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 473, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 494 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 494, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 536 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 536, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 557 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 557, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 578 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 578.

[00183] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 453 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 453, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 474 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 474, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 495 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 495, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 537 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 537, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 558 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 558, and an LCDR3

comprising the amino acid sequence of SEQ ID NO: 579 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 579.

[00184] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 454 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 454, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 475 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 475, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 496 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 496, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 538 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 538, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 559 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 559, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 580 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 580.

[00185] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 455 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 455, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 476 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 476, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 497 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 497, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 539 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 539, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 560 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 560, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 581 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 581.

[00186] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 456 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 456, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 477 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 477, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 498 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 498, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 540 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 540, an LCDR2

comprising the amino acid sequence of SEQ ID NO: 561 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 561, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 582 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 582.

[00187] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 457 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 457, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 478 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 478, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 499 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 499, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 541 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 541, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 562 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 562, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 583 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 583.

[00188] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 458 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 458, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 479 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 479, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 500 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 500, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 542 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 542, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 563 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 563, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 584 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 584.

[00189] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 459 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 459, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 480 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 480, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 501 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 501, an LCDR1

comprising the amino acid sequence of SEQ ID NO: 543 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 543, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 564 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 564, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 585 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 585.

[00190] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 460 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 460, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 481 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 481, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 502 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 502, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 544 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 544, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 565 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 565, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 586 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 586.

[00191] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 461 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 461, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 482 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 482, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 503 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 503, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 545 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 545, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 566 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 566, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 587 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 587.

[00192] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 462 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 462, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 483 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 483, an

HCDR3 comprising the amino acid sequence of SEQ ID NO: 504 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 504, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 546 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 546, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 567 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 567, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 588 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 588.

[00193] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 463 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 463, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 484 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 484, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 505 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 505, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 547 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 547, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 568 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 568, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 589 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 589.

[00194] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 464 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 464, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 485 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 485, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 506 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 506, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 548 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 548, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 569 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 569, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 590 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 590.

[00195] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 465 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO:

465, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 486 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 486, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 507 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 507, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 549 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 549, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 570 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 570, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 591 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 591.

[00196] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 466 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 466, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 487 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 487, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 508 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 508, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 550 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 550, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 571 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 571, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 592 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 592.

[00197] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 467 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 467, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 488 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 488, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 509 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 509, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 551 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 551, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 572 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 572, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 593 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 593.

[00198] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 468 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 468, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 489 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 489, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 510 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 510, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 552 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 552, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 573 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 573, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 594 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 594.

[00199] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 469 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 469, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 490 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 490, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 511 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 511, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 553 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 553, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 574 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 574, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 595 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 595.

[00200] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 470 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 470, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 491 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 491, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 512 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 512, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 554 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 554, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 575 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 575, and an LCDR3

comprising the amino acid sequence of SEQ ID NO: 596 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 596.

[00201] In some embodiments, the CD117-binding antibody or antigen-binding fragment thereof comprises: an HCDR1 comprising the amino acid sequence of SEQ ID NO: 471 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 471, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 492 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 492, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 513 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 513, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 555 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 555, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 576 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 576, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 597 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 597.

[00202] In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 514-534. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 95% sequence identity to any one of SEQ ID NOs: 514-534. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 97% sequence identity to any one of SEQ ID NOs: 514-534. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 99% sequence identity to any one of SEQ ID NOs: 514-534. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least or about 100% sequence identity to any one of SEQ ID NOs: 514-534. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a heavy chain variable domain comprising at least a portion having at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, or more than 150 amino acids of any one of SEQ ID NOs: 514-534.

[00203] In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 598-618. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a light chain

variable domain comprising at least or about 95% sequence identity to any one of SEQ ID NOs: 598-618. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 97% sequence identity to any one of SEQ ID NOs: 598-618. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 99% sequence identity to any one of SEQ ID NOs: 598-618. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least or about 100% sequence identity to any one of SEQ ID NOs: 598-618. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a light chain variable domain comprising at least a portion having at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, or more than 150 amino acids of any one of SEQ ID NOs: 598-618.

[00204] In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 619-639. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 95% sequence identity to any one of SEQ ID NOs: 619-639. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 97% sequence identity to any one of SEQ ID NOs: 619-639. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 99% sequence identity to any one of SEQ ID NOs: 619-639. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least or about 100% sequence identity to any one of SEQ ID NOs: 619-639. In some instances, the CD117 antibody or antigen-binding fragment thereof comprises a VH-VL sequence comprising at least a portion having at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, or more than 250 amino acids of any one of SEQ ID NOs: 619-639.

[00205] Variant Libraries

[00206] Codon variation

[00207] Variant nucleic acid libraries described herein may comprise a plurality of nucleic acids, wherein each nucleic acid encodes for a variant codon sequence compared to a reference nucleic acid sequence. In some instances, each nucleic acid of a first nucleic acid population contains a variant at a single variant site. In some instances, the first nucleic acid population contains a plurality of variants at a single variant site such that the first nucleic acid population contains more than one variant at the same variant site. The first nucleic acid population may comprise nucleic

acids collectively encoding multiple codon variants at the same variant site. The first nucleic acid population may comprise nucleic acids collectively encoding up to 19 or more codons at the same position. The first nucleic acid population may comprise nucleic acids collectively encoding up to 60 variant triplets at the same position, or the first nucleic acid population may comprise nucleic acids collectively encoding up to 61 different triplets of codons at the same position. Each variant may encode for a codon that results in a different amino acid during translation. **Table 1** provides a listing of each codon possible (and the representative amino acid) for a variant site.

Table 1. List of codons and amino acids

Amino Acids	One letter code	Three letter code	Codons					
Alanine	A	Ala	GCA	GCC	GCG	GCT		
Cysteine	C	Cys	TGC	TGT				
Aspartic acid	D	Asp	GAC	GAT				
Glutamic acid	E	Glu	GAA	GAG				
Phenylalanine	F	Phe	TTC	TTT				
Glycine	G	Gly	GGA	GGC	GGG	GGT		
Histidine	H	His	CAC	CAT				
Isoleucine	I	Iso	ATA	ATC	ATT			
Lysine	K	Lys	AAA	AAG				
Leucine	L	Leu	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	M	Met	ATG					
Asparagine	N	Asn	AAC	AAT				
Proline	P	Pro	CCA	CCC	CCG	CCT		
Glutamine	Q	Gln	CAA	CAG				

Arginine	R	Arg	AGA	AGG	CGA	CGC	CGG	CGT
Serine	S	Ser	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	T	Thr	ACA	ACC	ACG	ACT		
Valine	V	Val	GTA	GTC	GTG	GTT		
Tryptophan	W	Trp	TGG					
Tyrosine	Y	Tyr	TAC	TAT				

[00208] A nucleic acid population may comprise varied nucleic acids collectively encoding up to 20 codon variations at multiple positions. In such cases, each nucleic acid in the population comprises variation for codons at more than one position in the same nucleic acid. In some instances, each nucleic acid in the population comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more codons in a single nucleic acid. In some instances, each variant long nucleic acid comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more codons in a single long nucleic acid. In some instances, the variant nucleic acid population comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more codons in a single nucleic acid. In some instances, the variant nucleic acid population comprises variation for codons in at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more codons in a single long nucleic acid.

[00209] Highly Parallel Nucleic Acid Synthesis

[00210] Provided herein is a platform approach utilizing miniaturization, parallelization, and vertical integration of the end-to-end process from polynucleotide synthesis to gene assembly within nanowells on silicon to create a revolutionary synthesis platform. Devices described herein provide, with the same footprint as a 96-well plate, a silicon synthesis platform is capable of increasing throughput by a factor of up to 1,000 or more compared to traditional synthesis methods, with production of up to approximately 1,000,000 or more polynucleotides, or 10,000 or more genes in a single highly-parallelized run.

[00211] With the advent of next-generation sequencing, high resolution genomic data has become an important factor for studies that delve into the biological roles of various genes in both normal biology and disease pathogenesis. At the core of this research is the central dogma of molecular biology and the concept of “residue-by-residue transfer of sequential information.”

Genomic information encoded in the DNA is transcribed into a message that is then translated into the protein that is the active product within a given biological pathway.

[00212] Another exciting area of study is on the discovery, development and manufacturing of therapeutic molecules focused on a highly-specific cellular target. High diversity DNA sequence libraries are at the core of development pipelines for targeted therapeutics. Gene mutants are used to express proteins in a design, build, and test protein engineering cycle that ideally culminates in an optimized gene for high expression of a protein with high affinity for its therapeutic target. As an example, consider the binding pocket of a receptor. The ability to test all sequence permutations of all residues within the binding pocket simultaneously will allow for a thorough exploration, increasing chances of success. Saturation mutagenesis, in which a researcher attempts to generate all possible mutations at a specific site within the receptor, represents one approach to this development challenge. Though costly and time and labor-intensive, it enables each variant to be introduced into each position. In contrast, combinatorial mutagenesis, where a few selected positions or short stretch of DNA may be modified extensively, generates an incomplete repertoire of variants with biased representation.

[00213] To accelerate the drug development pipeline, a library with the desired variants available at the intended frequency in the right position available for testing—in other words, a precision library, enables reduced costs as well as turnaround time for screening. Provided herein are methods for synthesizing nucleic acid synthetic variant libraries which provide for precise introduction of each intended variant at the desired frequency. To the end user, this translates to the ability to not only thoroughly sample sequence space but also be able to query these hypotheses in an efficient manner, reducing cost and screening time. Genome-wide editing can elucidate important pathways, libraries where each variant and sequence permutation can be tested for optimal functionality, and thousands of genes can be used to reconstruct entire pathways and genomes to re-engineer biological systems for drug discovery.

[00214] In a first example, a drug itself can be optimized using methods described herein. For example, to improve a specified function of an antibody, a variant polynucleotide library encoding for a portion of the antibody is designed and synthesized. A variant nucleic acid library for the antibody can then be generated by processes described herein (e.g., PCR mutagenesis followed by insertion into a vector). The antibody is then expressed in a production cell line and screened for enhanced activity. Example screens include examining modulation in binding affinity to an antigen, stability, or effector function (e.g., ADCC, complement, or apoptosis). Exemplary regions to optimize the antibody include, without limitation, the Fc region, Fab region, variable region of the

Fab region, constant region of the Fab region, variable domain of the heavy chain or light chain (V_H or V_L), and specific complementarity-determining regions (CDRs) of V_H or V_L .

[00215] In some embodiments, an antibody or antigen-binding fragment thereof comprises an Fc region having one or more amino acid modification(s) with respect to a wildtype Fc region that improves the serum half-life of the antibody or antigen-binding fragment thereof. For example, an antibody or antigen-binding fragment thereof can comprise a modified IgG Fc region for improved serum half-life having one or more of the following modifications with respect to a wildtype IgG Fc region: M252Y, S254T, T256E, M428L, N434S, T256D, T307R, Q311V, N315D, N286D, T307R, H285N, or T307Q. In some embodiments, an antibody or antigen-binding fragment thereof can comprise a modified IgG Fc region for improved serum half-life having one of the following sets of modifications: M252Y/S254T/T256E, M428L/N434S, T256D/T307R/Q311V, T256D/N315D/A378V, T256D/N286D/T307R/Q311V, H285N/T307Q/N315D, T256D/T307R/Q311V/A378V, H285D/Q311V/A378V, T256D/H285D/A378V, T256D/Q311V/A378V, T256D/H285D/N286D/T307R/A378V, T256D/H286D/T307R/Q311V/A378V, T307Q/Q311V/A378V, H285D/T307Q/A378V, or T256D/H285D/T307R/Q311V/A378V. In some embodiments, an antibody or antigen-binding fragment thereof can comprise an Fc region having one or more deletions with respect to a wildtype Fc region for improved serum half-life. For example, an Fc region can comprise a deletion of a CH2 domain, a CH3 domain, or a portion thereof for improved serum half-life. In some embodiments, an Fc region can comprise a deletion of a C-terminal amino acid in a CH3 domain, such as a C-terminal lysine, for improved serum half-life.

[00216] Nucleic acid libraries synthesized by methods described herein may be expressed in various cells associated with a disease state. Cells associated with a disease state include cell lines, tissue samples, primary cells from a subject, cultured cells expanded from a subject, or cells in a model system. Exemplary model systems include, without limitation, plant and animal models of a disease state.

[00217] To identify a variant molecule associated with prevention, reduction or treatment of a disease state, a variant nucleic acid library described herein is expressed in a cell associated with a disease state, or one in which a cell a disease state can be induced. In some instances, an agent is used to induce a disease state in cells. Exemplary tools for disease state induction include, without limitation, a Cre/Lox recombination system, LPS inflammation induction, and streptozotocin to induce hypoglycemia. The cells associated with a disease state may be cells from a model system or cultured cells, as well as cells from a subject having a particular disease condition. Exemplary disease conditions include a bacterial, fungal, viral, autoimmune, or proliferative disorder (e.g.,

cancer). In some instances, the variant nucleic acid library is expressed in the model system, cell line, or primary cells derived from a subject, and screened for changes in at least one cellular activity. Exemplary cellular activities include, without limitation, proliferation, cycle progression, cell death, adhesion, migration, reproduction, cell signaling, energy production, oxygen utilization, metabolic activity, and aging, response to free radical damage, or any combination thereof.

[00218] Substrates

[00219] Devices used as a surface for polynucleotide synthesis may be in the form of substrates which include, without limitation, homogenous array surfaces, patterned array surfaces, channels, beads, gels, and the like. Provided herein are substrates comprising a plurality of clusters, wherein each cluster comprises a plurality of loci that support the attachment and synthesis of polynucleotides. In some instances, substrates comprise a homogenous array surface. For example, the homogenous array surface is a homogenous plate. The term “locus” as used herein refers to a discrete region on a structure which provides support for polynucleotides encoding for a single predetermined sequence to extend from the surface. In some instances, a locus is on a two dimensional surface, *e.g.*, a substantially planar surface. In some instances, a locus is on a three-dimensional surface, *e.g.*, a well, microwell, channel, or post. In some instances, a surface of a locus comprises a material that is actively functionalized to attach to at least one nucleotide for polynucleotide synthesis, or preferably, a population of identical nucleotides for synthesis of a population of polynucleotides. In some instances, polynucleotide refers to a population of polynucleotides encoding for the same nucleic acid sequence. In some cases, a surface of a substrate is inclusive of one or a plurality of surfaces of a substrate. The average error rates for polynucleotides synthesized within a library described here using the systems and methods provided are often less than 1 in 1000, less than about 1 in 2000, less than about 1 in 3000 or less often without error correction.

[00220] Provided herein are surfaces that support the parallel synthesis of a plurality of polynucleotides having different predetermined sequences at addressable locations on a common support. In some instances, a substrate provides support for the synthesis of more than 50, 100, 200, 400, 600, 800, 1000, 1200, 1400, 1600, 1800, 2,000; 5,000; 10,000; 20,000; 50,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; 10,000,000 or more non-identical polynucleotides. In some cases, the surfaces provide support for the synthesis of more than 50, 100, 200, 400, 600, 800, 1000, 1200, 1400, 1600, 1800, 2,000; 5,000; 10,000; 20,000; 50,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000;

1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; 10,000,000 or more polynucleotides encoding for distinct sequences. In some instances, at least a portion of the polynucleotides have an identical sequence or are configured to be synthesized with an identical sequence. In some instances, the substrate provides a surface environment for the growth of polynucleotides having at least 80, 90, 100, 120, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500 bases or more.

[00221] Provided herein are methods for polynucleotide synthesis on distinct loci of a substrate, wherein each locus supports the synthesis of a population of polynucleotides. In some cases, each locus supports the synthesis of a population of polynucleotides having a different sequence than a population of polynucleotides grown on another locus. In some instances, each polynucleotide sequence is synthesized with 1, 2, 3, 4, 5, 6, 7, 8, 9 or more redundancy across different loci within the same cluster of loci on a surface for polynucleotide synthesis. In some instances, the loci of a substrate are located within a plurality of clusters. In some instances, a substrate comprises at least 10, 500, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000, 13000, 14000, 15000, 20000, 30000, 40000, 50000 or more clusters. In some instances, a substrate comprises more than 2,000; 5,000; 10,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,100,000; 1,200,000; 1,300,000; 1,400,000; 1,500,000; 1,600,000; 1,700,000; 1,800,000; 1,900,000; 2,000,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; or 10,000,000 or more distinct loci. In some instances, a substrate comprises about 10,000 distinct loci. The number of loci within a single cluster is varied in different instances. In some cases, each cluster includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 130, 150, 200, 300, 400, 500 or more loci. In some instances, each cluster includes about 50-500 loci. In some instances, each cluster includes about 100-200 loci. In some instances, each cluster includes about 100-150 loci. In some instances, each cluster includes about 109, 121, 130 or 137 loci. In some instances, each cluster includes about 19, 20, 61, 64 or more loci. Alternatively or in combination, polynucleotide synthesis occurs on a homogenous array surface.

[00222] In some instances, the number of distinct polynucleotides synthesized on a substrate is dependent on the number of distinct loci available in the substrate. In some instances, the density of loci within a cluster or surface of a substrate is at least or about 1, 10, 25, 50, 65, 75, 100, 130, 150, 175, 200, 300, 400, 500, 1,000 or more loci per mm². In some cases, a substrate comprises 10-500, 25-400, 50-500, 100-500, 150-500, 10-250, 50-250, 10-200, or 50-200 mm². In some instances, the distance between the centers of two adjacent loci within a cluster or surface is from about 10-500,

from about 10-200, or from about 10-100 μm . In some instances, the distance between two centers of adjacent loci is greater than about 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 μm . In some instances, the distance between the centers of two adjacent loci is less than about 200, 150, 100, 80, 70, 60, 50, 40, 30, 20 or 10 μm . In some instances, each locus has a width of about 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 μm . In some cases, each locus has a width of about 0.5-100, 0.5-50, 10-75, or 0.5-50 μm .

[00223] In some instances, the density of clusters within a substrate is at least or about 1 cluster per 100 mm^2 , 1 cluster per 10 mm^2 , 1 cluster per 5 mm^2 , 1 cluster per 4 mm^2 , 1 cluster per 3 mm^2 , 1 cluster per 2 mm^2 , 1 cluster per 1 mm^2 , 2 clusters per 1 mm^2 , 3 clusters per 1 mm^2 , 4 clusters per 1 mm^2 , 5 clusters per 1 mm^2 , 10 clusters per 1 mm^2 , 50 clusters per 1 mm^2 or more. In some instances, a substrate comprises from about 1 cluster per 10 mm^2 to about 10 clusters per 1 mm^2 . In some instances, the distance between the centers of two adjacent clusters is at least or about 50, 100, 200, 500, 1000, 2000, or 5000 μm . In some cases, the distance between the centers of two adjacent clusters is between about 50-100, 50-200, 50-300, 50-500, and 100-2000 μm . In some cases, the distance between the centers of two adjacent clusters is between about 0.05-50, 0.05-10, 0.05-5, 0.05-4, 0.05-3, 0.05-2, 0.1-10, 0.2-10, 0.3-10, 0.4-10, 0.5-10, 0.5-5, or 0.5-2 mm. In some cases, each cluster has a cross section of about 0.5 to about 2, about 0.5 to about 1, or about 1 to about 2 mm. In some cases, each cluster has a cross section of about 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 mm. In some cases, each cluster has an interior cross section of about 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.15, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 mm.

[00224] In some instances, a substrate is about the size of a standard 96 well plate, for example between about 100 and about 200 mm by between about 50 and about 150 mm. In some instances, a substrate has a diameter less than or equal to about 1000, 500, 450, 400, 300, 250, 200, 150, 100 or 50 mm. In some instances, the diameter of a substrate is between about 25-1000, 25-800, 25-600, 25-500, 25-400, 25-300, or 25-200 mm. In some instances, a substrate has a planar surface area of at least about 100; 200; 500; 1,000; 2,000; 5,000; 10,000; 12,000; 15,000; 20,000; 30,000; 40,000; 50,000 mm^2 or more. In some instances, the thickness of a substrate is between about 50-2000, 50-1000, 100-1000, 200-1000, or 250-1000 mm.

[00225] *Surface materials*

[00226] Substrates, devices, and reactors provided herein are fabricated from any variety of materials suitable for the methods, compositions, and systems described herein. In certain instances, substrate materials are fabricated to exhibit a low level of nucleotide binding. In some instances, substrate materials are modified to generate distinct surfaces that exhibit a high level of nucleotide binding. In some instances, substrate materials are transparent to visible and/or UV light.

In some instances, substrate materials are sufficiently conductive, *e.g.*, are able to form uniform electric fields across all or a portion of a substrate. In some instances, conductive materials are connected to an electric ground. In some instances, the substrate is heat conductive or insulated. In some instances, the materials are chemical resistant and heat resistant to support chemical or biochemical reactions, for example polynucleotide synthesis reaction processes. In some instances, a substrate comprises flexible materials. For flexible materials, materials can include, without limitation: nylon, both modified and unmodified, nitrocellulose, polypropylene, and the like. In some instances, a substrate comprises rigid materials. For rigid materials, materials can include, without limitation: glass; fused silica; silicon, plastics (for example polytetrafluoroethylene, polypropylene, polystyrene, polycarbonate, and blends thereof, and the like); metals (for example, gold, platinum, and the like). The substrate, solid support or reactors can be fabricated from a material selected from the group consisting of silicon, polystyrene, agarose, dextran, cellulosic polymers, polyacrylamides, polydimethylsiloxane (PDMS), and glass. The substrates/solid supports or the microstructures, reactors therein may be manufactured with a combination of materials listed herein or any other suitable material known in the art.

[00227] Surface Architecture

[00228] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates have a surface architecture suitable for the methods, compositions, and systems described herein. In some instances, a substrate comprises raised and/or lowered features. One benefit of having such features is an increase in surface area to support polynucleotide synthesis. In some instances, a substrate having raised and/or lowered features is referred to as a three-dimensional substrate. In some cases, a three-dimensional substrate comprises one or more channels. In some cases, one or more loci comprise a channel. In some cases, the channels are accessible to reagent deposition via a deposition device such as a material deposition device. In some cases, reagents and/or fluids collect in a larger well in fluid communication one or more channels. For example, a substrate comprises a plurality of channels corresponding to a plurality of loci with a cluster, and the plurality of channels are in fluid communication with one well of the cluster. In some methods, a library of polynucleotides is synthesized in a plurality of loci of a cluster.

[00229] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates are configured for polynucleotide synthesis. In some instances, the structure is configured to allow for controlled flow and mass transfer paths for polynucleotide synthesis on a surface. In some instances, the configuration of a substrate allows for the controlled and even distribution of mass transfer paths, chemical exposure times, and/or wash efficacy during

polynucleotide synthesis. In some instances, the configuration of a substrate allows for increased sweep efficiency, for example by providing sufficient volume for a growing polynucleotide such that the excluded volume by the growing polynucleotide does not take up more than 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1%, or less of the initially available volume that is available or suitable for growing the polynucleotide. In some instances, a three-dimensional structure allows for managed flow of fluid to allow for the rapid exchange of chemical exposure.

[00230] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates comprise structures suitable for the methods, compositions, and systems described herein. In some instances, segregation is achieved by physical structure. In some instances, segregation is achieved by differential functionalization of the surface generating active and passive regions for polynucleotide synthesis. In some instances, differential functionalization is achieved by alternating the hydrophobicity across the substrate surface, thereby creating water contact angle effects that cause beading or wetting of the deposited reagents. Employing larger structures can decrease splashing and cross-contamination of distinct polynucleotide synthesis locations with reagents of the neighboring spots. In some cases, a device, such as a material deposition device, is used to deposit reagents to distinct polynucleotide synthesis locations. Substrates having three-dimensional features are configured in a manner that allows for the synthesis of a large number of polynucleotides (*e.g.*, more than about 10,000) with a low error rate (*e.g.*, less than about 1:500, 1:1000, 1:1500, 1:2,000, 1:3,000, 1:5,000, or 1:10,000). In some cases, a substrate comprises features with a density of about or greater than about 1, 5, 10, 20, 30, 40, 50, 60, 70, 80, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400 or 500 features per mm².

[00231] A well of a substrate may have the same or different width, height, and/or volume as another well of the substrate. A channel of a substrate may have the same or different width, height, and/or volume as another channel of the substrate. In some instances, the diameter of a cluster or the diameter of a well comprising a cluster, or both, is between about 0.05-50, 0.05-10, 0.05-5, 0.05-4, 0.05-3, 0.05-2, 0.05-1, 0.05-0.5, 0.05-0.1, 0.1-10, 0.2-10, 0.3-10, 0.4-10, 0.5-10, 0.5-5, or 0.5-2 mm. In some instances, the diameter of a cluster or well or both is less than or about 5, 4, 3, 2, 1, 0.5, 0.1, 0.09, 0.08, 0.07, 0.06, or 0.05 mm. In some instances, the diameter of a cluster or well or both is between about 1.0 and 1.3 mm. In some instances, the diameter of a cluster or well, or both is about 1.150 mm. In some instances, the diameter of a cluster or well, or both is about 0.08 mm. The diameter of a cluster refers to clusters within a two-dimensional or three-dimensional substrate.

[00232] In some instances, the height of a well is from about 20-1000, 50-1000, 100- 1000, 200-1000, 300-1000, 400-1000, or 500-1000 μm . In some cases, the height of a well is less than about 1000, 900, 800, 700, or 600 μm .

[00233] In some instances, a substrate comprises a plurality of channels corresponding to a plurality of loci within a cluster, wherein the height or depth of a channel is 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, or 10-50 μm . In some cases, the height of a channel is less than 100, 80, 60, 40, or 20 μm .

[00234] In some instances, the diameter of a channel, locus (*e.g.*, in a substantially planar substrate) or both channel and locus (*e.g.*, in a three-dimensional substrate wherein a locus corresponds to a channel) is from about 1-1000, 1-500, 1-200, 1-100, 5-100, or 10-100 μm , for example, about 90, 80, 70, 60, 50, 40, 30, 20 or 10 μm . In some instances, the diameter of a channel, locus, or both channel and locus is less than about 100, 90, 80, 70, 60, 50, 40, 30, 20 or 10 μm . In some instances, the distance between the center of two adjacent channels, loci, or channels and loci is from about 1-500, 1-200, 1-100, 5-200, 5-100, 5-50, or 5-30, for example, about 20 μm .

[00235] Surface Modifications

[00236] Provided herein are methods for polynucleotide synthesis on a surface, wherein the surface comprises various surface modifications. In some instances, the surface modifications are employed for the chemical and/or physical alteration of a surface by an additive or subtractive process to change one or more chemical and/or physical properties of a substrate surface or a selected site or region of a substrate surface. For example, surface modifications include, without limitation, (1) changing the wetting properties of a surface, (2) functionalizing a surface, *i.e.*, providing, modifying or substituting surface functional groups, (3) defunctionalizing a surface, *i.e.*, removing surface functional groups, (4) otherwise altering the chemical composition of a surface, *e.g.*, through etching, (5) increasing or decreasing surface roughness, (6) providing a coating on a surface, *e.g.*, a coating that exhibits wetting properties that are different from the wetting properties of the surface, and/or (7) depositing particulates on a surface.

[00237] In some cases, the addition of a chemical layer on top of a surface (referred to as adhesion promoter) facilitates structured patterning of loci on a surface of a substrate. Exemplary surfaces for application of adhesion promotion include, without limitation, glass, silicon, silicon dioxide and silicon nitride. In some cases, the adhesion promoter is a chemical with a high surface energy. In some instances, a second chemical layer is deposited on a surface of a substrate. In some cases, the second chemical layer has a low surface energy. In some cases, surface energy of a chemical layer coated on a surface supports localization of droplets on the surface. Depending on

the patterning arrangement selected, the proximity of loci and/or area of fluid contact at the loci are alterable.

[00238] In some instances, a substrate surface, or resolved loci, onto which nucleic acids or other moieties are deposited, *e.g.*, for polynucleotide synthesis, are smooth or substantially planar (*e.g.*, two-dimensional) or have irregularities, such as raised or lowered features (*e.g.*, three-dimensional features). In some instances, a substrate surface is modified with one or more different layers of compounds. Such modification layers of interest include, without limitation, inorganic and organic layers such as metals, metal oxides, polymers, small organic molecules and the like.

[00239] In some instances, resolved loci of a substrate are functionalized with one or more moieties that increase and/or decrease surface energy. In some cases, a moiety is chemically inert. In some cases, a moiety is configured to support a desired chemical reaction, for example, one or more processes in a polynucleotide synthesis reaction. The surface energy, or hydrophobicity, of a surface is a factor for determining the affinity of a nucleotide to attach onto the surface. In some instances, a method for substrate functionalization comprises: (a) providing a substrate having a surface that comprises silicon dioxide; and (b) silanizing the surface using, a suitable silanizing agent described herein or otherwise known in the art, for example, an organofunctional alkoxysilane molecule. Methods and functionalizing agents are described in U.S. Patent No. 5474796, which is herein incorporated by reference in its entirety.

[00240] In some instances, a substrate surface is functionalized by contact with a derivatizing composition that contains a mixture of silanes, under reaction conditions effective to couple the silanes to the substrate surface, typically via reactive hydrophilic moieties present on the substrate surface. Silanization generally covers a surface through self-assembly with organofunctional alkoxysilane molecules. A variety of siloxane functionalizing reagents can further be used as currently known in the art, *e.g.*, for lowering or increasing surface energy. The organofunctional alkoxysilanes are classified according to their organic functions.

[00241] Polynucleotide Synthesis

[00242] Methods of the current disclosure for polynucleotide synthesis may include processes involving phosphoramidite chemistry. In some instances, polynucleotide synthesis comprises coupling a base with phosphoramidite. Polynucleotide synthesis may comprise coupling a base by deposition of phosphoramidite under coupling conditions, wherein the same base is optionally deposited with phosphoramidite more than once, *i.e.*, double coupling. Polynucleotide synthesis may comprise capping of unreacted sites. In some instances, capping is optional. Polynucleotide synthesis may also comprise oxidation or an oxidation step or oxidation steps. Polynucleotide synthesis may comprise deblocking, detritylation, and sulfurization. In some instances,

polynucleotide synthesis comprises either oxidation or sulfurization. In some instances, between one or each step during a polynucleotide synthesis reaction, the device is washed, for example, using tetrazole or acetonitrile. Time frames for any one step in a phosphoramidite synthesis method may be less than about 2 min, 1 min, 50 sec, 40 sec, 30 sec, 20 sec and 10 sec.

[00243] Polynucleotide synthesis using a phosphoramidite method may comprise a subsequent addition of a phosphoramidite building block (*e.g.*, nucleoside phosphoramidite) to a growing polynucleotide chain for the formation of a phosphite triester linkage. Phosphoramidite polynucleotide synthesis proceeds in the 3' to 5' direction. Phosphoramidite polynucleotide synthesis allows for the controlled addition of one nucleotide to a growing nucleic acid chain per synthesis cycle. In some instances, each synthesis cycle comprises a coupling step. Phosphoramidite coupling involves the formation of a phosphite triester linkage between an activated nucleoside phosphoramidite and a nucleoside bound to the substrate, for example, via a linker. In some instances, the nucleoside phosphoramidite is provided to the device activated. In some instances, the nucleoside phosphoramidite is provided to the device with an activator. In some instances, nucleoside phosphoramidites are provided to the device in a 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100-fold excess or more over the substrate-bound nucleosides. In some instances, the addition of nucleoside phosphoramidite is performed in an anhydrous environment, for example, in anhydrous acetonitrile. Following addition of a nucleoside phosphoramidite, the device is optionally washed. In some instances, the coupling step is repeated one or more additional times, optionally with a wash step between nucleoside phosphoramidite additions to the substrate. In some instances, a polynucleotide synthesis method used herein comprises 1, 2, 3 or more sequential coupling steps. Prior to coupling, in many cases, the nucleoside bound to the device is de-protected by removal of a protecting group, where the protecting group functions to prevent polymerization. A common protecting group is 4,4'-dimethoxytrityl (DMT).

[00244] Following coupling, phosphoramidite polynucleotide synthesis methods optionally comprise a capping step. In a capping step, the growing polynucleotide is treated with a capping agent. A capping step is useful to block unreacted substrate-bound 5'-OH groups after coupling from further chain elongation, preventing the formation of polynucleotides with internal base deletions. Further, phosphoramidites activated with 1H-tetrazole may react, to a small extent, with the O6 position of guanosine. Without being bound by theory, upon oxidation with I₂ /water, this side product, possibly via O6-N7 migration, may undergo depurination. The apurinic sites may end up being cleaved in the course of the final deprotection of the polynucleotide thus reducing the yield of the full-length product. The O6 modifications may be removed by treatment with the

capping reagent prior to oxidation with I₂/water. In some instances, inclusion of a capping step during polynucleotide synthesis decreases the error rate as compared to synthesis without capping. As an example, the capping step comprises treating the substrate-bound polynucleotide with a mixture of acetic anhydride and 1-methylimidazole. Following a capping step, the device is optionally washed.

[00245] In some instances, following addition of a nucleoside phosphoramidite, and optionally after capping and one or more wash steps, the device bound growing nucleic acid is oxidized. The oxidation step comprises the phosphite triester is oxidized into a tetracoordinated phosphate triester, a protected precursor of the naturally occurring phosphate diester internucleoside linkage. In some instances, oxidation of the growing polynucleotide is achieved by treatment with iodine and water, optionally in the presence of a weak base (*e.g.*, pyridine, lutidine, collidine). Oxidation may be carried out under anhydrous conditions using, *e.g.* *tert*-Butyl hydroperoxide or (1*S*)-(+)-(10-camphorsulfonyl)-oxaziridine (CSO). In some methods, a capping step is performed following oxidation. A second capping step allows for device drying, as residual water from oxidation that may persist can inhibit subsequent coupling. Following oxidation, the device and growing polynucleotide is optionally washed. In some instances, the step of oxidation is substituted with a sulfurization step to obtain polynucleotide phosphorothioates, wherein any capping steps can be performed after the sulfurization. Many reagents are capable of the efficient sulfur transfer, including but not limited to 3-(Dimethylaminomethylidene)amino)-3*H*-1,2,4-dithiazole-3-thione, DDTT, 3*H*-1,2-benzodithiol-3-one 1,1-dioxide, also known as Beaucage reagent, and *N,N,N',N'*-Tetraethylthiuram disulfide (TETD).

[00246] In order for a subsequent cycle of nucleoside incorporation to occur through coupling, the protected 5' end of the device bound growing polynucleotide is removed so that the primary hydroxyl group is reactive with a next nucleoside phosphoramidite. In some instances, the protecting group is DMT and deblocking occurs with trichloroacetic acid in dichloromethane. Conducting detritylation for an extended time or with stronger than recommended solutions of acids may lead to increased depurination of solid support-bound polynucleotide and thus reduces the yield of the desired full-length product. Methods and compositions of the disclosure described herein provide for controlled deblocking conditions limiting undesired depurination reactions. In some instances, the device bound polynucleotide is washed after deblocking. In some instances, efficient washing after deblocking contributes to synthesized polynucleotides having a low error rate.

[00247] Methods for the synthesis of polynucleotides typically involve an iterating sequence of the following steps: application of a protected monomer to an actively functionalized surface (*e.g.*,

locus) to link with either the activated surface, a linker or with a previously deprotected monomer; deprotection of the applied monomer so that it is reactive with a subsequently applied protected monomer; and application of another protected monomer for linking. One or more intermediate steps include oxidation or sulfurization. In some instances, one or more wash steps precede or follow one or all of the steps.

[00248] Methods for phosphoramidite-based polynucleotide synthesis comprise a series of chemical steps. In some instances, one or more steps of a synthesis method involve reagent cycling, where one or more steps of the method comprise application to the device of a reagent useful for the step. For example, reagents are cycled by a series of liquid deposition and vacuum drying steps. For substrates comprising three-dimensional features such as wells, microwells, channels and the like, reagents are optionally passed through one or more regions of the device via the wells and/or channels.

[00249] Methods and systems described herein relate to polynucleotide synthesis devices for the synthesis of polynucleotides. The synthesis may be in parallel. For example, at least or about at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 1000, 10000, 50000, 75000, 100000 or more polynucleotides can be synthesized in parallel. The total number polynucleotides that may be synthesized in parallel may be from 2-100000, 3-50000, 4-10000, 5-1000, 6-900, 7-850, 8-800, 9-750, 10-700, 11-650, 12-600, 13-550, 14-500, 15-450, 16-400, 17-350, 18-300, 19-250, 20-200, 21-150, 22-100, 23-50, 24-45, 25-40, 30-35. Those of skill in the art appreciate that the total number of polynucleotides synthesized in parallel may fall within any range bound by any of these values, for example 25-100. The total number of polynucleotides synthesized in parallel may fall within any range defined by any of the values serving as endpoints of the range. Total molar mass of polynucleotides synthesized within the device or the molar mass of each of the polynucleotides may be at least or at least about 10, 20, 30, 40, 50, 100, 250, 500, 750, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 25000, 50000, 75000, 100000 picomoles, or more. The length of each of the polynucleotides or average length of the polynucleotides within the device may be at least or about at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 150, 200, 300, 400, 500 nucleotides, or more. The length of each of the polynucleotides or average length of the polynucleotides within the device may be at most or about at most 500, 400, 300, 200, 150, 100, 50, 45, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10 nucleotides, or less. The length of each of the polynucleotides or average length of the polynucleotides within the device may fall from 10-500, 9-400, 11-300, 12-200, 13-150, 14-100, 15-50, 16-45, 17-40, 18-35, 19-25. Those of skill in the art appreciate that the length of each of the polynucleotides or average

length of the polynucleotides within the device may fall within any range bound by any of these values, for example 100-300. The length of each of the polynucleotides or average length of the polynucleotides within the device may fall within any range defined by any of the values serving as endpoints of the range.

[00250] Methods for polynucleotide synthesis on a surface provided herein allow for synthesis at a fast rate. As an example, at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 125, 150, 175, 200 nucleotides per hour, or more are synthesized. Nucleotides include adenine, guanine, thymine, cytosine, uridine building blocks, or analogs/modified versions thereof. In some instances, libraries of polynucleotides are synthesized in parallel on substrate. For example, a device comprising about or at least about 100; 1,000; 10,000; 30,000; 75,000; 100,000; 1,000,000; 2,000,000; 3,000,000; 4,000,000; or 5,000,000 resolved loci is able to support the synthesis of at least the same number of distinct polynucleotides, wherein polynucleotide encoding a distinct sequence is synthesized on a resolved locus. In some instances, a library of polynucleotides is synthesized on a device with low error rates described herein in less than about three months, two months, one month, three weeks, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 days, 24 hours or less. In some instances, larger nucleic acids assembled from a polynucleotide library synthesized with low error rate using the substrates and methods described herein are prepared in less than about three months, two months, one month, three weeks, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 days, 24 hours or less.

[00251] In some instances, methods described herein provide for generation of a library of nucleic acids comprising variant nucleic acids differing at a plurality of codon sites. In some instances, a nucleic acid may have 1 site, 2 sites, 3 sites, 4 sites, 5 sites, 6 sites, 7 sites, 8 sites, 9 sites, 10 sites, 11 sites, 12 sites, 13 sites, 14 sites, 15 sites, 16 sites, 17 sites, 18 sites, 19 sites, 20 sites, 30 sites, 40 sites, 50 sites, or more of variant codon sites.

[00252] In some instances, the one or more sites of variant codon sites may be adjacent. In some instances, the one or more sites of variant codon sites may not be adjacent and separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more codons.

[00253] In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein all the variant codon sites are adjacent to one another, forming a stretch of variant codon sites. In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein none the variant codon sites are adjacent to one another. In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein some the variant codon sites are adjacent to one another, forming a stretch of variant codon sites, and some of the variant codon sites are not adjacent to one another.

[00254] Referring to the Figures, **FIG. 1** illustrates an exemplary process workflow for synthesis of nucleic acids (e.g., genes) from shorter nucleic acids. The workflow is divided generally into phases: (1) de novo synthesis of a single stranded nucleic acid library, (2) joining nucleic acids to form larger fragments, (3) error correction, (4) quality control, and (5) shipment. Prior to de novo synthesis, an intended nucleic acid sequence or group of nucleic acid sequences is preselected. For example, a group of genes is preselected for generation.

[00255] Once large nucleic acids for generation are selected, a predetermined library of nucleic acids is designed for de novo synthesis. Various suitable methods are known for generating high density polynucleotide arrays. In the workflow example, a device surface layer is provided. In the example, chemistry of the surface is altered in order to improve the polynucleotide synthesis process. Areas of low surface energy are generated to repel liquid while areas of high surface energy are generated to attract liquids. The surface itself may be in the form of a planar surface or contain variations in shape, such as protrusions or microwells which increase surface area. In the workflow example, high surface energy molecules selected serve a dual function of supporting DNA chemistry, as disclosed in International Patent Application Publication WO/2015/021080, which is herein incorporated by reference in its entirety.

[00256] In situ preparation of polynucleotide arrays is generated on a solid support and utilizes single nucleotide extension process to extend multiple oligomers in parallel. A deposition device, such as a material deposition device, is designed to release reagents in a step wise fashion such that multiple polynucleotides extend, in parallel, one residue at a time to generate oligomers with a predetermined nucleic acid sequence **102**. In some instances, polynucleotides are cleaved from the surface at this stage. Cleavage includes gas cleavage, e.g., with ammonia or methylamine.

[00257] The generated polynucleotide libraries are placed in a reaction chamber. In this exemplary workflow, the reaction chamber (also referred to as “nanoreactor”) is a silicon coated well, containing PCR reagents and lowered onto the polynucleotide library **103**. Prior to or after the sealing **104** of the polynucleotides, a reagent is added to release the polynucleotides from the substrate. In the exemplary workflow, the polynucleotides are released subsequent to sealing of the nanoreactor **105**. Once released, fragments of single stranded polynucleotides hybridize in order to span an entire long range sequence of DNA. Partial hybridization **105** is possible because each synthesized polynucleotide is designed to have a small portion overlapping with at least one other polynucleotide in the pool.

[00258] After hybridization, a PCA reaction is commenced. During the polymerase cycles, the polynucleotides anneal to complementary fragments and gaps are filled in by a polymerase. Each cycle increases the length of various fragments randomly depending on which polynucleotides find

each other. Complementarity amongst the fragments allows for forming a complete large span of double stranded DNA **106**.

[00259] After PCA is complete, the nanoreactor is separated from the device **107** and positioned for interaction with a device having primers for PCR **108**. After sealing, the nanoreactor is subject to PCR **109** and the larger nucleic acids are amplified. After PCR **110**, the nanochamber is opened **111**, error correction reagents are added **112**, the chamber is sealed **113** and an error correction reaction occurs to remove mismatched base pairs and/or strands with poor complementarity from the double stranded PCR amplification products **114**. The nanoreactor is opened and separated **115**. Error corrected product is next subject to additional processing steps, such as PCR and molecular bar coding, and then packaged **122** for shipment **123**.

[00260] In some instances, quality control measures are taken. After error correction, quality control steps include for example interaction with a wafer having sequencing primers for amplification of the error corrected product **116**, sealing the wafer to a chamber containing error corrected amplification product **117**, and performing an additional round of amplification **118**. The nanoreactor is opened **119** and the products are pooled **120** and sequenced **121**. After an acceptable quality control determination is made, the packaged product **122** is approved for shipment **123**.

[00261] In some instances, a nucleic acid generated by a workflow such as that in **FIG. 1** is subject to mutagenesis using overlapping primers disclosed herein. In some instances, a library of primers are generated by in situ preparation on a solid support and utilize single nucleotide extension process to extend multiple oligomers in parallel. A deposition device, such as a material deposition device, is designed to release reagents in a step wise fashion such that multiple polynucleotides extend, in parallel, one residue at a time to generate oligomers with a predetermined nucleic acid sequence **102**.

[00262] Computer systems

[00263] Any of the systems described herein, may be operably linked to a computer and may be automated through a computer either locally or remotely. In various instances, the methods and systems of the disclosure may further comprise software programs on computer systems and use thereof. Accordingly, computerized control for the synchronization of the dispense/vacuum/refill functions such as orchestrating and synchronizing the material deposition device movement, dispense action and vacuum actuation are within the bounds of the disclosure. The computer systems may be programmed to interface between the user specified base sequence and the position of a material deposition device to deliver the correct reagents to specified regions of the substrate.

[00264] The computer system **200** illustrated in **FIG. 2** may be understood as a logical apparatus that can read instructions from media **211** and/or a network port **205**, which can optionally be

connected to server **209** having fixed media **212**. The system, such as shown in **FIG. 2** can include a CPU **201**, disk drives **203**, optional input devices such as keyboard **215** and/or mouse **216** and optional monitor **207**. Data communication can be achieved through the indicated communication medium to a server at a local or a remote location. The communication medium can include any means of transmitting and/or receiving data. For example, the communication medium can be a network connection, a wireless connection or an internet connection. Such a connection can provide for communication over the World Wide Web. It is envisioned that data relating to the present disclosure can be transmitted over such networks or connections for reception and/or review by a party **222** as illustrated in **FIG. 2**.

[00265] As illustrated in **FIG. 3**, a high speed cache **304** can be connected to, or incorporated in, the processor **302** to provide a high speed memory for instructions or data that have been recently, or are frequently, used by processor **302**. The processor **302** is connected to a north bridge **306** by a processor bus **308**. The north bridge **306** is connected to random access memory (RAM) **310** by a memory bus **312** and manages access to the RAM **310** by the processor **302**. The north bridge **306** is also connected to a south bridge **314** by a chipset bus **316**. The south bridge **314** is, in turn, connected to a peripheral bus **318**. The peripheral bus can be, for example, PCI, PCI-X, PCI Express, or other peripheral bus. The north bridge and south bridge are often referred to as a processor chipset and manage data transfer between the processor, RAM, and peripheral components on the peripheral bus **318**. In some alternative architectures, the functionality of the north bridge can be incorporated into the processor instead of using a separate north bridge chip. In some instances, system **300** can include an accelerator card **322** attached to the peripheral bus **318**. The accelerator can include field programmable gate arrays (FPGAs) or other hardware for accelerating certain processing. For example, an accelerator can be used for adaptive data restructuring or to evaluate algebraic expressions used in extended set processing.

[00266] Software and data are stored in external storage **324** and can be loaded into RAM **310** and/or cache **304** for use by the processor. The system **300** includes an operating system for managing system resources; non-limiting examples of operating systems include: Linux, WindowsTM, MACOSTM, BlackBerry OSTM, iOSTM, and other functionally-equivalent operating systems, as well as application software running on top of the operating system for managing data storage and optimization in accordance with example instances of the present disclosure. In this example, system **300** also includes network interface cards (NICs) **320** and **321** connected to the peripheral bus for providing network interfaces to external storage, such as Network Attached Storage (NAS) and other computer systems that can be used for distributed parallel processing.

[00267] **FIG. 4** is a diagram showing a network **400** with a plurality of computer systems **402a**, and **402b**, a plurality of cell phones and personal data assistants **402c**, and Network Attached Storage (NAS) **404a**, and **404b**. In example instances, systems **402a**, **402b**, and **402c** can manage data storage and optimize data access for data stored in Network Attached Storage (NAS) **404a** and **404b**. A mathematical model can be used for the data and be evaluated using distributed parallel processing across computer systems **402a**, and **402b**, and cell phone and personal data assistant systems **402c**. Computer systems **402a**, and **402b**, and cell phone and personal data assistant systems **402c** can also provide parallel processing for adaptive data restructuring of the data stored in Network Attached Storage (NAS) **404a** and **404b**. **FIG. 4** illustrates an example only, and a wide variety of other computer architectures and systems can be used in conjunction with the various instances of the present disclosure. For example, a blade server can be used to provide parallel processing. Processor blades can be connected through a back plane to provide parallel processing. Storage can also be connected to the back plane or as Network Attached Storage (NAS) through a separate network interface. In some example instances, processors can maintain separate memory spaces and transmit data through network interfaces, back plane or other connectors for parallel processing by other processors. In other instances, some or all of the processors can use a shared virtual address memory space.

[00268] **FIG. 5** is a block diagram of a multiprocessor computer system **500** using a shared virtual address memory space in accordance with an example instance. The system includes a plurality of processors **502a-f** that can access a shared memory subsystem **504**. The system incorporates a plurality of programmable hardware memory algorithm processors (MAPs) **506a-f** in the memory subsystem **504**. Each MAP **506a-f** can comprise a memory **508a-f** and one or more field programmable gate arrays (FPGAs) **510a-f**. The MAP provides a configurable functional unit and particular algorithms or portions of algorithms can be provided to the FPGAs **510a-f** for processing in close coordination with a respective processor. For example, the MAPs can be used to evaluate algebraic expressions regarding the data model and to perform adaptive data restructuring in example instances. In this example, each MAP is globally accessible by all of the processors for these purposes. In one configuration, each MAP can use Direct Memory Access (DMA) to access an associated memory **508a-f**, allowing it to execute tasks independently of, and asynchronously from the respective microprocessor **502a-f**. In this configuration, a MAP can feed results directly to another MAP for pipelining and parallel execution of algorithms.

[00269] The above computer architectures and systems are examples only, and a wide variety of other computer, cell phone, and personal data assistant architectures and systems can be used in connection with example instances, including systems using any combination of general

processors, co-processors, FPGAs and other programmable logic devices, system on chips (SOCs), application specific integrated circuits (ASICs), and other processing and logic elements. In some instances, all or part of the computer system can be implemented in software or hardware. Any variety of data storage media can be used in connection with example instances, including random access memory, hard drives, flash memory, tape drives, disk arrays, Network Attached Storage (NAS) and other local or distributed data storage devices and systems.

[00270] In example instances, the computer system can be implemented using software modules executing on any of the above or other computer architectures and systems. In other instances, the functions of the system can be implemented partially or completely in firmware, programmable logic devices such as field programmable gate arrays (FPGAs) as referenced in **FIG. 3**, system on chips (SOCs), application specific integrated circuits (ASICs), or other processing and logic elements. For example, the Set Processor and Optimizer can be implemented with hardware acceleration through the use of a hardware accelerator card, such as accelerator card **322** illustrated in **FIG. 3**.

[00271] The following examples are set forth to illustrate more clearly the principle and practice of embodiments disclosed herein to those skilled in the art and are not to be construed as limiting the scope of any claimed embodiments. Unless otherwise stated, all parts and percentages are on a weight basis.

EXAMPLES

[00272] The following examples are given for the purpose of illustrating various embodiments of the disclosure and are not meant to limit the present disclosure in any fashion. The present examples, along with the methods described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the disclosure. Changes therein and other uses which are encompassed within the spirit of the disclosure as defined by the scope of the claims will occur to those skilled in the art.

[00273] Example 1: Functionalization of a device surface

[00274] A device was functionalized to support the attachment and synthesis of a library of polynucleotides. The device surface was first wet cleaned using a piranha solution comprising 90% H₂SO₄ and 10% H₂O₂ for 20 minutes. The device was rinsed in several beakers with DI water, held under a DI water gooseneck faucet for 5 min, and dried with N₂. The device was subsequently soaked in NH₄OH (1:100; 3 mL:300 mL) for 5 min, rinsed with DI water using a handgun, soaked in three successive beakers with DI water for 1 min each, and then rinsed again with DI water using

the handgun. The device was then plasma cleaned by exposing the device surface to O₂. A SAMCO PC-300 instrument was used to plasma etch O₂ at 250 watts for 1 min in downstream mode.

[00275] The cleaned device surface was actively functionalized with a solution comprising N-(3-triethoxysilylpropyl)-4-hydroxybutyramide using a YES-1224P vapor deposition oven system with the following parameters: 0.5 to 1 torr, 60 min, 70 °C, 135 °C vaporizer. The device surface was resist coated using a Brewer Science 200X spin coater. SPR™ 3612 photoresist was spin coated on the device at 2500 rpm for 40 sec. The device was pre-baked for 30 min at 90 °C on a Brewer hot plate. The device was subjected to photolithography using a Karl Suss MA6 mask aligner instrument. The device was exposed for 2.2 sec and developed for 1 min in MSF 26A. Remaining developer was rinsed with the handgun and the device soaked in water for 5 min. The device was baked for 30 min at 100 °C in the oven, followed by visual inspection for lithography defects using a Nikon L200. A descum process was used to remove residual resist using the SAMCO PC-300 instrument to O₂ plasma etch at 250 watts for 1 min.

[00276] The device surface was passively functionalized with a 100 µL solution of perfluorooctyltrichlorosilane mixed with 10 µL light mineral oil. The device was placed in a chamber, pumped for 10 min, and then the valve was closed to the pump and left to stand for 10 min. The chamber was vented to air. The device was resist stripped by performing two soaks for 5 min in 500 mL NMP at 70 °C with ultrasonication at maximum power (9 on Crest system). The device was then soaked for 5 min in 500 mL isopropanol at room temperature with ultrasonication at maximum power. The device was dipped in 300 mL of 200 proof ethanol and blown dry with N₂. The functionalized surface was activated to serve as a support for polynucleotide synthesis.

[00277] Example 2: Synthesis of a 50-mer sequence on an oligonucleotide synthesis device

[00278] A two-dimensional oligonucleotide synthesis device was assembled into a flowcell, which was connected to a flowcell (Applied Biosystems (ABI394 DNA Synthesizer"). The two-dimensional oligonucleotide synthesis device was uniformly functionalized with N-(3-TRIETHOXYSYLYLPROPYL)-4-HYDROXYBUTYRAMIDE (Gelest) was used to synthesize an exemplary polynucleotide of 50 bp ("50-mer polynucleotide") using polynucleotide synthesis methods described herein.

[00279] The sequence of the 50-mer was as described below:

5'AGACAATCAACCATTTGGGGTGGACAGCCTTGACCTCTAGACTTCGGCAT##TTTTTTT TTT3' (SEQ ID NO: 640), where # denotes Thymidine-succinyl hexamide CED phosphoramidite (CLP-2244 from ChemGenes), which is a cleavable linker enabling the release of oligos from the surface during deprotection.

[00280] The synthesis was done using standard DNA synthesis chemistry (coupling, capping, oxidation, and deblocking) according to the protocol in **Table 2** and an ABI synthesizer.

Table 2: Synthesis protocols

Table 2		
General DNA Synthesis Process Name	Process Step	Time (sec)
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	23
	N2 System Flush	4
	Acetonitrile System Flush	4
DNA BASE ADDITION (Phosphoramidite + Activator Flow)	Activator Manifold Flush	2
	Activator to Flowcell	6
	Activator + Phosphoramidite to Flowcell	6
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Incubate for 25sec	25
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
DNA BASE ADDITION (Phosphoramidite + Activator Flow)	Activator Manifold Flush	2
	Activator to Flowcell	5
	Activator + Phosphoramidite to Flowcell	18
	Incubate for 25sec	25
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
CAPPING (CapA+B, 1:1, Flow)	CapA+B to Flowcell	15
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	Acetonitrile System Flush	4

Table 2		
General DNA Synthesis Process Name	Process Step	Time (sec)
OXIDATION (Oxidizer Flow)	Oxidizer to Flowcell	18
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	23
	N2 System Flush	4
	Acetonitrile System Flush	4
DEBLOCKING (Deblock Flow)	Deblock to Flowcell	36
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	18
	N2 System Flush	4.13
	Acetonitrile System Flush	4.13
	Acetonitrile to Flowcell	15

[00281] The phosphoramidite/activator combination was delivered similar to the delivery of bulk reagents through the flowcell. No drying steps were performed as the environment stays "wet" with reagent the entire time.

[00282] The flow restrictor was removed from the ABI 394 synthesizer to enable faster flow. Without flow restrictor, flow rates for amidites (0.1M in ACN), Activator, (0.25M Benzoylthiotetrazole ("BTT"; 30-3070-xx from GlenResearch) in ACN), and Ox (0.02M I2 in 20% pyridine, 10% water, and 70% THF) were roughly ~100uL/sec, for acetonitrile ("ACN") and capping reagents (1:1 mix of CapA and CapB, wherein CapA is acetic anhydride in THF/Pyridine and CapB is 16% 1-methylimidazole in THF), roughly ~200uL/sec, and for Deblock (3% dichloroacetic acid in toluene), roughly ~300uL/sec (compared to ~50uL/sec for all reagents with flow restrictor). The time to completely push out Oxidizer was observed, the timing for chemical flow times was adjusted accordingly and an extra ACN wash was introduced between different chemicals. After polynucleotide synthesis, the chip was deprotected in gaseous ammonia overnight at 75 psi. Five drops of water were applied to the surface to recover polynucleotides. The recovered polynucleotides were then analyzed on a BioAnalyzer small RNA chip.

[00283] **Example 3: Synthesis of a 100-mer sequence on an oligonucleotide synthesis device**

[00284] The same process as described in Example 2 for the synthesis of the 50-mer sequence was used for the synthesis of a 100-mer polynucleotide ("100-mer polynucleotide"; 5' CGGGATCCTTATCGTCATCGTCGTACAGATCCCGACCCATTTGCTGTCCACCAGTCATG CTAGCCATACCATGATGATGATGATGATGAGAACCCCGCAT##TTTTTTTTTTT3' (SEQ ID NO: 641) , where # denotes Thymidine-succinyl hexamide CED phosphoramidite (CLP-2244 from ChemGenes) on two different silicon chips, the first one uniformly functionalized with N-(3-TRIETHOXYSYLYLPROPYL)-4-HYDROXYBUTYRAMIDE and the second one functionalized with 5/95 mix of 11-acetoxyundecyltriethoxysilane and n-decyltriethoxysilane, and the polynucleotides extracted from the surface were analyzed on a BioAnalyzer instrument.

[00285] All ten samples from the two chips were further PCR amplified using a forward (5'ATGCGGGGTTCTCATCATC3') (SEQ ID NO:642) and a reverse (5'CGGGATCCTTATCGTCATCG3') (SEQ ID NO:643) primer in a 50uL PCR mix (25uL NEB Q5 mastermix, 2.5uL 10uM Forward primer, 2.5uL 10uM Reverse primer, 1uL polynucleotide extracted from the surface, and water up to 50uL) using the following thermalcycling program:

98 °C, 30 sec

98 °C, 10 sec; 63 °C, 10 sec; 72 °C, 10 sec; repeat 12 cycles

72 °C, 2min

[00286] The PCR products were also run on a BioAnalyzer, demonstrating sharp peaks at the 100-mer position. Next, the PCR amplified samples were cloned, and Sanger sequenced. **Table 3** summarizes the results from the Sanger sequencing for samples taken from spots 1-5 from chip 1 and for samples taken from spots 6-10 from chip 2.

Table 3: Sequencing results

Spot	Error rate	Cycle efficiency
1	1/763 bp	99.87%
2	1/824 bp	99.88%
3	1/780 bp	99.87%
4	1/429 bp	99.77%
5	1/1525 bp	99.93%
6	1/1615 bp	99.94%
7	1/531 bp	99.81%
8	1/1769 bp	99.94%
9	1/854 bp	99.88%

Spot	Error rate	Cycle efficiency
10	1/1451 bp	99.93%

[00287] Thus, the high quality and uniformity of the synthesized polynucleotides were repeated on two chips with different surface chemistries. Overall, 89% of the 100-mers that were sequenced were perfect sequences with no errors, corresponding to 233 out of 262.

[00288] **Table 4** summarizes error characteristics for the sequences obtained from the polynucleotide samples from spots 1-10.

Table 4: Error characteristics

Sample ID/Spot no.	OSA_0 046/1	OSA_0 047/2	OSA_0 048/3	OSA_0 049/4	OSA_0 050/5	OSA_0 051/6	OSA_0 052/7	OSA_0 053/8	OSA_0 054/9	OSA_00 55/10
Total Sequences	32	32	32	32	32	32	32	32	32	32
Sequencing Quality	25 of 28	27 of 27	26 of 30	21 of 23	25 of 26	29 of 30	27 of 31	29 of 31	28 of 29	25 of 28
Oligo Quality	23 of 25	25 of 27	22 of 26	18 of 21	24 of 25	25 of 29	22 of 27	28 of 29	26 of 28	20 of 25
ROI Match Count	2500	2698	2561	2122	2499	2666	2625	2899	2798	2348
ROI Mutation	2	2	1	3	1	0	2	1	2	1
ROI Multi Base Deletion	0	0	0	0	0	0	0	0	0	0
ROI Small Insertion	1	0	0	0	0	0	0	0	0	0
ROI Single Base Deletion	0	0	0	0	0	0	0	0	0	0
Large Deletion Count	0	0	1	0	0	1	1	0	0	0
Mutation: G>A	2	2	1	2	1	0	2	1	2	1
Mutation: T>C	0	0	0	1	0	0	0	0	0	0
ROI Error Count	3	2	2	3	1	1	3	1	2	1
ROI Error Rate	Err: ~1 in 834	Err: ~1 in 1350	Err: ~1 in 1282	Err: ~1 in 708	Err: ~1 in 2500	Err: ~1 in 2667	Err: ~1 in 876	Err: ~1 in 2900	Err: ~1 in 1400	Err: ~1 in 2349
ROI Minus Primer Error Rate	MP Err: ~1 in 763	MP Err: ~1 in 824	MP Err: ~1 in 780	MP Err: ~1 in 429	MP Err: ~1 in 1525	MP Err: ~1 in 1615	MP Err: ~1 in 531	MP Err: ~1 in 1769	MP Err: ~1 in 854	MP Err: ~1 in 1451

[00289] Example 4: Antibody Libraries for SIGLEC-8

[00290] Two expression cassettes for SIGLEC-8, pTT5-SIGLEC-8 P2A mVenus (**FIG. 6A**) and pTT5-SIGLEC-8 mVenus (**FIG. 6B**), were designed to determine the transient expression profile and localization of SIGLEC-8. SIGLEC-8 was shown to localize to the membrane (**FIGs. 6C-6E**). The transient expression of SIGLEC-8 was validated with a control antibody (**FIGs. 6F-6G**).

[00291] Synthetic antibody libraries were developed, and SIGLEC-8 candidates were panned using a bead-based panning strategy over four rounds (**FIGs. 7A-7B**). Clonal ELISA screening found 52 total unique clonotypes in panning rounds 3 and 4 (**FIGs. 8A-8C**). SIGLEC-8 antibodies were expressed and purified for further assays (**FIGs. 9A-9C**).

[00292] Kinetics studies were performed using Carterra SPR (**FIGs. 10A-10B**). Titration assays showed that specific binding to the transient line and showed correlation with K_D (**FIGs. 11A-11O**). Cross-reactivity profiles were evaluated using SPR with related SIGLEC proteins (**FIGs. 12A-12B**). Sub-nanomolar clones were identified for SIGLEC-8 (**FIGs. 13A-13B**). SIGLEC-8 mAbs were tested for cross-reactivity with other SIGLEC proteins (**FIG. 13C**). Binning for SIGLEC-8 leads was performed (**FIG. 14A**), and SIGLEC-8 leads were compared for relatedness (**FIG. 14B**). When compared to lirentelimab, a monoclonal antibody known to target SIGLEC-8, antibodies disclosed herein, such as antibody SIGLEC-8-40, were shown to target the same SIGLEC-8 epitope as is targeted by lirentelimab (**FIGs. 15A-15B**).

[00293] A summary of the binding affinity and cell binding EC50 of the SIGLEC-8 antibodies is shown in Table 5.

Table 5: SIGLEC-8 Antibody Binding Affinity and Cell Binding

Clone	KD (nM)	Cell Binding EC50 (nM)
SIGLEC-8-1	0.292	1.258
SIGLEC-8-2	160000	8.276
SIGLEC-8-3	242	6.464
SIGLEC-8-4	0.189	2.376
SIGLEC-8-6	4.68	2.433
SIGLEC-8-7	1.12	0.8133
SIGLEC-8-8	1.65	1.299
SIGLEC-8-9	8080	1592
SIGLEC-8-10	3.17	1.087
SIGLEC-8-11	0.217	2.192
SIGLEC-8-13	N.B. (Non-Binding)	50.72

SIGLEC-8-14	65.4	20.76
SIGLEC-8-15	2.57	N.B.
SIGLEC-8-16	2.02	2.874
SIGLEC-8-17	8.89	1.255
SIGLEC-8-19	4.86	N.B. (Non-Binding)
SIGLEC-8-20	0.0764	0.9721
SIGLEC-8-23	10.1	0.8546
SIGLEC-8-24	0.822	1.047
SIGLEC-8-25	50.6	7.627
SIGLEC-8-27	N/A	903.8
SIGLEC-8-28	3.49	1.022
SIGLEC-8-29	326	355.4
SIGLEC-8-30	0.856	1.498
SIGLEC-8-31	0.37	1.332
SIGLEC-8-32	19.2	3.811
SIGLEC-8-33	2.5	133.1
SIGLEC-8-34	9.23	1.951
SIGLEC-8-38	46200	10.55
SIGLEC-8-39	159	4.466
SIGLEC-8-40	0.0225	0.6086
SIGLEC-8-43	13.9	1.667
SIGLEC-8-44	0.517	1.073
SIGLEC-8-45	0.574	1.811
SIGLEC-8-46	152000	32.8
SIGLEC-8-47	32.7	1.882
SIGLEC-8-48	336	12.26
SIGLEC-8-49	88.8	1.403
SIGLEC-8-50	1.21	1.153
SIGLEC-8-51	10	N.B.
SIGLEC-8-52	0.733	4.072
SIGLEC-8-53	0.185	0.6896
SIGLEC-8-54	1.06	0.5268
SIGLEC-8-55	1.61	3.011
SIGLEC-8-56	0.271	1.017
SIGLEC-8-57	990	1.728
SIGLEC-8-58	0.97	0.9139

SIGLEC-8-59	31.2	0.9387
SIGLEC-8-60	0.895	0.6534
SIGLEC-8-61	0.0942	0.4943

[00294] Example 5: Antibody Libraries for CD117

[00295] Two expression cassettes for CD117, pTT5- CD117 P2A mVenus (**FIG. 16A**) and pTT5- CD117 mVenus (**FIG. 16B**), were designed to determine the transient expression profile and localization of CD117. CD117 was shown to localize to the membrane (**FIG. 6C** and **FIGS. 16C-16D**).

[00296] Synthetic antibody libraries were developed, and CD117 candidates were panned using a bead-based panning strategy over five rounds (**FIGS. 18A-18B**). NGS analysis was performed on CD117 panning phage outputs, showing an increase in cluster enrichment from round 4 to round 5 (**FIGS. 19A-19B**). CDR3 enrichment was also observed throughout the panning rounds (**FIGS. 19C-19E**).

[00297] The transient expression of CD117 was validated with a control antibody, Expi293 (**FIGS. 17A-17B**). Expi293, the primary antibody, was transiently transfected with CD117 48-hours post-transfection. The secondary antibody used was APC Goat anti-human IgG (diluted 1:400). 100,000 cells per well were blocked with 1x PBS + 0.5% BSA for 1 hour, stained with 100 uL of the primary antibody for 1 hour, and stained with the secondary antibody for one hour, all with 3x washes in between each staining. Several candidates were shown to bind to the transient cell line by FACS (**FIGS. 20A-20C**). Specific binding by FACS showed functional screen leads of antibodies CD117-7, CD117-10, CD117-17, CD117-11, CD117-18, CD117-14, and CD117-6 (**FIGS. 21A-21X**). Cell binding EC50s are summarized in Table 6.

Table 6. CD117 Antibody Cell Binding

Clone	Cell Binding (EC50 nM)
CD117-1	23.79
CD117-2	0.742
CD117-3	31.57
CD117-4	3.419
CD117-5	6.882
CD117-6	0.1162
CD117-7	4.013
CD117-8	351.3
CD117-9	1.386
CD117-10	91.28

CD117-11	4.307
CD117-12	1209
CD117-13	11
CD117-14	0.07182
CD117-15	7.323
CD117-16	190.2
CD117-17	7.581
CD117-18	20.03
CD117-19	3.288
CD117-20	6.24
CD117-21	20.66

[00298] Clonal ELISA screening top hits were identified as CD117-2, CD117-14, CD117-6, and CD117-9, as measured using half-maximal effective concentration (EC₅₀) (**FIGs. 22A-22E**).

[00299] Reporter assays using CD117 (c-kit) were performed using Stem Cell Factor (SCF or c-kit ligand). SCF binding to CD117 causes dimerization and subsequent activation of the ERK pathway. ERK phosphorylation leads to binding of the transcription factor serum response factor (SRF) which targets promoters of target genes that contain serum response elements (SRE). The binding of the SRF transcription factor to SREs leads to increased cell proliferation. The functional reporter assay used here transiently overexpressed CD117-GFP and SRF reporter in HEK293T cells to screen for CD117 antibodies. SCF was titrated on cells overexpressing CD117. SCF caused a increase in SRF activation – over a two-fold increase in signal was observed. The EC₅₀ of SCF for CD117 activation was observed to be around 585 pM (**FIG. 23**), and this concentration was used to test the activity of the CD117 antibodies.

[00300] Titration of four CD117 control antibodies against the standard 585 pM SCF concentration (**FIG. 24A**). All four controls showed a strong inhibition of SRF reporter activity. A SIGLEC-8 antibody, used as a control, showed no effect against SCF signaling. In another control experiment, neither CD117 antibodies nor SIGLEC-8 antibodies showed any effect on EGF signaling (**FIG. 24B**).

[00301] Primary screens for top agonists were performed using 10 nM of SCF-stimulated cells. The top blockers identified included CD117-6, CD117-7, CD117-10, CD117-11, CD117-14, CD117-17, CD117-18, CD117-79, CD117-125, CD117-131, and CD117-150 (**FIGs. 25A-25B**). However, MFI binding analysis showed that top binders were not the top antagonists (**FIG. 25C**). The transcriptional reporter assay showed the ability to readily assay the functional activity of further CD117 antibodies as the SRF reporter showed a robust increase when

CD117-overexpressing HEK cells were stimulated with SCF. This response was inhibited in the control assays (**FIGs. 26A-26B**). Additionally, the EC₅₀ for CD117 activation was found to be around 10 nM, and this concentration was used to test the activity of the top leads (CD117-6, CD117-7, CD117-10, CD117-11, CD117-14, CD117-17, CD117-18, CD117-79, CD117-125, CD117-131, and CD117-150).

[00302] Secondary screening titrations were performed on the potential antagonists. Binding was tested on top candidates CD117-1, CD117-2, CD117-6, CD117-7, and CD117-14 to determine the concentration of antigen that blocks antibody-phage binding to immobilized antigen (IC₅₀) (**FIGs. 27A-27D** and **FIGs. 28A-28H**). The top three antagonists identified were CD117-6, CD117-7, and CD117-14.

[00303] To further evaluate the antibodies discovered during the screens, 21 clones were selected for detailed characterization and were analyzed for target binding kinetics by a Carterra SPR instrument. The binding kinetics of the anti-CD117 antibodies for human CD117, cynomolgus monkey CD117, and murine CD117 are shown in **FIG. 29A-29B**.

[00304] CD117 epitope binning was also evaluated using classical epitope binning with CD117. Table 7 shows the epitope bins for the anti-CD117 antibodies. For comparison, four prior art antibodies were also epitope binned and found to bind a distinct epitope from the anti-CD117 antibodies provided herein.

Table 7. CD117 epitope bins

Bin1	Bin 2
CD117-1	CD117-9
CD117-2	
CD117-3	
CD117-5	
CD117-7	Bin 3
CD117-10	Prior art Ab1
CD117-11	Prior art Ab2
CD117-12	Prior art Ab3
CD117-13	Prior art Ab4
CD117-14	
CD117-15	
CD117-17	
CD117-18	
CD117-19	
CD117-20	

[00305] Example 6. SIGLEC-8 Antibody Efficacy in Mouse Asthma Model

[0001] Ovalbumin (OVA) + Al(OH)₃ Induced Asthma Mouse Model: OVA + Al(OH)₃ was injected intraperitoneally on days 0, 7, and 14 during the sensitization phase of asthma induction, followed by intranasal dosing with 2% OVA for 30 min daily on days 22 – 25, during the challenge phase. Six different test groups were assessed, as summarized in Table 8, with 8 animals per group.

Table 8. Experimental Design

Group No.	Test Material	Dose Level	Dose Regimen	Total No. of Doses	Route	Number of animals
1	Isotype Control	10 mg/kg	BIW	2	IP	8
2	Positive control	10 mg/kg	BIW	2	IP	8
3	SIGLEC-8-33	10 mg/kg	BIW	2	IP	8
4	SIBLEC8-40	10 mg/kg	BIW	2	IP	8
5	SIGLEC-8-55	10 mg/kg	BIW	2	IP	8
6	SIGLEC-8-61	10 mg/kg	BIW	2	IP	8

BIW = twice/week (twice weekly); IP = intraperitoneal injection

[00306] Mice (n=8/group) were injected with SIGLEC-8 antibodies or control on days 21 and 24 according to the dosing regimen in Table 6. Number of leucocytes, eosinophils, and proportion of eosinophils to CD45⁺ cells from bronchoalveolar lavage fluid (BALF) was assessed. OVA/HDM-specific IgE/total IgE in serum was also detected. The results are shown in **Figures 30-40**.

[00307] The frequency of mCD45⁺ cells in live cells is shown in FIG. 30A and the number of mCD45⁺ cells per milliliter BALF is shown in FIG. 30B. SIGLEC-8-55 administration resulted in significantly higher mCD45⁺ cell percentage in live cells compared to the isotype control group. Every SIGLEC-8 antibody group (and the positive control) resulted in significantly lower mCD45⁺ cells/mL BALF than the isotype control group.

[00308] The frequency of mCD3⁺ cells in mCD45⁺ is shown in FIG. 31A, and the number of mCD3⁺ cells per milliliter BALF is shown in FIG. 31B. SIGLEC-8-33 administration resulted in significantly higher mCD3⁺ cell percentage in mCD45⁺ cells compared to the isotype control group. Administration of SIGLEC-55 or SIGLEC-61 resulted in significantly lower mCD3⁺ cells/mL BALF than the isotype control group.

[00309] The frequency of mCD3⁻ cells in mCD45⁺ is shown in FIG. 32A, and the number of mCD3⁻ cells per milliliter BALF is shown in FIG. 32B. SIGLEC-8-33 administration resulted in significantly lower mCD3⁻ cell percentage of CD45⁺ cells compared to isotype control, and all

SIGLEC-8 antibody groups except SIGLEC-8-55 resulted in significantly lower mCD3- cells/mL compared to isotype control.

[00310] The frequency of NK cells in mCD3- is shown in FIG. 33A and the number of NK cells per milliliter BALF is shown in FIG. 33B. All SIGLEC-8 antibodies resulted in significantly lower NK cells/mL of BALF compared to isotype control.

[00311] The frequency of Siglec-F+ cells in mCD3- is shown in FIG. 34A and the number of Siglec-F+ cells per ml of BALF is shown in FIG. 34B. Administration of SIGLEC-8-33 resulted in significantly lower level of Siglec-F+ cell percentage in CD3- cells compared to isotype control, while all of the SIGLEC 8 antibodies except SIGLEC-8-55 resulted in significantly lower Siglec-F+ cells/mL BALF compared to isotype control.

[00312] Serum IgE Levels were evaluated by ELISA and are shown in FIG. 35. Administration of SIGLEC-8 antibodies did not significantly reduce anti-OVA IgE level in mice.

[00313] The frequency of mCD19+ cells in mCD3- is shown in FIG. 36A and the number of mCD19+ cells per milliliter BALF is shown in FIG. 36B. No significant differences were observed between the SIGLEC-8 antibody groups and the isotype control.

[00314] The frequency of mCD11b+ cells in CD3- cells is shown in FIG. 37A and the number of mCD11b+ cells is shown in FIG. 37B. Administration of SIGLEC-8-33 resulted in significantly higher percentages of mCD11b+ cells compared to isotype control. SIGLEC-8-55 and SIGLEC-8-61 administration resulted in significantly lower mCD11b+ cells/mL BALF than isotype control.

[00315] The frequency of macrophages (F4/80+) cells in mCD11b+ cells is shown in FIG. 38A and the number of macrophages (F4/80+) cells is shown in FIG. 38B. Administration of SIGLEC-8-55 or SIGLEC-8-61 resulted in significantly higher percentages of macrophages in mCD11b+ cells compared to isotype control.

[00316] The frequency of mCD11c+ cells in mCD45+ cells is shown in FIG. 39A and the number of mCD11c+ cells is shown in FIG. 39B. No significant differences were observed between the SIGLEC-8 antibody groups and the isotype control.

[00317] The frequency of macrophages (F4/80+) cells in mCD11c+ cells is shown in FIG. 40A and the number of macrophages (F4/80+) mCD11c+ cells is shown in FIG. 40B. Administration of SIGLEC-8-40, SIGLEC-8-55, or SIGLEC-8-61 resulted in significantly higher percentages of macrophages in mCD11c+ cells than the isotype control.

[00318] Example 7. Exemplary Sequences

[00319] Sequences for SIGLEC-8 immunoglobulins are seen in **Table 9**. Sequences for CD117 immunoglobulins are seen in **Table 10**.

Table 9. SIGLEC-8 sequences

Variable Heavy Chain CDR1 (HCDR1)		
SEQ ID NO:	Description	Amino Acid Sequence
1	SIGLEC-8-1	GFTFSNFP
2	SIGLEC-8-2	GFTFSKHA
3	SIGLEC-8-3	GFTFSTYD
4	SIGLEC-8-4	GFSFSSDA
5	SIGLEC-8-6	GFSFSSYG
6	SIGLEC-8-7	GFTFSNHA
7	SIGLEC-8-8	GFTFNYYA
8	SIGLEC-8-9	GFTFSSYA
9	SIGLEC-8-10	GFTFNYYA
10	SIGLEC-8-11	GLTFSNYD
11	SIGLEC-8-13	GFTFSSYD
12	SIGLEC-8-14	GFSFSNHA
13	SIGLEC-8-15	GFTFSTYT
14	SIGLEC-8-16	GFTFSDYG
15	SIGLEC-8-17	GFPFSNYA
16	SIGLEC-8-19	GFTFRTYD
17	SIGLEC-8-20	GFTFSSFD
18	SIGLEC-8-23	GLTFSSYA
19	SIGLEC-8-24	GFTFSSTA
20	SIGLEC-8-25	GFTFSKYA
21	SIGLEC-8-27	GFTFSNHV
22	SIGLEC-8-28	GSPFSNYA
23	SIGLEC-8-29	GFTFSRHA
24	SIGLEC-8-30	GFTFSHYA
25	SIGLEC-8-31	GFTFSTDA
26	SIGLEC-8-32	GFTLSSYV
27	SIGLEC-8-33	GFAFSDYA
28	SIGLEC-8-34	GFTFSRHA
29	SIGLEC-8-38	GFTFSPYA
30	SIGLEC-8-39	GFTFSRYG
31	SIGLEC-8-40	GFTFSFFD
32	SIGLEC-8-43	GFTFSSYA
33	SIGLEC-8-44	GFTISSSA
34	SIGLEC-8-45	GFTFSSGA
35	SIGLEC-8-46	GLTFSRYA
36	SIGLEC-8-47	GFTFSTHA
37	SIGLEC-8-48	GFNFRSYA
38	SIGLEC-8-49	GFTFSTYA
39	SIGLEC-8-50	GFTLSNYA
40	SIGLEC-8-51	GFTFPRYG
41	SIGLEC-8-52	GFTFRSYV
42	SIGLEC-8-53	GFTFSSSA
43	SIGLEC-8-54	GFTFNYYA
44	SIGLEC-8-55	GFTFDDYA
45	SIGLEC-8-56	GLTFSSSA
46	SIGLEC-8-57	GFAFSRYA
47	SIGLEC-8-58	GFTFRTSA
48	SIGLEC-8-59	GFTFTSYA
49	SIGLEC-8-60	GFTLSNYA
50	SIGLEC-8-61	GFTFSSSA
Variable Heavy Chain CDR2 (HCDR2)		
SEQ ID NO:	Description	Amino Acid Sequence
51	SIGLEC-8-1	ISGTGSST

52	SIGLEC-8-2	ISGSGART
53	SIGLEC-8-3	IGGSGRST
54	SIGLEC-8-4	ISGGGSA
55	SIGLEC-8-6	ISGSGGGT
56	SIGLEC-8-7	ISGSAAST
57	SIGLEC-8-8	ISGSGGTT
58	SIGLEC-8-9	ISGSGGST
59	SIGLEC-8-10	ISGSGSSP
60	SIGLEC-8-11	ISTSGGGSGGST
61	SIGLEC-8-13	ISGSGVGT
62	SIGLEC-8-14	ISGSSGST
63	SIGLEC-8-15	ISGSGDDT
64	SIGLEC-8-16	ISGSGATT
65	SIGLEC-8-17	ISASGSST
66	SIGLEC-8-19	ISGGGGST
67	SIGLEC-8-20	ISGGGGST
68	SIGLEC-8-23	ISGSGVGT
69	SIGLEC-8-24	ISGTGGST
70	SIGLEC-8-25	ISGSGGTT
71	SIGLEC-8-27	ISGSGAST
72	SIGLEC-8-28	ISGGGAST
73	SIGLEC-8-29	ISSSGDNT
74	SIGLEC-8-30	ISGSGDIT
75	SIGLEC-8-31	VSGSGAST
76	SIGLEC-8-32	ISGSGATT
77	SIGLEC-8-33	ITGSGDYT
78	SIGLEC-8-34	ISGSGYST
79	SIGLEC-8-38	IGGSGGST
80	SIGLEC-8-39	TSGSGGTT
81	SIGLEC-8-40	ISSETGRRT
82	SIGLEC-8-43	ISGSGGST
83	SIGLEC-8-44	ISGGGGTT
84	SIGLEC-8-45	ISGSGAST
85	SIGLEC-8-46	VSGSGVST
86	SIGLEC-8-47	ISGSGDIT
87	SIGLEC-8-48	ISGSGGSA
88	SIGLEC-8-49	ISASGGST
89	SIGLEC-8-50	VSGSGAST
90	SIGLEC-8-51	TSGSGGTT
91	SIGLEC-8-52	ISLGGGST
92	SIGLEC-8-53	ISDSGGST
93	SIGLEC-8-54	ISGSGSSP
94	SIGLEC-8-55	ISGSGGST
95	SIGLEC-8-56	ISGYGGST
96	SIGLEC-8-57	ISGSGGRT
97	SIGLEC-8-58	VSGSGSST
98	SIGLEC-8-59	ISGSGGSA
99	SIGLEC-8-60	VSGSGAST
100	SIGLEC-8-61	ISESGGST
Variable Heavy Chain CDR3 (HCDR3)		
SEQ ID NO:	Description	Amino Acid Sequence
101	SIGLEC-8-1	VREGRYFYAMDV
102	SIGLEC-8-2	ARQSRGGSLGMDV
103	SIGLEC-8-3	ARGSASAWFAFDY
104	SIGLEC-8-4	AREGASNYAAFDI
105	SIGLEC-8-6	AREESGKYLSLDH
106	SIGLEC-8-7	ARDLLALPYAFDI
107	SIGLEC-8-8	ARRGGWYSFDI

108	SIGLEC-8-9	ARVGYDSSGYYYIGSRGGH
109	SIGLEC-8-10	ARDQIVAMDV
110	SIGLEC-8-11	AREANNYYYGMDV
111	SIGLEC-8-13	SKDVRWSPGGMDV
112	SIGLEC-8-14	AREGRVAAFYDS
113	SIGLEC-8-15	TRAGEQHHYYGMDV
114	SIGLEC-8-16	AREGGSTYYSLDY
115	SIGLEC-8-17	AREDSGKYLSLDY
116	SIGLEC-8-19	ARDSSYRWFSMDV
117	SIGLEC-8-20	AREDGSGSYSMDV
118	SIGLEC-8-23	AKHTSSSWYPLDY
119	SIGLEC-8-24	ARESDYDYFGMDV
120	SIGLEC-8-25	VRAGLVGYDFDI
121	SIGLEC-8-27	ARAPIAVAGTADH
122	SIGLEC-8-28	AREKDNSWFGMDV
123	SIGLEC-8-29	ARIHRNGHAFDI
124	SIGLEC-8-30	AKATYFYDSSGYRRATYFDY
125	SIGLEC-8-31	AREDSGKYLSLDY
126	SIGLEC-8-32	AREVAGIFYDY
127	SIGLEC-8-33	ARDTGGMVDV
128	SIGLEC-8-34	ARENGQYYYGMDV
129	SIGLEC-8-38	ARDYGGYYFDY
130	SIGLEC-8-39	ARVGGSGWYPNDY
131	SIGLEC-8-40	ATAEDEQGYDY
132	SIGLEC-8-43	ARTESGGNDHDY
133	SIGLEC-8-44	AREGAGYYYGMDV
134	SIGLEC-8-45	AREGSSSWNAFDI
135	SIGLEC-8-46	ARARGGSSRYYYGMDV
136	SIGLEC-8-47	ARQSRGGSLGMDV
137	SIGLEC-8-48	AREGYNWAVDY
138	SIGLEC-8-49	AKSGGADYYYGMDV
139	SIGLEC-8-50	AREDSGKYLSLDY
140	SIGLEC-8-51	ARDESSGWYPKDY
141	SIGLEC-8-52	AREESGKYLSLDH
142	SIGLEC-8-53	AREESGKYLSLDH
143	SIGLEC-8-54	ARDQIVAMDV
144	SIGLEC-8-55	AKYRRYDSGLGGFDY
145	SIGLEC-8-56	AREAGYYYGMDV
146	SIGLEC-8-57	ARQSRGGSLGMDV
147	SIGLEC-8-58	AKEGSYYYGMDV
148	SIGLEC-8-59	ARDTVGYGMDV
149	SIGLEC-8-60	ARENSGKYLSLDY
150	SIGLEC-8-61	AREGGDYYYGIDV
Variable Heavy Chain		
SEQ ID NO:	Description	Amino Acid Sequence
151	SIGLEC-8-1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNFPMSWVRQAPGKGLEWVSS ISGTGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVREG RYFYYAMDVWGQGTLLTVSS
152	SIGLEC-8-2	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKHMSWVRQAPGKGLEWVS GISGSGARTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQ SRGGSGLGMDVWGQGTLLTVSS
153	SIGLEC-8-3	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYDMTWVRQAPGKGLEWVSS IGGSGRSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGS ASAWFAFDYWGQGTLLTVSS
154	SIGLEC-8-4	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSDAMSWVRQAPGKGLEWVSG ISGGGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG ASNYAAFDIWGQGTLLTVSS

155	SIGLEC-8-6	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYGMSWVRQAPGKGLEWVST ISGSGGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREE SGKYLSDLHWGQGLTVTVSS
156	SIGLEC-8-7	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNHAMAWVRQAPGKGLEWVS GISGSAASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD LLALPYAFDIWGQGLTVTVSS
157	SIGLEC-8-8	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYALSWVRQAPGKGLEWVS GISGSGGTTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARR GGWYSFDIWGQGLTVTVSS
158	SIGLEC-8-9	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVS AISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARV GYYDSSGYYYIGSRGGHWGQGLTVTVSS
159	SIGLEC-8-10	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMAWVRQAPGKGLEWVS AISGSGSPYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD QIVAMDVWGQGLTVTVSS
160	SIGLEC-8-11	EVQLLESGGGLVQPGGSLRLSCAASGLTFSNYDMSWVRQAPGKGLEWVS AISTSGGGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYY CAREANNYYYGMDVWGQGLTVTVSS
161	SIGLEC-8-13	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMNWVRQAPGKGLEWVS AISGSGVGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCSKD VRWSPGGMDVWGQGLTVTVSS
162	SIGLEC-8-14	EVQLLESGGGLVQPGGSLRLSCAASGFSFSNHAMTWVRQAPGKGLEWVS GISGSSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE GRVAAYFDSWGQGLTVTVSS
163	SIGLEC-8-15	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYTMNWVRQAPGKGLEWVS VISGSGDDTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRA GEQHYYGMDVWGQGLTVTVSS
164	SIGLEC-8-16	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYGMSWVRQAPGKGLEWVL AISGSGATTYYADSVKGRFTISRDN SKNTLYLQMDSLRAEDTAVYYCARE GGSTYYSLDYWGQGLTVTVSS
165	SIGLEC-8-17	EVQLLESGGGLVQPGGSLRLSCAASGFPFSNYAMGWVRQAPGKGLEWVS GISASGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE DSGKYLSDLDYWGQGLTVTVSS
166	SIGLEC-8-19	EVQLLESGGGLVQPGGSLRLSCAASGFTFRTYDMSWVRQAPGKGLEWVS AISGGGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SSYRWFSMDVWGQGLTVTVSS
167	SIGLEC-8-20	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFDMTWVRQAPGKGLEWVSS ISGGGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARED GSGSYSMDVWGQGLTVTVSS
168	SIGLEC-8-23	EVQLLESGGGLVQPGGSLRLSCAASGLTFSSYAMSWVRQAPGKGLEWVS AISGSGVGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKH TSSSWYPLDYWGQGLTVTVSS
169	SIGLEC-8-24	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSTAMSWVRQAPGKGLEWVSA ISGTGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARES DYDYFGMDVWGQGLTVTVSS
170	SIGLEC-8-25	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYAMDWVRQAPGKGLEWVS DISGSGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRA GLVGYDFDIWGQGLTVTVSS
171	SIGLEC-8-27	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNHVMSWVRQAPGKGLEWVS AISGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARA PIAVAGTADHWGQGLTVTVSS
172	SIGLEC-8-28	EVQLLESGGGLVQPGGSLRLSCAASGSPFSNYAMSWVRQAPGKGLEWVSS ISGGGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREK DNSWFGMDVWGQGLTVTVSS
173	SIGLEC-8-29	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRHAMTWVRQAPGKGLEWVS AISSSGDNTYYVDSVKGRYTISRDN SKNTLYLQMNSLRAEDTAVYYCARI HRNGHAFDIWGQGLTVTVSS
174	SIGLEC-8-30	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYALSWVRQAPGKGLEWVSII SGSGDDTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKATY FYDSSGYRRATYFDYWGQGLTVTVSS

175	SIGLEC-8-31	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTDAMSWVRQAPGKGLEWVST VSGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARED SGKYLSLDYWGQGLTVTVSS
176	SIGLEC-8-32	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYVMSWVRQAPGKGLEWVS AISGSGATTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE VAGIFDYWGQGLTVTVSS
177	SIGLEC-8-33	EVQLLESGGGLVQPGGSLRLSCAASGFAFSDYAMSWVRQAPGKGLEWVS AITGSGDYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD TGGMDVWGQGLTVTVSS
178	SIGLEC-8-34	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRHAMGWVRQAPGKGLEWVS SISGSGYSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE NGQYYYGMDVWGQGLTVTVSS
179	SIGLEC-8-38	EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYAMSWVRQAPGKGLEWVS GIGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD YGGYYFDYWGQGLTVTVSS
180	SIGLEC-8-39	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVS ATSGSGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARV GGSGWYPNDYWGQGLTVTVSS
181	SIGLEC-8-40	EVQLLESGGGLVQPGGSLRLSCAASGFTSFDDMMWVRQAPGKGLEWVS QISETGRRTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATA EDEQGYDYWGQGLTVTVSS
182	SIGLEC-8-43	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVS AISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCART ESGGNDHDYWGQGLTVTVSS
183	SIGLEC-8-44	EVQLLESGGGLVQPGGSLRLSCAASGFTISSAMTWVRQAPGKGLEWVSSI SGGGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG AGYYYGMDVWGQGLTVTVSS
184	SIGLEC-8-45	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSGAMSWVRQAPGKGLEWVST ISGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG SSSWNAFDIWGQGLTVTVSS
185	SIGLEC-8-46	EVQLLESGGGLVQPGGSLRLSCAASGLTFSRYAMSWVRQAPGKGLEWVS TVSGSGVSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARA RGGSSRYYYGMDVWGQGLTVTVSS
186	SIGLEC-8-47	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTHAMSWVRQAPGKGLEWVST ISGSGDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQSR GGSLGMDVWGQGLTVTVSS
187	SIGLEC-8-48	EVQLLESGGGLVQPGGSLRLSCAASGFNFRSYAMSWVRQAPGKGLEWVS GISGSGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE GYNWAVDYWGQGLTVTVSS
188	SIGLEC-8-49	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMHWVRQAPGKGLEWVS TISASGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKS GGADYYYYGMDVWGQGLTVTVSS
189	SIGLEC-8-50	EVQLLESGGGLVQPGGSLRLSCAASGFTLSNYAMTWVRQAPGKGLEWVS TVSGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE DSGKYLSLDYWGQGLTVTVSS
190	SIGLEC-8-51	EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYGMSWVRQAPGKGLEWVT ATSGSGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD ESSGWYPKDYWGQGLTVTVSS
191	SIGLEC-8-52	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYVMSWVRQAPGKGLEWVSS ISLGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREES GKYLSLDHWGQGLTVTVSS
192	SIGLEC-8-53	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMA WVRQAPGKGLEWVSE ISDSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREES GKYLSLDHWGQGLTVTVSS
193	SIGLEC-8-54	EVQLLESGGGLVQPGGSLRLSCAASGFTFN NYAMAWVRQAPGKGLEWVS AISGSGSSPYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD QIVAMDVWGQGLTVTVSS
194	SIGLEC-8-55	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVS YISGSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKY RRYDSGLGGFDYWGQGLTVTVSS

195	SIGLEC-8-56	EVQLLESGGGLVQPGGSLRLSCAASGLTFSSSAMS WVRQAPGKGLEWVSA ISGYGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREA GYYYYGMDVWGQGT LVTVSS
196	SIGLEC-8-57	EVQLLESGGGLVQPGGSLRLSCAASGFAFSRYAMS WVRQAPGKGLEWVS GISGSGRTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQ SRGGS LGMDVWGQGT LVTVSS
197	SIGLEC-8-58	EVQLLESGGGLVQPGGSLRLSCAASGFTFRTSAMS WVRQAPGKGLEWVSS VSGSGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEG SYYYYGMDVWGQGT LVTVSS
198	SIGLEC-8-59	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAVSWVRQAPGKGLEWVSS ISGSGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDT VGYGMDVWGQGT LVTVSS
199	SIGLEC-8-60	EVQLLESGGGLVQPGGSLRLSCAASGFTLSNYAMTWVRQAPGKGLEWVS TVSGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE NSGKYLSDYWGQGT LVTVSS
200	SIGLEC-8-61	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMTWVRQAPGKGLEWVTA ISESGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG GDYYYGIDVWGQGT LVTVSS
Variable Light Chain CDR1 (LCDR1)		
SEQ ID NO:	Description	Amino Acid Sequence
201	SIGLEC-8-1	QNIAGY
202	SIGLEC-8-2	QRISSY
203	SIGLEC-8-3	QSIARY
204	SIGLEC-8-4	QSITPY
205	SIGLEC-8-6	QTIRSY
206	SIGLEC-8-7	QSTSSY
207	SIGLEC-8-8	QIISTY
208	SIGLEC-8-9	QTISTY
209	SIGLEC-8-10	QSISSY
210	SIGLEC-8-11	QTISSY
211	SIGLEC-8-13	QSVSIY
212	SIGLEC-8-14	QGISGY
213	SIGLEC-8-15	QTISTS
214	SIGLEC-8-16	QSIGSY
215	SIGLEC-8-17	QSISSH
216	SIGLEC-8-19	QSISTY
217	SIGLEC-8-20	QSIDNY
218	SIGLEC-8-23	QSITTY
219	SIGLEC-8-24	QSVSSY
220	SIGLEC-8-25	ESISSY
221	SIGLEC-8-27	QSIGSD
222	SIGLEC-8-28	QSIDRY
223	SIGLEC-8-29	QSIHTY
224	SIGLEC-8-30	QGISRH
225	SIGLEC-8-31	QSITNY
226	SIGLEC-8-32	QSISTY
227	SIGLEC-8-33	QSIHSY
228	SIGLEC-8-34	QTITTY
229	SIGLEC-8-38	QYISNY
230	SIGLEC-8-39	QSVSRF
231	SIGLEC-8-40	QSINFW
232	SIGLEC-8-43	QSISTH
233	SIGLEC-8-44	QSIGNY
234	SIGLEC-8-45	QTIAN Y
235	SIGLEC-8-46	QTIDKY
236	SIGLEC-8-47	QTISRY
237	SIGLEC-8-48	QSIGSF
238	SIGLEC-8-49	QSIGYY
239	SIGLEC-8-50	QSIGSY

240	SIGLEC-8-51	QSVSRF
241	SIGLEC-8-52	QSVSNF
242	SIGLEC-8-53	QTIINY
243	SIGLEC-8-54	QSISSY
244	SIGLEC-8-55	RSIDTY
245	SIGLEC-8-56	QKITSY
246	SIGLEC-8-57	QSIGSY
247	SIGLEC-8-58	QTIGRY
248	SIGLEC-8-59	QTISGY
249	SIGLEC-8-60	QNIASY
250	SIGLEC-8-61	QSINRY
Variable Light Chain CDR2 (LCDR2)		
SEQ ID NO:	Description	Amino Acid Sequence
251	SIGLEC-8-1	AAS
252	SIGLEC-8-2	GAS
253	SIGLEC-8-3	GAS
254	SIGLEC-8-4	ATS
255	SIGLEC-8-6	AAS
256	SIGLEC-8-7	AVS
257	SIGLEC-8-8	SAS
258	SIGLEC-8-9	DAS
259	SIGLEC-8-10	SAS
260	SIGLEC-8-11	AAS
261	SIGLEC-8-13	ATS
262	SIGLEC-8-14	GAS
263	SIGLEC-8-15	GAS
264	SIGLEC-8-16	ATS
265	SIGLEC-8-17	AAS
266	SIGLEC-8-19	GAS
267	SIGLEC-8-20	AAS
268	SIGLEC-8-23	AAS
269	SIGLEC-8-24	GAS
270	SIGLEC-8-25	GAS
271	SIGLEC-8-27	GAS
272	SIGLEC-8-28	GAS
273	SIGLEC-8-29	GAS
274	SIGLEC-8-30	AES
275	SIGLEC-8-31	ASS
276	SIGLEC-8-32	AAS
277	SIGLEC-8-33	AAS
278	SIGLEC-8-34	AAS
279	SIGLEC-8-38	ATS
280	SIGLEC-8-39	GAS
281	SIGLEC-8-40	GTT
282	SIGLEC-8-43	DAS
283	SIGLEC-8-44	AAS
284	SIGLEC-8-45	AAS
285	SIGLEC-8-46	GAS
286	SIGLEC-8-47	AAS
287	SIGLEC-8-48	GAS
288	SIGLEC-8-49	GTS
289	SIGLEC-8-50	SAS
290	SIGLEC-8-51	GAS
291	SIGLEC-8-52	AAS
292	SIGLEC-8-53	GAS
293	SIGLEC-8-54	DAS
294	SIGLEC-8-55	DAS
295	SIGLEC-8-56	AAS

296	SIGLEC-8-57	GSS
297	SIGLEC-8-58	GAS
298	SIGLEC-8-59	SAS
299	SIGLEC-8-60	ATS
300	SIGLEC-8-61	GAS
Variable Light Chain CDR3 (LCDR3)		
SEQ ID NO:	Description	Amino Acid Sequence
301	SIGLEC-8-1	QQSYSTPLA
302	SIGLEC-8-2	QESYSTPFT
303	SIGLEC-8-3	QQSYRTSYT
304	SIGLEC-8-4	QQSHSSPLT
305	SIGLEC-8-6	QQSYTTPIT
306	SIGLEC-8-7	QQSYSVPLT
307	SIGLEC-8-8	QQSFSAPDT
308	SIGLEC-8-9	QQNYITPNT
309	SIGLEC-8-10	QQSYGTPLT
310	SIGLEC-8-11	QQSSSTPLT
311	SIGLEC-8-13	QQSHSTPYT
312	SIGLEC-8-14	QQSYTTPIT
313	SIGLEC-8-15	RQSYSTPIT
314	SIGLEC-8-16	QQSYKTPYT
315	SIGLEC-8-17	QQSYNTPPT
316	SIGLEC-8-19	QQTyrTPLT
317	SIGLEC-8-20	QQSYKTPVT
318	SIGLEC-8-23	QQSHTTPLT
319	SIGLEC-8-24	QQSYSVPVT
320	SIGLEC-8-25	QQSYSPIT
321	SIGLEC-8-27	QQTFTNTPLT
322	SIGLEC-8-28	QQTYSTPIT
323	SIGLEC-8-29	QQSYSTPLL
324	SIGLEC-8-30	QQTyTLPYT
325	SIGLEC-8-31	QQSYITPLT
326	SIGLEC-8-32	QQSYDTPLT
327	SIGLEC-8-33	QQSYITPYS
328	SIGLEC-8-34	QQSYSTPLS
329	SIGLEC-8-38	QQGYSPVWT
330	SIGLEC-8-39	QQSYTTPHT
331	SIGLEC-8-40	QQTATWPFT
332	SIGLEC-8-43	QH
333	SIGLEC-8-44	QQSYSTPLS
334	SIGLEC-8-45	QQSYNTPIT
335	SIGLEC-8-46	QQSYTTPT
336	SIGLEC-8-47	QQSFATPYT
337	SIGLEC-8-48	QQTYSTPRS
338	SIGLEC-8-49	QQSYSTPLN
339	SIGLEC-8-50	QQTYNTPIT
340	SIGLEC-8-51	QQSYTTPHT
341	SIGLEC-8-52	QQTYSTPIT
342	SIGLEC-8-53	QQSYVTPPT
343	SIGLEC-8-54	QQSYRTPIT
344	SIGLEC-8-55	QQSYVTPPT
345	SIGLEC-8-56	QQSYGTPLT
346	SIGLEC-8-57	QQSYSPVWT
347	SIGLEC-8-58	QQSYKTPVT
348	SIGLEC-8-59	QQGYSTPLT
349	SIGLEC-8-60	QQTynIPLT
350	SIGLEC-8-61	QQSFTTPLT
Variable Light Chain		

SEQ ID NO:	Description	Amino Acid Sequence
351	SIGLEC-8-1	DIQMTQSPSSLSASVGDRVTITCRASQNIAGYLNWYQQKPGKAPKLLIYAA SNLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLAFGGGTK VEIK
352	SIGLEC-8-2	DIQMTQSPSSLSASVGDRVTITCRASQRISSYLNWYQQKPGKAPKLLIYGAS ILQTGVPSRFSGSGSGTDFTLTINSLQPEDFATYYCQESYSTPFTFGGGTKVE IK
353	SIGLEC-8-3	DIQMTQSPSSLSASVGDRVTITCRASQSIARYLNWYQQKPGKAPKLLIYGA SDLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRTSYTFGGGTK VEIK
354	SIGLEC-8-4	DIQMTQSPSSLSASVEDRVTITCRAGQSITPYLNWYQQKPGKAPKLLIYATS SLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSPLTFGGGTKV EIK
355	SIGLEC-8-6	DIQMTQSPSSLSASVGDRVTITCRASQTIRSYLNWYQQKPGKAPKLLIYAA SSLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTTPITFGGGTKV EIK
356	SIGLEC-8-7	DIQMTQSPSSLSASVGDRVTITCRASQSTSSYLSWYQQKPGKAPKLLIYAVS TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSVPLTFGGGTKV EIK
357	SIGLEC-8-8	DIQMTQSPSTLSAYVGDRVTITCRASQIISTYLNWYQQKPGKAPKLLIYSAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSAPDTFGGGTKV EIK
358	SIGLEC-8-9	DIQMTQSPSSLSASVGDRVTITCRTSTISTYLNWYQQKPGKAPKLLIYDAS DLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPNTFGGGTKV EIK
359	SIGLEC-8-10	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYSAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYGTPLTFGGGTKV EIK
360	SIGLEC-8-11	DIQMTQSPSSLSASVGDRVTITCRASQTISSYLHWYQQKPGKAPKLLIYAAS SLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPLTFGGGTKVE IK
361	SIGLEC-8-13	DIQMTQSPSSLSASVGDRVTITCRASQSVSIYLNWYQQKPGKAPKLLIYATS NLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSTPYTFGGGTKV EIK
362	SIGLEC-8-14	DIQMTQSPSSLSASVGDRVTITCRASQGISGYLNWYQQKPGKAPKLLIYGA SRLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTTPITFGGGTK VEIK
363	SIGLEC-8-15	DIQMTQSPSSLSASVGDRVTITCRASQTISTSLNWYQQKPGKAPKLLIYGAS TLQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPITFGGGTKVE IK
364	SIGLEC-8-16	DIQMTQSPSSLSASVGDRVTITCRTSQSIGSYLNWYQQKPGKAPKLLIYATS NLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPYTFGGGTKV EIK
365	SIGLEC-8-17	DIQMTQSPSSLSASVGDRVTITCRTSQSISSHLNWYQQKPGKAPKLLIYAAS SLQPGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPTFGGGTKV EIK
366	SIGLEC-8-19	DIQMTQSPSSLSASVGDRVTITCRAGQSISTYLNWYQQKPGKAPKLLIYGA SKLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYRTPLTFGGGTK VEIK
367	SIGLEC-8-20	DIQMTQSPSSLSASVGDRVTITCRASQSIDNYLHWYQQKPGKAPKLLIYAA SNLEGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPVTFGGGTK VEIK
368	SIGLEC-8-23	DIQMTQSPSSLSASVGDRVTITCRSSQSITTYLNWYQQKPGKAPKLLIYAAS NL YSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHTTPLTFGGGTKV EIK
369	SIGLEC-8-24	DIQMTQSPSSLSASVGDRVTITCRASQSVSSYVNWYQQKPGKAPKLLIYGA SSLQDGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSVPTFGGGTK VEIK

370	SIGLEC-8-25	DIQMTQSPSSLSASVGDRVITITCRASESISSYLNWYQQKPGKAPKLLIYGAS ILQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSPITFGGGTKVE IK
371	SIGLEC-8-27	DIQMTQSPSSLSASVGDRVITITCRASQSIGSDLNWYQQKPGKAPKLLIYGA SRLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTFTNTPLTFGGGGTK VEIK
372	SIGLEC-8-28	DIQMTQSPSSLSASVGDRVITITCRASQSIDRYLNWYQQKPGKAPKLLIYGA STLQTGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYSTPITFGGGTKV EIK
373	SIGLEC-8-29	DIQMTQSPSSLSASVGDRVITITCRASQSIHTYLNWYQQKPGKAPKLLIYGA STLRSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPLLTFGGGGTK VEIK
374	SIGLEC-8-30	DIQMTQSPSSLSASVGDRVITITCRASQGISRHLNWYQQKPGKAPKLLIYAE STLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYTLPYTFGGGGTK VEIK
375	SIGLEC-8-31	DIQMTQSPSSLSASVGDRVITITCRASQSITNYLNWYQQKPGKAPKLLIYASS TLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYITPLTFGGGGTKVE IK
376	SIGLEC-8-32	DIQMTQSPSSLSASVGDRVITITCRSSQSISTYLNWYQQKPGKAPKLLIYAAS YLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYDTPLTFGGGGTKV EIK
377	SIGLEC-8-33	DIQMTQSTSSLSASVGDRVITITCRASQSIHSYLNWYQQKPGKAPILIYAASS LERGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYITPYSFGGGGTKVEI K
378	SIGLEC-8-34	DIQMTQSPSSLSASVGDRVITITCRASQTITTYLNWYQQKPGKAPKLLIYAA SHLQTGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPLSFGGGGTK VEIK
379	SIGLEC-8-38	DIQMTQSPSSLSASVGDRVITITCRASQYISNYLNWYQQKPGKAPKLLIYAT STLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQGYSPWTFGGGGTK VEIK
380	SIGLEC-8-39	DIQMTQSPSSLSASVGDRVITITCRASQSVSRFLNWYQQKPGKAPKLLIYGA STLQTGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYTTPHTFGGGGTK VEIK
381	SIGLEC-8-40	DIQMTQSPSSLSASVGDRVITITCRASQSINFWLRWYQQKPGKAPKLLIYGT TSLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQATWPFTFGQGGTK VEIK
382	SIGLEC-8-43	DIQMTQSPSSLSASVGDRVITINCRASQSISTHLNWYQQKPGKAPKLLIYDA SSLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQHFGGGGTKVEIK
383	SIGLEC-8-44	DIQMTQSPSSLSASVGDRVITITCRASQSIGNYNWYQQKPGKAPKLLIYAA SRLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPLSFGGGGTK VEIK
384	SIGLEC-8-45	DIQMTQSPSSLSASVGDRVITITCRASQTIANYNWYQQKPGKAPKLLIYAA SNLEDGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYNTPTITFGGGTK VEIK
385	SIGLEC-8-46	DIQMTQSPSSLSASVGDRVITITCRASQTIDKYNWYQQKPGKAPKLLIYGA SRLQNGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYTTPTFGGGTKV EIK
386	SIGLEC-8-47	DIQMTQSPSSLSASVGDRVITITCRASQTISRYLNWYQQKPGKAPKLLIYAA SNLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSFATPYTFGGGGTK VEIK
387	SIGLEC-8-48	DIQMTQSPSSLSASVGDRVITITCRASQSIGFLNWYQQKPGKAPKLLIYGAS ILQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYSTPRSFGGGTKVE IK
388	SIGLEC-8-49	DIQMTQSPSSLSASVGDRVITITCRASQSIGYYLNWYQQKPGKAPKLLIYGT SSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPLNFGGGGTK VEIK
389	SIGLEC-8-50	DIQMTQSPSSLSASVGDRVITITCRASQSIGSYLNWYQQKPGKAPKLLIYSAS SLQTGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYNTPTITFGGGTKV EIK

390	SIGLEC-8-51	DIQMTQSPSSLSASVGDRVITITCRASQSVSRFLNWWYQQKPGKAPKLLIYGA SNLEGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYTTPHTFGGGTK VEIK
391	SIGLEC-8-52	DIQMTQSPSSLSASVGDRVITITCRASQSVSNFLNWWYQQKPGKAPKLLIYAA SNLEGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYSTPITFGGGTK VEIK
392	SIGLEC-8-53	DIQMTQSPSSLSASVGDRVITITCRASQTIINYNWWYQQKPGKAPKLLIYGAS NVQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYVTPPTFGGGTKV EIK
393	SIGLEC-8-54	DIQMTQSPSSLSASVGDRVITITCRGSQSISSYNWWYQQKPGKAPKLLIYDAS SLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYRTPITFGGGTKVE IK
394	SIGLEC-8-55	DIQMTQSPSSLSASVGDRVITITCRASRSIDTYLNWWYQQKPGKAPKLLIYDA STLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYVTPPTFGGGTK VEIK
395	SIGLEC-8-56	DIQMTQSPSSLSASVGDRVITITCRASQKITSYNWWYQQKPGKAPKLLIYAA SSLHDGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYGTPLTFGGGK VEIK
396	SIGLEC-8-57	DIQMTQSPSSLSASVGDRVITITCRASQSIGYNWWYQQKPGKAPKLLIYGSS TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSPWTFGGGK EIK
397	SIGLEC-8-58	DIQMTQSPSSLSASVGDRVITITCRASQTIGRYLNWWYQQKPGKAPKLLIYGA SSLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYKTPVTFGGGK VEIK
398	SIGLEC-8-59	DIQMTQSPSSLSASVGDRVITITCRASQTISGYLSWWYQQKPGKAPKLLIYAS RLHSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQGYSTPLTFGGGK EIK
399	SIGLEC-8-60	DIQMTQSPSSLSASVGDRVITITCRASQNIASYNWWYQQKPGKAPKLLIYAT SDLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYNIPLTFGGGK VEIK
400	SIGLEC-8-61	DIQMTQSPSSLSASVGDRVITITCRAGQSINRYLNWWYQQKPGKAPKLLIYGA SNLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSFTTPLTFGGGK VEIK
Variable Light Chain-Variable Heavy Chain		
SEQ ID NO:	Description	Amino Acid Sequence
401	SIGLEC-8-1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNFPMSWVRQAPGKGLEWVSS ISGTGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVREG RYFYYAMDVWGQGTLLTVSSDIQMTQSPSSLSASVGDRVITITCRASQNI GYLNWWYQQKPGKAPKLLIYAASNLHTGVPSRFSGSGSGTDFTLTISLQPE DFATYYCQQSYSTPLAFGGGKVEIK
402	SIGLEC-8-2	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKHAMS WVRQAPGKGLEWVS GISGSGARTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQ SRGGS LGMDVWGQGTLLTVSSDIQMTQSPSSLSASVGDRVITITCRASQRI SYLNWWYQQKPGKAPKLLIYGASILQTGVPSRFSGSGSGTDFTLTINS LQPE DFATYYCQESYSTPFTFGGGKVEIK
403	SIGLEC-8-3	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYDMTWVRQAPGKGLEWVSS IGGSGRSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGS ASAWFAFDYWGQGTLLTVSSDIQMTQSPSSLSASVGDRVITITCRASQSIAR YLNWWYQQKPGKAPKLLIYGASDLQSGVPSRFSGSGSGTDFTLTISLQPE DFATYYCQQSYRTSYTFGGGKVEIK
404	SIGLEC-8-4	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSDAMS WVRQAPGKGLEWVSG ISGGGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG ASNYYAFDIWGQGTLLTVSSDIQMTQSPSSLSASVEDRVITITCRAGQSITPY LNWWYQQKPGKAPKLLIYATSSLHSGVPSRFSGSGSGTDFTLTISLQPE DFATYYCQQSHSSPLTFGGGKVEIK
405	SIGLEC-8-6	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYGMS WVRQAPGKGLEWVST ISGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREE SGKYLSLDHWGQGTLLTVSSDIQMTQSPSSLSASVGDRVITITCRASQTIRS YLNWWYQQKPGKAPKLLIYAASLHTGVPSRFSGSGSGTDFTLTISLQPE DFATYYCQQSYTTPITFGGGKVEIK

406	SIGLEC-8-7	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNHAMAWVRQAPGKGLEWVS GISGSAASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD LLALPYAFDIWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSTSS YLSWYQQKPGKAPKLLIYAVSTLQSGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYSVPLTFGGGKVEIK
407	SIGLEC-8-8	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYALSWVRQAPGKGLEWVS GISGSGGTTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARR GGWYSFDIWGQGT LVT VSSDIQMTQSPSTLSAYVGDRVTITCRASQIISTYL NWXQQKPGKAPKLLIYASSSLQSGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQSFSAPDTFGGGKVEIK
408	SIGLEC-8-9	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVS AISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARV GYYDSSGYYYIGSRGGHWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITC RTSQTISTYLNWYQQKPGKAPKLLIYDASDLQSGVPSRFSGSGSGTDFTLT ISLQPEDFATYYCQQNYITPNTFGGGKVEIK
409	SIGLEC-8-10	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMAWVRQAPGKGLEWVS AISGSGSSPYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD QIVAMDVWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYASSSLQSGVPSRFSGSGSGTDFTLTISLQPEDFAT YYCQQSYGTPLTFGGGKVEIK
410	SIGLEC-8-11	EVQLLESGGGLVQPGGSLRLSCAASGLTFSNYDMSWVRQAPGKGLEWVS AISTSGGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYY CAREANNYYYGMDVWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRA SQTISYLNWYQQKPGKAPKLLIYAASSLHTGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQSSSTPLTFGGGKVEIK
411	SIGLEC-8-13	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMNWVRQAPGKGLEWVS AISGSGVGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCSKD VRWSPGGMDVWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSV SIYLNWYQQKPGKAPKLLIYATSNLHSGVPSRFSGSGSGTDFTLTISLQPE DFATYYCQQSHSTPYTFGGGKVEIK
412	SIGLEC-8-14	EVQLLESGGGLVQPGGSLRLSCAASGFSSFNHAMTWVRQAPGKGLEWVS GISGSSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE GRVAAYFDSWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQGISG YLNWYQQKPGKAPKLLIYGASRLQNGVPSRFSGSGSGTDFTLTISLQPED FATYYCQQSYTPTTFGGGKVEIK
413	SIGLEC-8-15	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYTMNWVRQAPGKGLEWVS VISGSGDDTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRA GEQHYYGMDVWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQT ISTSLNWYQQKPGKAPKLLIYGASTLQRGVPSRFSGSGSGTDFTLTISLQPE DFATYYCRQSYSTPITFGGGKVEIK
414	SIGLEC-8-16	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYGMSWVRQAPGKGLEWVL AISGSGATTYYADSVKGRFTISRDN SKNTLYLQMDSLRAEDTAVYYCARE GGSTYYSLDYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRTSQSIG YLNWYQQKPGKAPKLLIYATSNLHSGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYKTPYTFGGGKVEIK
415	SIGLEC-8-17	EVQLLESGGGLVQPGGSLRLSCAASGFPPFSNYAMGWVRQAPGKGLEWVS GISASGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE DSGKYLSDYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRTSQSISS HLNWYQQKPGKAPKLLIYAASSLQPGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYNTPTFGGGKVEIK
416	SIGLEC-8-19	EVQLLESGGGLVQPGGSLRLSCAASGFTFRTYDMSWVRQAPGKGLEWVS AISGGGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SSYRWFSMDVWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRAGQSIS TYLNWYQQKPGKAPKLLIYGASKLQSGVPSRFSGSGSGTDFTLTISLQPED FATYYCQQT YRTPLTFGGGKVEIK
417	SIGLEC-8-20	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFDMTWVRQAPGKGLEWVSS ISGGGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARED GSGSYSMDVWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSIDN YLHWYQQKPGKAPKLLIYAASNLEGGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQSYKTPVTFGGGKVEIK

418	SIGLEC-8-23	EVQLLESGGGLVQPGGSLRLSCAASGLTFSSYAMSWVRQAPGKGLEWVS AISGSGVGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKH TSSSWYPLDYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRSSQSITT YLNWYQQKPGKAPKLLIY AASNLYSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSHTTPLTFGGG TKVEIK
419	SIGLEC-8-24	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSTAMSWVRQAPGKGLEWVSA ISGTGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARES DYDYFGMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASQSVS SYVNWYQQKPGKAPKLLIYGASSLQDGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQQSYSPVPTFGGG TKVEIK
420	SIGLEC-8-25	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYAMDWVRQAPGKGLEWVS DISGSGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRA GLVGYDFDIWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASESISSY LNWYQQKPGKAPKLLIYGASILQGGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSYSPITFGGG TKVEIK
421	SIGLEC-8-27	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNHVMSWVRQAPGKGLEWVS AISGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARA PIAVAGTADHWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASQSIGS DLNWYQQKPGKAPKLLIYGASRLQESGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQTFTNTPLTFGGG TKVEIK
422	SIGLEC-8-28	EVQLLESGGGLVQPGGSLRLSCAASGSPFSNYAMSWVRQAPGKGLEWVSS ISGGGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREK DNSWFGMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASQSID RYLNWYQQKPGKAPKLLIYGASTLQTGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQTYSTPITFGGG TKVEIK
423	SIGLEC-8-29	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRHAMTWVRQAPGKGLEWVS AISSGDN TYYVDSVKGRYTISRDN SKNTLYLQMNSLRAEDTAVYYCARI HRNGHAFDIWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASQSIHT YLNWYQQKPGKAPKLLIYGASTLRSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSYSTPLTFGGG TKVEIK
424	SIGLEC-8-30	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYALSWVRQAPGKGLEWVSII SGSGDTTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKATY FYDSSGYRRATYFDYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRA SQISRHLNWYQQKPGKAPKLLIYAESTLQSGVPSRFSGSGSGTDFTLTIS LQPEDFATYYCQQTYTLPYTFGGG TKVEIK
425	SIGLEC-8-31	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTDAMSWVRQAPGKGLEWVST VSGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARED SGKYLSLDYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASQSITN YLNWYQQKPGKAPKLLIYASSTLESGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSYITPLTFGGG TKVEIK
426	SIGLEC-8-32	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYVMSWVRQAPGKGLEWVS AISGSGATTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE VAGIFDYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRSSQSISTYLN WYQQKPGKAPKLLIYAASYLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYDTPLTFGGG TKVEIK
427	SIGLEC-8-33	EVQLLESGGGLVQPGGSLRLSCAASGFAFSDYAMSWVRQAPGKGLEWVS AITGSGDYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD TGGMDVWGQGT LVTVSSDIQMTQSTSSLSASVGDRVITICRASQSIHSYLN WYQQKPGKAPILY AASSLERGVPSRFSGSGSGTDFTLTISSLQPEDFATYY CQQSYITPYSFGGG TKVEIK
428	SIGLEC-8-34	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRHAMGWVRQAPGKGLEWVS SISGSGYSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE NGQYYYGMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASQTI TTYLNWYQQKPGKAPKLLIYAASHLQTGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQQSYSTPLSFGGG TKVEIK
429	SIGLEC-8-38	EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYAMSWVRQAPGKGLEWVS GIGGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD YGGYYFDYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITICRASQYISNY LNWYQQKPGKAPKLLIYATSTLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQGYSPVPTFGGG TKVEIK

430	SIGLEC-8-39	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVS ATSGSGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARV GGSGWYPNDYWGGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQSV SRFLN WYQQKPGKAPKLLIYGASTLQTGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQQSYTTPHTFGGGTKVEIK
431	SIGLEC-8-40	EVQLLESGGGLVQPGGSLRLSCAASGFTFSFFDMMWVRQAPGKGLEWVS QISETGRRTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATA EDEQGYDYWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQSINFV LRWYQQKPGKAPKLLIYGTTSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQTATWPFTFGQGTKVEIK
432	SIGLEC-8-43	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVS AISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCART ESGNDHDYWGQTLVTVSSDIQMTQSPSSLSASVGDRVITINCRASQSIST HLN WYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQHFGGGTKVEIK
433	SIGLEC-8-44	EVQLLESGGGLVQPGGSLRLSCAASGFTISSAMTWVRQAPGKGLEWVSSI SGGGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG AGYYYGMDVWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQSIG NYLN WYQQKPGKAPKLLIYAASRLQGGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQQSYSTPLSFGGGTKVEIK
434	SIGLEC-8-45	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSGAMSWVRQAPGKGLEWVST ISGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG SSSWNAFDIWGGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQTIAN YLN WYQQKPGKAPKLLIYAASNLEDGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSYNTPIITFGGGTKVEIK
435	SIGLEC-8-46	EVQLLESGGGLVQPGGSLRLSCAASGLTFSRYAMSWVRQAPGKGLEWVS TVSGSGVSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARA RGGSSRYYYGMDVWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRAS QTIDKYN WYQQKPGKAPKLLIYGASRLQNGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYTTPHTFGGGTKVEIK
436	SIGLEC-8-47	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTHAMSWVRQAPGKGLEWVST ISGSGDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQSR GGSLGMDVWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQTISRY LN WYQQKPGKAPKLLIYAASNLVSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSFATPYTFGGGTKVEIK
437	SIGLEC-8-48	EVQLLESGGGLVQPGGSLRLSCAASGFNFRSYAMSWVRQAPGKGLEWVS GISGSGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE GYNWAVDYWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQSIGF LN WYQQKPGKAPKLLIYGASILQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQTYSTPRSFSGGGTKVEIK
438	SIGLEC-8-49	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMHWVRQAPGKGLEWVS TISASGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKS GGADYYYYGMDVWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRAS QSIGYYLN WYQQKPGKAPKLLIYGTTSSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSTPLNFGGGTKVEIK
439	SIGLEC-8-50	EVQLLESGGGLVQPGGSLRLSCAASGFTLSNYAMTWVRQAPGKGLEWVS TVSGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE DSGKYLSLDYWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQSIG SYLN WYQQKPGKAPKLLIYASSLQTGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQTYNTPIITFGGGTKVEIK
440	SIGLEC-8-51	EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYGMSWVRQAPGKGLEWVT ATSGSGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD ESSGWYPKDYWGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQSVS RFLN WYQQKPGKAPKLLIYGASNLEGGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYTTPHTFGGGTKVEIK
441	SIGLEC-8-52	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYVMSWVRQAPGKGLEWVSS ISLGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREES GKYLSLDHWGGQTLVTVSSDIQMTQSPSSLSASVGDRVITICRASQSVSNF LN WYQQKPGKAPKLLIYAASNLEGGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQTYSTPIITFGGGTKVEIK

442	SIGLEC-8-53	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMAWVRQAPGKGLEWVSE ISDSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREES GKYLSDLHWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRASQTII NYL NWYQQKPGKAPKLLIYGASNVQSGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSYVTPPTFGGGTKVEIK
443	SIGLEC-8-54	EVQLLESGGGLVQPGGSLRLSCAASGFTFN NYAMAWVRQAPGKGLEWVS AISGSGSSPYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD QIVAMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRGSQSISSYL NWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSYRTPITFGGGTKVEIK
444	SIGLEC-8-55	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVS YISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKY RRYDSGLGGFDYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRASRS IDTYLNWYQQKPGKAPKLLIYDASTLQGGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYVTPPTFGGGTKVEIK
445	SIGLEC-8-56	EVQLLESGGGLVQPGGSLRLSCAASGLTFSSSAMS WVRQAPGKGLEWVSA ISGYGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREA GYYYYGMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRASQKIT SYLNWYQQKPGKAPKLLIYAASSLHDGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYGTPLTFGGG TKVEIK
446	SIGLEC-8-57	EVQLLESGGGLVQPGGSLRLSCAASGFAFSRYAMSWVRQAPGKGLEWVS GISGSGGRTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQ SRGGS LGMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRASQSI GYLNWYQQKPGKAPKLLIYGSS TLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYSPWTFGGG TKVEIK
447	SIGLEC-8-58	EVQLLESGGGLVQPGGSLRLSCAASGFTFR TSAMSWVRQAPGKGLEWVSS VSGSGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEG SYYYYGMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRASQTIG RYLNWYQQKPGKAPKLLIYGASSLYSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYKTPVTFGGG TKVEIK
448	SIGLEC-8-59	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAVSWVRQAPGKGLEWVSS ISGSGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDT VGYGMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRASQTISGYL SWYQQKPGKAPKLLIYASRLHSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQGYSTPLTFGGG TKVEIK
449	SIGLEC-8-60	EVQLLESGGGLVQPGGSLRLSCAASGFTLSNYAMTWVRQAPGKGLEWVS TVSGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE NSGKYLSDYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRASQNI SYLNWYQQKPGKAPKLLIYATSDLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQT YNIPLTFGGG TKVEIK
450	SIGLEC-8-61	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMTWVRQAPGKGLEWVTA ISESGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREG GDYYYGIDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVITITCRAGQSINR YLNWYQQKPGKAPKLLIYGASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSFTPLTFGGG TKVEIK
SIGLEC-8 Heavy Chains		
SEQ ID NO:	Description	Amino Acid Sequence
650	SIGLEC-8-1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNFPMSWVRQAPGKGLEWVSSISGT GSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVREGRYFY YAM DVWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT VDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYK CKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVM HEALHNHYTQKSLSLSPG
651	SIGLEC-8-2	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKHAMS WVRQAPGKGLEWVSGISGS GARTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQSRGGS LGM DVWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW

		NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
652	SIGLEC-8-3	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYDMTWVRQAPGKGLEWVSSIGGS GRSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGSASAWFAF DYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
653	SIGLEC-8-4	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSDAMSWVRQAPGKGLEWVSGISGG GGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGASNYAAF DIWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
654	SIGLEC-8-6	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYGMSWVRQAPGKGLEWVSTISGS GGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREESGKYL SL DHWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
655	SIGLEC-8-7	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNHAMAWVRQAPGKGLEWVSGISG SAASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLALPYAF DIWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
656	SIGLEC-8-8	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYALSWVRQAPGKGLEWVSGISGS GGTTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGGWYSFDI WGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPG
657	SIGLEC-8-9	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVGYDSSGY YYIGSRGGHWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPG

658	SIGLEC-8-10	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMAWVRQAPGKGLEWVSAISG SGSSPYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQIVAMDV WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPG
659	SIGLEC-8-11	EVQLLESGGGLVQPGGSLRLSCAASGLTFSNYDMSWVRQAPGKGLEWVSAISTS GGGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREANNY YYGMDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG
660	SIGLEC-8-13	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLEWVSAISGS GVGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKSDVRWSPGG MDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
661	SIGLEC-8-14	EVQLLESGGGLVQPGGSLRLSCAASGFSFSNHAMTWVRQAPGKGLEWVSGISGS SGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGRVAAYFD SWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPG
662	SIGLEC-8-15	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYTMNWVRQAPGKGLEWVSVISGS GDDTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRAGEQHYY GMDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG
663	SIGLEC-8-16	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYGMSWVRQAPGKGLEWVLAISG SGATTYYADSVKGRFTISRDN SKNTLYLQMDSLRAEDTAVYYCAREGGSTYY LDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
664	SIGLEC-8-17	EVQLLESGGGLVQPGGSLRLSCAASGFPSNYAMGWVRQAPGKGLEWVSGISA SGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREDSGKYL DYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS

		DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
665	SIGLEC-8-19	EVQLLESGGGLVQPGGSLRLSCAASGFTFRITYDMSWVRQAPGKGLEWVSAISG GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDSSYRWFS MDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
666	SIGLEC-8-20	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFDMTWVRQAPGKGLEWVSSISGG GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREDGSGSYSM DVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
667	SIGLEC-8-23	EVQLLESGGGLVQPGGSLRLSCAASGLTFSSYAMSWVRQAPGKGLEWVSAISGS GVGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHTSSSWYPL DYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
668	SIGLEC-8-24	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSTAMSWVRQAPGKGLEWVSAISGT GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARESDYDYFGM DVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
669	SIGLEC-8-25	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYAMDWVRQAPGKGLEWVSDISG SGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRAGLVGYDF DIWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
670	SIGLEC-8-27	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNHVMSWVRQAPGKGLEWVSAISGS GASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARAPIAVAGTA DHWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
671	SIGLEC-8-28	EVQLLESGGGLVQPGGSLRLSCAASGSPFSNYAMSWVRQAPGKGLEWVSSISGG GASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREKDNSWFG MDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH

		HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVM HEALHNHYTQKSLSLSPG
672	SIGLEC-8-29	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRHAMTWVRQAPGKGLEWVSAISS GDNTYYVDSVKGRYTISRDN SKNTLYLQMNSLRAEDTAVYYCARIHRNGHAFD IWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEA LHNHYTQKSLSLSPG
673	SIGLEC-8-30	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYALSWVRQAPGKGLEWVSIISGS GDTTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKATYFYDSSG YRRATYFDYWGGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCFSVMHEALHNHYTQKSLSLSPG
674	SIGLEC-8-31	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTDAMSWVRQAPGKGLEWVSTVSG SGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREDSGKYL DYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVM HEALHNHYTQKSLSLSPG
675	SIGLEC-8-32	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYVMSWVRQAPGKGLEWVSAISGS GATTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREVAGIFDYW GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEAL HNHYTQKSLSLSPG
676	SIGLEC-8-33	EVQLLESGGGLVQPGGSLRLSCAASGFAFSDYAMSWVRQAPGKGLEWVSAITG SGDYTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDTGGM DVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEA LHNHYTQKSLSLSPG
677	SIGLEC-8-34	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRHAMGWVRQAPGKGLEWVSSISGS GYSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARENGQYYG MDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVM HEALHNHYTQKSLSLSPG
678	SIGLEC-8-38	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYAMSWVRQAPGKGLEWVSGIGGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDYGGYYFDY WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS

		GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPG
679	SIGLEC-8-39	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVSATSG SGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVGGSGWYP NDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
680	SIGLEC-8-40	EVQLLESGGGLVQPGGSLRLSCAASGFTFSFFDMMWVRQAPGKGLEWVSQISET GRRTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATAEDEQGYDY WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPG
681	SIGLEC-8-43	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARTESGGNDHD YWQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPG
682	SIGLEC-8-44	EVQLLESGGGLVQPGGSLRLSCAASGFTISSAMTWVRQAPGKGLEWVSSISGG GGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGAGYYYG MDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
683	SIGLEC-8-45	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSGAMSWVRQAPGKGLEWVSTISGS GASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGSSSWNAF DIWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
684	SIGLEC-8-46	EVQLLESGGGLVQPGGSLRLSCAASGLTFSRYAMSWVRQAPGKGLEWVSTVSG SGVSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARARGGSSRY YYGMDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG

685	SIGLEC-8-47	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTHAMS WVRQAPGKGLEWVSTISGS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQSRGGSLGM DVWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTK VDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV HEALHNHYTQKSLSLSPG
686	SIGLEC-8-48	EVQLLESGGGLVQPGGSLRLSCAASGFNFRSY AMSWVRQAPGKGLEWVSGISG SGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGYNWAV DYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTK VDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV HEALHNHYTQKSLSLSPG
687	SIGLEC-8-49	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMH WVRQAPGKGLEWVSTISAS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSGGADYYYY GMDVWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT V SWNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTK V DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPG
688	SIGLEC-8-50	EVQLLESGGGLVQPGGSLRLSCAASGFTLSNYAMT WVRQAPGKGLEWVSTVSG SGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREDSGKYLSL DYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTK VDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV HEALHNHYTQKSLSLSPG
689	SIGLEC-8-51	EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYGM SWVRQAPGKGLEWVTATSG SGGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDSSGWYP KDYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT V WNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTK V KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV HEALHNHYTQKSLSLSPG
690	SIGLEC-8-52	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYVMS WVRQAPGKGLEWVSSISLS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREESGKYLSL DHWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTK VDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV HEALHNHYTQKSLSLSPG
691	SIGLEC-8-53	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMAWVRQAPGKGLEWVSEISDS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREESGKYLSL DHWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTK VDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS

		DIAVEWESNGQPENNYKTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
692	SIGLEC-8-54	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMAWVRQAPGKGLEWVSAISG SGSSPYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQIVAMDV WGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPG
693	SIGLEC-8-55	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSYISG SGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYRRYDSGL GGFDYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
694	SIGLEC-8-56	EVQLLESGGGLVQPGGSLRLSCAASGLTFSSAMSWVRQAPGKGLEWVSAISGY GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREAGYYYG MDVWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT V WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
695	SIGLEC-8-57	EVQLLESGGGLVQPGGSLRLSCAASGFAFSRYAMSWVRQAPGKGLEWVSGISG SGGRTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQSRGGSGLG MDVWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT V WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
696	SIGLEC-8-58	EVQLLESGGGLVQPGGSLRLSCAASGFTFRTSAMSWVRQAPGKGLEWVSSVSG SGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEGSYYYG MDVWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT V WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
697	SIGLEC-8-59	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAVSWVRQAPGKGLEWVSSISGS GGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDTVGYGMD VWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPG
698	SIGLEC-8-60	EVQLLESGGGLVQPGGSLRLSCAASGFTLSNYAMTWVRQAPGKGLEWVSTVSG SGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARENSGKYLSL DYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH

		EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
699	SIGLEC-8-61	EVQLLESQGGGLVQPGGSLRLSCAASGFTFSSSAMTWVRQAPGKGLEWVTAISESGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAREGGDYYYGIDVWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
SIGLEC-8 Light Chains		
SEQ ID NO:	Description	Amino Acid Sequence
700	SIGLEC-8-1	DIQMTQSPSSLSASVGDRVTITCRASQNIAGYLNWYQQKPGKAPKLLIYAASNLHTGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLAFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
701	SIGLEC-8-2	DIQMTQSPSSLSASVGDRVTITCRASQRISSYLNWYQQKPGKAPKLLIYGASILQTVPSRFGSGSGTDFTLTISSLQPEDFATYYCQESYSTPFTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
702	SIGLEC-8-3	DIQMTQSPSSLSASVGDRVTITCRASQSIARYLNWYQQKPGKAPKLLIYGASDLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYRTSYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
703	SIGLEC-8-4	DIQMTQSPSSLSASVEDRVTITCRAGQSITPYLNWYQQKPGKAPKLLIYATSSLHSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSHSSPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
704	SIGLEC-8-6	DIQMTQSPSSLSASVGDRVTITCRASQTIRSYLNWYQQKPGKAPKLLIYAASSLHTGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYTTPITFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
705	SIGLEC-8-7	DIQMTQSPSSLSASVGDRVTITCRASQSTSSYLSWYQQKPGKAPKLLIYAVSTLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSVPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
706	SIGLEC-8-8	DIQMTQSPSTLSAYVGDRVTITCRASQIISTYLNWYQQKPGKAPKLLIYSASSLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSFAPDTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
707	SIGLEC-8-9	DIQMTQSPSSLSASVGDRVTITCRSTQISTYLNWYQQKPGKAPKLLIYDASDLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQNYITPNTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
708	SIGLEC-8-10	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYSASSLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYGTPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
709	SIGLEC-8-11	DIQMTQSPSSLSASVGDRVTITCRASQTSIYLNWYQQKPGKAPKLLIYAASSLHTGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
710	SIGLEC-8-13	DIQMTQSPSSLSASVGDRVTITCRASQSVSIYLNWYQQKPGKAPKLLIYATSNLHSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSHSTPYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

711	SIGLEC-8-14	DIQMTQSPSSLSASVGDRVTTITCRASQGISGYLNWYQQKPGKAPKLLIYGASRLQ NGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYTTPITFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
712	SIGLEC-8-15	DIQMTQSPSSLSASVGDRVTTITCRASQTISTSLNWYQQKPGKAPKLLIYGASTLQ RGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPITFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
713	SIGLEC-8-16	DIQMTQSPSSLSASVGDRVTTITCRSQTISQSYLNWYQQKPGKAPKLLIYATSNLH SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPYTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
714	SIGLEC-8-17	DIQMTQSPSSLSASVGDRVTTITCRSQTISSHLNWYQQKPGKAPKLLIYAASSLQ GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPTFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
715	SIGLEC-8-19	DIQMTQSPSSLSASVGDRVTTITCRAGQSISTYLNWYQQKPGKAPKLLIYGASKLQ SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYRTPFTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
716	SIGLEC-8-20	DIQMTQSPSSLSASVGDRVTTITCRASQSIDNYLHWYQQKPGKAPKLLIYAASNLE GGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPVTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
717	SIGLEC-8-23	DIQMTQSPSSLSASVGDRVTTITCRSSQSITTYLNWYQQKPGKAPKLLIYAASNLY SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSHHTPLTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
718	SIGLEC-8-24	DIQMTQSPSSLSASVGDRVTTITCRASQSVSSYVNWYQQKPGKAPKLLIYGASSLQ DGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSPVTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
719	SIGLEC-8-25	DIQMTQSPSSLSASVGDRVTTITCRASESISYLNWYQQKPGKAPKLLIYGASILQG GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSPITFGGGKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
720	SIGLEC-8-27	DIQMTQSPSSLSASVGDRVTTITCRASQSIGSDLNWYQQKPGKAPKLLIYGASRLQ SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTFTNPTLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
721	SIGLEC-8-28	DIQMTQSPSSLSASVGDRVTTITCRASQSIDRYLNWYQQKPGKAPKLLIYGASTLQ TGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPITFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
722	SIGLEC-8-29	DIQMTQSPSSLSASVGDRVTTITCRASQSIHTYLNWYQQKPGKAPKLLIYGASTLR SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
723	SIGLEC-8-30	DIQMTQSPSSLSASVGDRVTTITCRASQGISRHLNWYQQKPGKAPKLLIYAESTLQ SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYTLPYTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
724	SIGLEC-8-31	DIQMTQSPSSLSASVGDRVTTITCRASQISITNYLNWYQQKPGKAPKLLIYASSTLES GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYITPLTFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
725	SIGLEC-8-32	DIQMTQSPSSLSASVGDRVTTITCRSSQSISTYLNWYQQKPGKAPKLLIYAASYLQS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

726	SIGLEC-8-33	DIQMTQSTSSLSASVGDRVTITCRASQSIHSYLNWYQQKPGKAPILIYAASSLERG VPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYITPYSGGGGKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTEQDS KDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
727	SIGLEC-8-34	DIQMTQSPSSLSASVGDRVTITCRASQTITTYLNWYQQKPGKAPKLLIYAASHLQ TGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLSFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
728	SIGLEC-8-38	DIQMTQSPSSLSASVGDRVTITCRASQYISNYLNWYQQKPGKAPKLLIYATSTLE SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQGYSPWTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVT EQDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
729	SIGLEC-8-39	DIQMTQSPSSLSASVGDRVTITCRASQSVSRFLNWYQQKPGKAPKLLIYGASTLQ TGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYTTPHTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
730	SIGLEC-8-40	DIQMTQSPSSLSASVGDRVTITCRASQSINFWLRWYQQKPGKAPKLLIYGTTSLQ SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTATWPFTFGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
731	SIGLEC-8-43	DIQMTQSPSSLSASVGDRVTINCRASQSISTHLNWYQQKPGKAPKLLIYDASSLES GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQHFGGGKVEIKRTVAAPSVFIFPP SDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTEQDSKDYSL STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
732	SIGLEC-8-44	DIQMTQSPSSLSASVGDRVTITCRASQSIGNYLNWYQQKPGKAPKLLIYAASRLQ GGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLSFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
733	SIGLEC-8-45	DIQMTQSPSSLSASVGDRVTITCRASQTIANYNWYQQKPGKAPKLLIYAASNLE DGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPTITFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
734	SIGLEC-8-46	DIQMTQSPSSLSASVGDRVTITCRASQTIDKYNWYQQKPGKAPKLLIYGASRLQ NGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYTTPTFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTEQ DSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
735	SIGLEC-8-47	DIQMTQSPSSLSASVGDRVTITCRASQTISRYLNWYQQKPGKAPKLLIYAASNLY SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSFATPYTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
736	SIGLEC-8-48	DIQMTQSPSSLSASVGDRVTITCRASQSIGFLNWYQQKPGKAPKLLIYGASILQS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPRSGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTEQ DSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
737	SIGLEC-8-49	DIQMTQSPSSLSASVGDRVTITCRASQSIGYYLNWYQQKPGKAPKLLIYGTSLLQ SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLNFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
738	SIGLEC-8-50	DIQMTQSPSSLSASVGDRVTITCRASQSIGSYLNWYQQKPGKAPKLLIYSASSLQT GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYNTPTITFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTEQ DSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
739	SIGLEC-8-51	DIQMTQSPSSLSASVGDRVTITCRASQSVSRFLNWYQQKPGKAPKLLIYGASNLE GGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYTTPHTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC
740	SIGLEC-8-52	DIQMTQSPSSLSASVGDRVTITCRASQSVSNFLNWYQQKPGKAPKLLIYAASNLE GGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPTITFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKQVQWKVDNALQSGNSQESVTE QDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC

741	SIGLEC-8-53	DIQMTQSPSSLSASVGDRVTTTCRASQTIINYLNWYQQKPGKAPKLLIYGASNVO SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYVTPPTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
742	SIGLEC-8-54	DIQMTQSPSSLSASVGDRVTTTCRGSQSISSYLNWYQQKPGKAPKLLIYDASSLQS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPTFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
743	SIGLEC-8-55	DIQMTQSPSSLSASVGDRVTTTCRASRSIDTYLNWYQQKPGKAPKLLIYDASTLQ GGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYVTPPTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
744	SIGLEC-8-56	DIQMTQSPSSLSASVGDRVTTTCRASQKITSYLNWYQQKPGKAPKLLIYAASSLH DGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYGTPLTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
745	SIGLEC-8-57	DIQMTQSPSSLSASVGDRVTTTCRASQISGYLNWYQQKPGKAPKLLIYGSSTLQS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSPWTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
746	SIGLEC-8-58	DIQMTQSPSSLSASVGDRVTTTCRASQTIGRYLNWYQQKPGKAPKLLIYGASSLY SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPVTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
747	SIGLEC-8-59	DIQMTQSPSSLSASVGDRVTTTCRASQTISGYLSWYQQKPGKAPKLLIYSASRLHS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPLTFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
748	SIGLEC-8-60	DIQMTQSPSSLSASVGDRVTTTCRASQNIASYLNWYQQKPGKAPKLLIYATSDLQ SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQTYNIPLTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
749	SIGLEC-8-61	DIQMTQSPSSLSASVGDRVTTTCRAGQSINRYLNWYQQKPGKAPKLLIYGASNLQ SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSFTTPLTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Table 10. CD117 Sequences

Variable Heavy Chain CDR1 (HCDR1)		
SEQ ID NO:	Description	Amino Acid Sequence
451	CD117-1	GFTLTSYA
452	CD117-2	GFSFGSYA
453	CD117-3	GFSFSSYA
454	CD117-4	GFTFSRSA
455	CD117-5	GFIFTNYA
456	CD117-6	GFTFSAYA
457	CD117-7	GFTFSDYA
458	CD117-8	GFTLTSYA
459	CD117-9	GFSFTNYA
460	CD117-10	GFIFSSYA
461	CD117-11	GFTFGNFA
462	CD117-12	GITFSSYA
463	CD117-13	GFTLTSYA
464	CD117-14	GFTFSDYA
465	CD117-15	GFTFSDYP
466	CD117-16	GFTFGNYA
467	CD117-17	GFTFSDYP

468	CD117-18	GFTFSDYS
469	CD117-19	GFSFSSYA
470	CD117-20	GFTFSSDA
471	CD117-21	GFTFSTYA
Variable Heavy Chain CDR2 (HCDR2)		
SEQ ID NO:	Description	Amino Acid Sequence
472	CD117-1	ISGSGGYT
473	CD117-2	ISGSGGTT
474	CD117-3	ISGTGGNT
475	CD117-4	ISAGGGNT
476	CD117-5	IGGSGSST
477	CD117-6	ISSSGGST
478	CD117-7	IGGSGGSA
479	CD117-8	ISGSGGYT
480	CD117-9	ISGSGGST
481	CD117-10	ISGRGGNT
482	CD117-11	ISGSGGNT
483	CD117-12	ISSSGTGT
484	CD117-13	ISGSGGYT
485	CD117-14	IGGSGGSA
486	CD117-15	IGGSGGDT
487	CD117-16	ITGS
488	CD117-17	IGGSGGDT
489	CD117-18	ITGSGGNT
490	CD117-19	ISGTGGNT
491	CD117-20	ISGSGGYT
492	CD117-21	ISGG
Variable Heavy Chain CDR3 (HCDR3)		
SEQ ID NO:	Description	Amino Acid Sequence
493	CD117-1	ARDSGYDRGLDY
494	CD117-2	ARDPDDYGDYYFDY
495	CD117-3	ARRNDFWSDAFDI
496	CD117-4	AREQDLWSGTFDY
497	CD117-5	VKGGYSYGDSFDF
498	CD117-6	ARVSRGYPRRSDS
499	CD117-7	ARGFDSTDGVDY
500	CD117-8	ARDSGYDRGLDY
501	CD117-9	ARGSGSYFGFDF
502	CD117-10	AKMMDDFYDAFNM
503	CD117-11	ARGDGVNGFDY
504	CD117-12	ARERAPKDFGSSGYSFDY
505	CD117-13	ARDSGYDRGLDY
506	CD117-14	ARGFDSTDGVDY
507	CD117-15	ARGAYDGEFDFY
508	CD117-16	AKEPWAGATTAPFDY
509	CD117-17	ARGAYDGEFDFY
510	CD117-18	ARSNYEQDVFDI
511	CD117-19	ARRNDFWSDAFDI
512	CD117-20	ARSGNVVGDGMDV
513	CD117-21	ANFGDYTSGYYPVDY
Variable Heavy Chain		
SEQ ID NO:	Description	Amino Acid Sequence
514	CD117-1	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGL DYWGQGTLVTVSS

515	CD117-2	EVQLLESGVGLVQPGGSLRLSCAASGFSFGSYAMSWVRQAPGKGLEWVSSISGS GGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPDDYGDY YFDYWGQGT LTVSS
516	CD117-3	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVSAISGT GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRNDFWSDA FDIWGQGT LTVSS
517	CD117-4	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRSAMSWVRQAPGKGLEWVSAISA GGGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREQDLWSG TFDYWGQGT LTVSS
518	CD117-5	EVQLLESGGGLVQPGGSLRLSCAASGFIFTNYAMSWVRQAPGKGLEWVSAIGG SGSSTYYADSVKGRFTVSRDN SKNTLYLQMNSLRAEDTAVYYCVKGGYSYGD SFDYWGQGT LTVSS
519	CD117-6	EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYALTWVRQAPGKGLEWVSAISS GGSTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVSRGYPRRS DSWGQGT LTVSS
520	CD117-7	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSGIGG SGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGFDSTDGV DYWGQGT LTVSS
521	CD117-8	EVQLLESGGGLVQPGGSLRLSCAASGFTLT SYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGL DYWGQGT LTVSS
522	CD117-9	EVQLLESGGGLVQPGGSLRLSCAASGFSFTNYAMSWVRQAPGKGLEWVSSISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGSGSYFGFD FWGQGT LTVSS
523	CD117-10	EVQLLESGGGLVQPGGSLRLSCAASGFISSYAMTWVRQAPGKGLEWVSSISGR GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKMMDDFYDA FNMWGQGT LTVSS
524	CD117-11	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNFAMSWVRQAPGKGLEWVSLISG SGGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGDGVNGF DYWGQGT LTVSS
525	CD117-12	EVQLLESGGGLVQPGGSLRLSCAASGITFSSYAMTWVRQAPGKGLEWVSAISS GTGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARERAPKDFGS SGYSFDYWGQGT LTVSS
526	CD117-13	EVQLLESGGGLVQPGGSLRLSCAASGFTLT SYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGL DYWGQGT LTVSS
527	CD117-14	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSGIGG SGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGFDSTDGV DYWGQGT LTVSS
528	CD117-15	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYPMSWVRQAPGKGLEWVSAIGG SGGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGAYDGEFG DYWGQGT LTVSS
529	CD117-16	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMSWVRQAPGKGLEWVSAITG SYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPWAGATTAPFD YWGQGT LTVSS
530	CD117-17	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYPMSWVRQAPGKGLEWVSAIGG SGGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGAYDGEFG DYWGQGT LTVSS
531	CD117-18	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYSMNWVRQAPGKGLEWVSAITG SGGNTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSNYEQDVF DIWGQGT LTVSS
532	CD117-19	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVSAISGT GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRNDFWSDA FDIWGQGT LTVSS
533	CD117-20	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSDAMNWVRQAPGKGLEWVSGISG SGGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSGNVVDG GMDVWGQGT LTVSS
534	CD117-21	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISG GYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCANFGDYTSGYYPV DYWGQGT LTVSS

Variable Light Chain CDR1 (LCDR1)		
SEQ ID NO:	Description	Amino Acid Sequence
535	CD117-1	QSVRTY
536	CD117-2	QSIGEY
537	CD117-3	QNIYTY
538	CD117-4	QSISSY
539	CD117-5	QSVRNY
540	CD117-6	QGISTY
541	CD117-7	QSIGNY
542	CD117-8	QSVRTY
543	CD117-9	QGIGTY
544	CD117-10	QSIRTY
545	CD117-11	QSIPTY
546	CD117-12	QSIDIY
547	CD117-13	QNIYTY
548	CD117-14	QSVSSY
549	CD117-15	QSIGSY
550	CD117-16	QSVNSIY
551	CD117-17	QTISGY
552	CD117-18	QTIYRY
553	CD117-19	QNIYTY
554	CD117-20	QNIRRY
555	CD117-21	QSISTY
Variable Light Chain CDR2 (LCDR2)		
SEQ ID NO:	Description	Amino Acid Sequence
556	CD117-1	DAS
557	CD117-2	ATS
558	CD117-3	DAS
559	CD117-4	DAS
560	CD117-5	DAS
561	CD117-6	GAS
562	CD117-7	AAS
563	CD117-8	DAS
564	CD117-9	AAS
565	CD117-10	DAS
566	CD117-11	ATS
567	CD117-12	KAS
568	CD117-13	DAS
569	CD117-14	GAS
570	CD117-15	SAS
571	CD117-16	ATS
572	CD117-17	DAS
573	CD117-18	DAS
574	CD117-19	DAS
575	CD117-20	DAS
576	CD117-21	GAS
Variable Light Chain CDR3 (LCDR3)		
SEQ ID NO:	Description	Amino Acid Sequence
577	CD117-1	QQSYSSSIT
578	CD117-2	QQSHTTPYT
579	CD117-3	QQSSSTPYT
580	CD117-4	QQSYKTPWT
581	CD117-5	QQGYSTPWT
582	CD117-6	QQGYSPWT
583	CD117-7	QQGYSTPYT
584	CD117-8	QQSYNTPLA

585	CD117-9	QQSYRPPFT
586	CD117-10	QQSFTTPYT
587	CD117-11	QQTYSTPYT
588	CD117-12	QQSYTVPIT
589	CD117-13	QQSSSTPYT
590	CD117-14	QQSYKTPWT
591	CD117-15	QQTYNTPWT
592	CD117-16	QQSGSSPPYS
593	CD117-17	QQNYRTPFT
594	CD117-18	QQSYSIPIT
595	CD117-19	QQSYSSSIT
596	CD117-20	QQSHHTPLT
597	CD117-21	QQTFNTPRT
Variable Light Chain		
SEQ ID NO:	Description	Amino Acid Sequence
598	CD117-1	DIQMTQSPSSLSASVGDRVTITCRASQSVRTYLNWYQQKPGKAPKLLIYDASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSSITFGGGTKVEIK
599	CD117-2	DIQMTQSPSSLSASVGDRVTITCRASQSIGEYLNWYQQKPGKAPKLLIYATSSLQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHHTPYTFGGGKVEIK
600	CD117-3	DIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKPGKAPKLLIYDASSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPYTFGGGKVEIK
601	CD117-4	DIQMTQSPSSLSASVGDRVTITCRARQSISSYLNWYQQKPGKAPKLLIYDASSLRSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPWTFGGGKVEIK
602	CD117-5	DIQMTQSPSSLSASVGDRVTITCRASQSVRNYLNWYQQKPGKAPKLLIYDASDLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPWTFGGGKVEIK
603	CD117-6	DIQMTQSPSSLSASVGDRVTITCRASQGISYLNWYQQKPGKAPKLLIYGASRLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSPWTFGGGKVEIK
604	CD117-7	DIQMTQSPSSLSASVGDRVTITCRASQSIGNYLNWYQQKPGKAPKLLIYAASDLQTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPYTFGGGKVEIK
605	CD117-8	DIQMTQSPSSLSASVGDRVTITCRASQSVRTYLNWYQQKPGKAPKLLIYDASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPLAFGGGKVEIK
606	CD117-9	DIQMTQSPSSLSASVGDRVTITCRASQGIGTYLNWYQQKPGKAPKLLIYAASSLQPGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRPPFTFGGGKVEIK
607	CD117-10	DIQMTQSPSSLSASVGDRVTITCRASQSIRTYLNWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFTTPYTFGGGKVEIK
608	CD117-11	DIQMTQSPSSLSASVGDRVTITCRASQSIPTYLNWYQQKPGKAPKLLIYATSTLES
609	CD117-12	DIQMTQSPSSLSASVGDRVTITCRASQSIDYLNWYQQKPGKAPKLLIYKASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTVPITFGGGKVEIK
610	CD117-13	DIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKPGKAPKLLIYDASSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPYTFGGGKVEIK
611	CD117-14	DIQMTQSPSSLSASVGDRVTITCQTSQSVSSYLNWYQQKPGKAPKLLIYGASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPWTFGGGKVEIK
612	CD117-15	DIQMTQSPSSLSASVGDRVTITCRTSQSIGSYLNWYQQKPGKAPKLLIYSASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYNTPWTFGGGKVEIK
613	CD117-16	EIVLTQSPGTLSPGERATLSCRASQSVNSIYLAWYQQKPGQAPRLIYATSSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSSPPYSFGQGKVEIK
614	CD117-17	DIQMTQSPSSLSASVGDRVTITCRASQTISGYLNWYQQKPGKAPKLLIYDASTLQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNYRTPFTFGGGKVEIK
615	CD117-18	DIQMTQSPSSLSASVGDRVTITCRASQTIYRYLNWYQQKPGKAPKLLIYDASDLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSIPITFGGGKVEIK
616	CD117-19	DIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKPGKAPKLLIYDASSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSSITFGGGKVEIK
617	CD117-20	DIQMTQSPSSLSASVGDRVTITCRASQNIYRYLNWYQQKPGKAPKLLIYDASTLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHHTPLTFGGGKVEIK
618	CD117-21	DIQMTQSPSSLSASVGDRVTITCRASQISYTYLNWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTFNTPRTFGQGKVEIK
Variable Light Chain-Variable Heavy Chain		

SEQ ID NO:	Description	Amino Acid Sequence
619	CD117-1	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGL DYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSVRTYLNWYQQKP GKAPKLLIYDASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSSIT FGGGTKVEIK
620	CD117-2	EVQLLESGVGLVQPGGSLRLSCAASGFSFGSYAMSWVRQAPGKGLEWVSSISGS GGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPDDYGDY YFDYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSIGEYLNWYQQK PGKAPKLLIYATSSLQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHTTP YTFGGGTKVEIK
621	CD117-3	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVSAISGT GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRNDFWSDA FDIWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKP GKAPKLLIYDASSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPY TFGGGTKVEIK
622	CD117-4	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRSAMSWVRQAPGKGLEWVSAISA GGGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREQDLWSG TFDYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRARQSISSYLNWYQQK PGKAPKLLIYDASSLRSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTP WTFGGGTKVEIK
623	CD117-5	EVQLLESGGGLVQPGGSLRLSCAASGFIFTNYAMSWVRQAPGKGLEWVSAIGG SGSSTYYADSVKGRFTVSRDN SKNTLYLQMNSLRAEDTAVYYCVKGGYSYGD SFDYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSVRNYLNWYQQK PGKAPKLLIYDASDLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSTP WTFGGGTKVEIK
624	CD117-6	EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYALTWVRQAPGKGLEWVSAISS GGSTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVSRGYPRRS DSWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQGISYTYLNWYQQKPG KAPKLLIYGASRLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSPFW TFGGGTKVEIK
625	CD117-7	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSGIGG SGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGFDSTDGV DYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSIGNLYNWYQQKPG KAPKLLIYAASDLQTVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPYT FGGGTKVEIK
626	CD117-8	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGL DYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSVRTYLNWYQQKP GKAPKLLIYDASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPL AFGGGTKVEIK
627	CD117-9	EVQLLESGGGLVQPGGSLRLSCAASGFSFTNYAMSWVRQAPGKGLEWVSSISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGSGSYFGFD FWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQGIGTYLNWYQQKPGK APKLLIYAASSLQPGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRPPFTF GGGTKVEIK
628	CD117-10	EVQLLESGGGLVQPGGSLRLSCAASGFIFSSYAMTWVRQAPGKGLEWVSSISGR GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKMMDDFYDA FNMWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSIRTYLNWYQQKP GKAPKLLIYDASSLESVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFTTPY TFGGGTKVEIK
629	CD117-11	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNFAMSWVRQAPGKGLEWVSLISG SGGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGDGVNGF DYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSIPTYLNWYQQKPG KAPKLLIYATSTLESVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPYT FGGGTKVEIK
630	CD117-12	EVQLLESGGGLVQPGGSLRLSCAASGITFSSYAMTWVRQAPGKGLEWVSAISS GTGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARERAPKDFGS SGYSFDYWGQGT LVT VSSDIQMTQSPSSLSASVGDRVTITCRASQSIDIYLNWYQ

		QKPGKAPKLLIYKASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYT VPITFGGGTKVEIK
631	CD117-13	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGL DYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKPG KAPKLLIYDASSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPYTF GGG TKVEIK
632	CD117-14	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSGIGG SGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGFDSTDGV DYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCQTSQSVSSYLNWYQQKPG KAPKLLIYGASRLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPWT FGG TKVEIK
633	CD117-15	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYPMSWVRQAPGKGLEWVSAIGG SGGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGAYDGEGF DYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCRTSQSIGSYLNWYQQKPG KAPKLLIYSASRLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYNTPWT FGG TKVEIK
634	CD117-16	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMSWVRQAPGKGLEWVSAITG SYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPWAGATTAPFD YWGQGT LVTVSSEIVLTQSPGTLSPGERATLSCRASQSVNSIYLAWYQQKPG QAPRLLIYATSSRATGIPDRFSGSGSGTDFTLTISSELPEDFAVYYCQQSGSSPPYS FGQ G TKVEIK
635	CD117-17	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYPMSWVRQAPGKGLEWVSAIGG SGGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGAYDGEGF DYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCRASQTISGYLNWYQQKPG KAPKLLIYDASTLQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNYRTPFT FGG TKVEIK
636	CD117-18	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYSMNWVRQAPGKGLEWVSAITG SGGNTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSNYEQDVF DIWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCRASQTIYRYLNWYQQKPG KAPKLLIYDASDLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSIPITF GGG TKVEIK
637	CD117-19	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVSAISGT GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRNDFWSDA FDIWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKPG GKAPKLLIYDASSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSSIT FGG TKVEIK
638	CD117-20	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSDAMNWVRQAPGKGLEWVSGISG SGGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSGNVVGD GMDVWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCRASQNIYRYLNWYQQ KPGKAPKLLIYDASTLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHTT PLTFGGG TKVEIK
639	CD117-21	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISG GYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCANFGDYTSGYYPV DYWGQGT LVTVSSDIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPG KAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTFNTPT FGQ G TKVEIK
CD117 Heavy Chains		
SEQ ID NO:	Description	Amino Acid Sequence
750	CD117-1	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGLD YWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVMHE ALHNHYTQKSLSLSPG

751	CD117-2	EVQLLESGVGLVQPGGSLRLSCAASGFSFGSYAMSWVRQAPGKGLEWVSSISGS GGTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPDDYGDYY FDYWGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
752	CD117-3	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVSAISGT GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRNDFWSDAF DIWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
753	CD117-4	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRSAMSWVRQAPGKGLEWVSAISAG GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREQDLWSGTF DYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
754	CD117-5	EVQLLESGGGLVQPGGSLRLSCAASGFIFTNYAMSWVRQAPGKGLEWVSAIGGS GSSTYYADSVKGRFTVSRDN SKNTLYLQMNSLRAEDTAVYYCVKGGYSYGDSF DFWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
755	CD117-6	EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYALTWVRQAPGKGLEWVSAISS GGSTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVSRGYPRRS SWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
756	CD117-7	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSGIGG SGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGFDSTDGV DYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
757	CD117-8	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVSTISGS GGYTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDSGYDRGLD YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG

		AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPG
758	CD117-9	EVQLLESGGGLVQPGGSLRLSCAASGFSFTNYAMSWVRQAPGKGLEWVSSISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGSGSYFGFDF WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPG
759	CD117-10	EVQLLESGGGLVQPGGSLRLSCAASGFISSYAMTWVRQAPGKGLEWVSSISGR GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKMMDDFYDA FNMWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
760	CD117-11	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNFAMSWVRQAPGKGLEWVSLISGS GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGDGVNGFD YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPG
761	CD117-12	EVQLLESGGGLVQPGGSLRLSCAASGITFSSYAMTWVRQAPGKGLEWVSAISS GTGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARERAPKDFGS SGYSFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG
762	CD117-13	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVSTISGS GGYTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SGYDRGLD YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPG
763	CD117-14	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSGIGG SGGSAYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGFDSTDGV DYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG
764	CD117-15	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYPMWVRQAPGKGLEWVSAIGGS GGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGAYDGEFGD YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSHE

		DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHE ALHNHYTQKSLSLSPG
765	CD117-16	EVQLLESGGGLVQPGGSLRLS CAASGFTFGNYAMSWVRQAPGKGLEWVSAITG SYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPWAGATTAPFD YWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHE ALHNHYTQKSLSLSPG
766	CD117-17	EVQLLESGGGLVQPGGSLRLS CAASGFTFSDYPMWVRQAPGKGLEWVSAIGGS GGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGAYDGEGFD YWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHE ALHNHYTQKSLSLSPG
767	CD117-18	EVQLLESGGGLVQPGGSLRLS CAASGFTFSDYS MNWVRQAPGKGLEWVSAITG SGGNTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARS NYEQDVF DIWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVM HEALHNHYTQKSLSLSPG
768	CD117-19	EVQLLESGGGLVQPGGSLRLS CAASGFSFSSYAMSWVRQAPGKGLEWVSAISGT GGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRNDFWSDAF DIWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVM HEALHNHYTQKSLSLSPG
769	CD117-20	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSDAMN WVRQAPGKGLEWVSGISGS GGYTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSGNVVDG MDVWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVM HEALHNHYTQKSLSLSPG
770	CD117-21	EVQLLESGGGLVQPGGSLRLS CAASGFTFSTYAMSWVRQAPGKGLEWVSAISG GYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCANFGDYTS GYYYPV DYWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVM HEALHNHYTQKSLSLSPG
CD117 Light Chains		
SEQ ID NO:	Description	Amino Acid Sequence

771	CD117-1	DIQMTQSPSSLSASVGDRVTTITCRASQSVRTYLNWYQQKPGKAPKLLIYDASTLQ SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSSITFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTEQ DSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
772	CD117-2	DIQMTQSPSSLSASVGDRVTTITCRASQSIGEYLNWYQQKPGKAPKLLIYATSSLQ RGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHHTPYTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
773	CD117-3	DIQMTQSPSSLSASVGDRVTTITCRASQNIYTYLNWYQQKPGKAPKLLIYDASSLH SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPYTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
774	CD117-4	DIQMTQSPSSLSASVGDRVTTITCRARQSISSYLNWYQQKPGKAPKLLIYDASSLRS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPWTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
775	CD117-5	DIQMTQSPSSLSASVGDRVTTITCRASQSVRNYLNWYQQKPGKAPKLLIYDASDL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPWTFGGGKVEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESV TEQDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
776	CD117-6	DIQMTQSPSSLSASVGDRVTTTTCRASQGISTYLNWYQQKPGKAPKLLIYGASRLQ GGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSPWTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVT EQDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
777	CD117-7	DIQMTQSPSSLSASVGDRVTTITCRASQSIGNYNWYQQKPGKAPKLLIYAASDLQ TGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSTPYTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
778	CD117-8	DIQMTQSPSSLSASVGDRVTTITCRASQSVRTYLNWYQQKPGKAPKLLIYDASTLQ SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPLAFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
779	CD117-9	DIQMTQSPSSLSASVGDRVTTITCRASQGIGTYLNWYQQKPGKAPKLLIYAASSLQ PGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRPPFTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
780	CD117-10	DIQMTQSPSSLSASVGDRVTTITCRASQSIRTYLNWYQQKPGKAPKLLIYDASSLES GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFTPYTFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTEQ DSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
781	CD117-11	DIQMTQSPSSLSASVGDRVTTITCRASQSIPTYLNWYQQKPGKAPKLLIYATSTLES GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPYTFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTEQ DSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
782	CD117-12	DIQMTQSPSSLSASVGDRVTTITCRASQSIDIYLNWYQQKPGKAPKLLIYKASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTPITFGGGKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTEQ DSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
783	CD117-13	DIQMTQSPSSLSASVGDRVTTITCRASQNIYTYLNWYQQKPGKAPKLLIYDASSLH SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPYTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
784	CD117-14	DIQMTQSPSSLSASVGDRVTTITCQTSQSVSSYLNWYQQKPGKAPKLLIYGASRL SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYKTPWTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVT EQDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
785	CD117-15	DIQMTQSPSSLSASVGDRVTTITCRSISYLNWYQQKPGKAPKLLIYSASRLS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYNTPWTFGGGKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPPREKAVQWKVDNALQSGNSQESVTE QDSKDDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

786	CD117-16	EIVLTQSPGTLSPGERATLSCRASQSVNSIYLAWYQQKPGQAPRLLIYATSSRA TGIPDRFSGSGSGTDFTLTISLSEPEDFAVYYCQQSGSSPPYSFGQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
787	CD117-17	DIQMTQSPSSLSASVGDRVTITCRASQTISGYLNWYQQKPGKAPKLLIYDASTLQ RGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQNYRTPFTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
788	CD117-18	DIQMTQSPSSLSASVGDRVTITCRASQTIYRYLNWYQQKPGKAPKLLIYDASDLQ SGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSHIPITFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
789	CD117-19	DIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKPGKAPKLLIYDASSLH SGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSSSITFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
790	CD117-20	DIQMTQSPSSLSASVGDRVTITCRASQNIYRYLNWYQQKPGKAPKLLIYDASTLE SGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSHTTPTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
791	CD117-21	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTFNTPRTFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

[00320] While preferred embodiments of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

WHAT IS CLAIMED IS:

1. An antibody or antigen-binding fragment thereof that binds Sialic acid-binding immunoglobulin-like lectin 8 (SIGLEC-8), wherein the antibody or antigen-binding fragment thereof comprises:
 - a) a heavy chain complementary determining region 1 (HCDR1) comprising the amino acid sequence of SEQ ID NO: 1 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 1, a heavy chain complementary determining region 2 (HCDR2) comprising the amino acid sequence of SEQ ID NO: 51 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 51, a heavy chain complementary determining region 3 (HCDR3) comprising the amino acid sequence of SEQ ID NO: 101 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 101, a light chain complementary determining region 1 (LCDR1) comprising the amino acid sequence of SEQ ID NO: 201 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 201, a light chain complementary determining region 2 (LCDR2) comprising the amino acid sequence of SEQ ID NO: 251 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 251, and a light chain complementary determining region 3 (LCDR3) comprising the amino acid sequence of SEQ ID NO: 301 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 301;
 - b) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 2 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 2, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 52 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 52, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 102 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 102, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 202 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 202, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 252 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 252, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 302 or a functional variant

- thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 302;
- c) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 3 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 3, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 53 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 53, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 103 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 103, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 203 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 203, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 253 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 253, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 303 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 303;
- d) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 4 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 4, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 54 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 54, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 104 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 104, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 204 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 204, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 254 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 254, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 304 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 304;
- e) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 5 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 5, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 55 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 55, an HCDR3

- comprising the amino acid sequence of SEQ ID NO: 105 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 105, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 205 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 205, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 255 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 255, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 305 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 305;
- f) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 6 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 6, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 56 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 56, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 106 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 106, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 206 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 206, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 256 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 256, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 306 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 306;
- g) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 7 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 7, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 57 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 57, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 107 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 107, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 207 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 207, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 257 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 257, and an

- LCDR3 comprising the amino acid sequence of SEQ ID NO: 307 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 307;
- h) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 8 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 8, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 58 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 58, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 108 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 108, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 208 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 208, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 258 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 258, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 308 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 308;
- i) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 9 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 9, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 59 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 59, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 109 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 109, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 209 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 209, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 259 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 259, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 309 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 309;
- j) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 10 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 10, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 60 or a functional variant thereof having one or two amino acid

substitutions with respect to the amino acid sequence of SEQ ID NO: 60, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 110 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 110, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 210 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 210, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 260 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 260, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 310 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 310;

- k) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 11 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 11, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 61 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 61, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 111 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 111, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 211 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 211, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 261 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 261, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 311 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 311;
- l) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 12 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 12, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 62 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 62, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 112 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 112, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 212 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 212, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 262 or a functional variant thereof having one or two amino

- acid substitutions with respect to the amino acid sequence of SEQ ID NO: 262, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 312 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 312;
- m) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 13 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 13, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 63 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 63, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 113 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 113, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 213 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 213, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 263 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 263, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 313 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 313;
- n) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 14 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 14, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 64 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 64, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 114 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 114, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 214 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 214, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 264 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 264, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 314 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 314;
- o) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 15 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 15, an HCDR2 comprising the amino acid sequence of

SEQ ID NO: 65 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 65, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 115 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 115, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 215 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 215, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 265 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 265, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 315 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 315;

- p) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 16 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 16, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 66 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 66, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 116 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 116, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 216 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 216, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 266 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 266, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 316 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 316;
- q) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 17 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 17, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 67 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 67, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 117 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 117, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 217 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 217, an LCDR2 comprising the amino acid

- sequence of SEQ ID NO: 267 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 267, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 317 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 317;
- r) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 18 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 18, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 68 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 68, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 118 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 118, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 218 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 218, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 268 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 268, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 318 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 318;
- s) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 19 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 19, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 69 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 69, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 119 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 119, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 219 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 219, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 269 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 269, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 319 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 319;
- t) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 20 or a functional variant thereof having one or two amino acid substitutions with respect to the amino

acid sequence of SEQ ID NO: 20, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 70 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 70, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 120 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 120, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 220 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 220, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 270 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 270, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 320 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 320;

- u) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 21 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 21, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 71 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 71, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 121 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 121, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 221 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 221, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 271 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 271, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 321 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 321;
- v) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 22 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 22, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 72 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 72, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 122 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 122, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 222 or a functional variant thereof having one or two amino acid substitutions with respect

- to the amino acid sequence of SEQ ID NO: 222, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 272 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 272, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 322 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 322;
- w) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 23 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 23, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 73 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 73, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 123 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 123, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 223 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 223, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 273 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 273, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 323 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 323;
- x) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 24 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 24, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 74 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 74, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 124 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 124, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 224 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 224, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 274 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 274, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 324 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 324;

- y) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 25 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 25, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 75 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 75, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 125 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 125, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 225 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 225, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 275 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 275, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 325 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 325;
- z) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 26 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 26, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 76 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 76, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 126 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 126, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 226 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 226, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 276 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 276, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 326 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 326;
- aa) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 27 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 27, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 77 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 77, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 127 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of

- SEQ ID NO: 127, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 227 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 227, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 277 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 277, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 327 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 327;
- bb) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 28 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 28, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 78 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 78, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 128 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 128, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 228 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 228, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 278 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 278, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 328 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 328;
- cc) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 29 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 29, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 79 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 79, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 129 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 129, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 229 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 229, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 279 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 279, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 329 or a functional variant

- thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 329;
- dd) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 30 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 30, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 80 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 80, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 130 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 130, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 230 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 230, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 280 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 280, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 330 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 330;
- ee) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 31 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 31, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 81 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 81, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 131 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 131, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 231 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 231, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 281 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 281, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 331 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 331;
- ff) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 32 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 32, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 82 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 82, an HCDR3

comprising the amino acid sequence of SEQ ID NO: 132 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 132, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 232 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 232, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 282 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 282, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 332 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 332;

gg) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 33 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 33, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 83 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 83, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 133 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 133, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 233 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 233, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 283 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 283, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 333 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 333;

hh) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 34 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 34, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 84 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 84, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 134 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 134, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 234 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 234, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 284 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 284, and an

- LCDR3 comprising the amino acid sequence of SEQ ID NO: 334 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 334;
- ii) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 35 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 35, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 85 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 85, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 135 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 135, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 235 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 235, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 285 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 285, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 335 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 335;
- jj) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 36 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 36, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 86 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 86, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 136 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 136, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 236 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 236, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 286 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 286, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 336 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 336;
- kk) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 37 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 37, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 87 or a functional variant thereof having one or two amino acid

substitutions with respect to the amino acid sequence of SEQ ID NO: 87, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 137 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 137, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 237 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 237, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 287 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 287, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 337 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 337;

- II) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 38 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 38, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 88 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 88, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 138 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 138, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 238 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 238, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 288 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 288, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 338 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 338;
- mm) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 39 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 39, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 89 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 89, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 139 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 139, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 239 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 239, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 289 or a functional variant thereof having one or two amino

- acid substitutions with respect to the amino acid sequence of SEQ ID NO: 289, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 339 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 339;
- nn) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 40 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 40, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 90 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 90, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 140 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 140, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 240 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 240, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 290 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 290, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 340 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 340;
- oo) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 41 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 41, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 91 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 91, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 141 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 141, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 241, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 291 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 291, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 341 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 341;
- pp) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 42 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 42, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 92 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 92, an HCDR3

comprising the amino acid sequence of SEQ ID NO: 142 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 142, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 242 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 242, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 292 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 292, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 342 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 342;

- qq) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 43 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 43, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 93 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 93, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 143 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 143, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 243 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 243, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 293 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 293, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 343 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 343;
- rr) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 44 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 44, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 94 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 94, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 144 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 144, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 244 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 244, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 294 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 294, and an

- LCDR3 comprising the amino acid sequence of SEQ ID NO: 344 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 344;
- ss) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 45 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 45, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 95 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 95, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 145 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 145, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 245 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 245, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 295 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 295, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 345 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 345;
- tt) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 46 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 46, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 96 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 96, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 146 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 146, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 246 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 246, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 296 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 296, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 346 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 346;
- uu) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 47 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 47, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 97 or a functional variant thereof having one or two amino acid

substitutions with respect to the amino acid sequence of SEQ ID NO: 97, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 147 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 147, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 247 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 247, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 297 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 297, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 347 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 347;

- vv) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 48 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 48, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 98 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 98, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 148 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 148, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 248 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 248, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 298 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 298, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 348 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 348;
- ww) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 49 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 49, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 99 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 99, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 149 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 149, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 249 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 249, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 299 or a functional variant thereof having one or two amino

acid substitutions with respect to the amino acid sequence of SEQ ID NO: 299, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 349 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 349; or

- xx) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 50 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 50, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 100 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 100, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 150 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 150, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 250 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 250, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 300 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 300, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 350 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 350.

2. An antibody or antigen-binding fragment thereof that binds Sialic acid-binding immunoglobulin-like lectin 8 (SIGLEC-8), wherein the antibody or antigen-binding fragment thereof comprises:

- a) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 151 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 351;
- b) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 152 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 352;
- c) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 153 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 353;
- d) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 154 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 354;
- e) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 155 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 355;

- [illegible]

- [illegible]

- [illegible]

- pp) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 192 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 392;
- qq) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 193 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 393;
- rr) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 194 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 394;
- ss) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 195 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 395;
- tt) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 196 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 396;
- uu) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 197 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 397;
- vv) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 198 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 398;
- ww) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 199 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 399;
or
- xx) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 200 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 400.

3. The antibody or antigen-binding fragment thereof of claim 1 or claim 2, wherein the antibody or antigen-binding fragment thereof is a humanized or chimeric antibody, or an antigen-binding fragment thereof.

4. The antibody or antigen-binding fragment thereof of claim 2, wherein the antigen or antigen-binding fragment thereof comprises:

- a) a VH comprising the amino acid sequence of SEQ ID NO: 151 and a VL comprising the amino acid sequence of SEQ ID NO: 351;
- b) a VH comprising the amino acid sequence of SEQ ID NO: 152 and a VL comprising the amino acid sequence of SEQ ID NO: 352;

- c) a VH comprising the amino acid sequence of SEQ ID NO: 153 and a VL comprising the amino acid sequence of SEQ ID NO: 353;
- d) a VH comprising the amino acid sequence of SEQ ID NO: 154 and a VL comprising the amino acid sequence of SEQ ID NO: 354;
- e) a VH comprising the amino acid sequence of SEQ ID NO: 155 and a VL comprising the amino acid sequence of SEQ ID NO: 355;
- f) a VH comprising the amino acid sequence of SEQ ID NO: 156 and a VL comprising the amino acid sequence of SEQ ID NO: 356;
- g) a VH comprising the amino acid sequence of SEQ ID NO: 157 and a VL comprising the amino acid sequence of SEQ ID NO: 357;
- h) a VH comprising the amino acid sequence of SEQ ID NO: 158 and a VL comprising the amino acid sequence of SEQ ID NO: 358;
- i) a VH comprising the amino acid sequence of SEQ ID NO: 159 and a VL comprising the amino acid sequence of SEQ ID NO: 359;
- j) a VH comprising the amino acid sequence of SEQ ID NO: 160 and a VL comprising the amino acid sequence of SEQ ID NO: 360;
- k) a VH comprising the amino acid sequence of SEQ ID NO: 161 and a VL comprising the amino acid sequence of SEQ ID NO: 361;
- l) a VH comprising the amino acid sequence of SEQ ID NO: 162 and a VL comprising the amino acid sequence of SEQ ID NO: 362;
- m) a VH comprising the amino acid sequence of SEQ ID NO: 163 and a VL comprising the amino acid sequence of SEQ ID NO: 363;
- n) a VH comprising the amino acid sequence of SEQ ID NO: 164 and a VL comprising the amino acid sequence of SEQ ID NO: 364;
- o) a VH comprising the amino acid sequence of SEQ ID NO: 165 and a VL comprising the amino acid sequence of SEQ ID NO: 365;
- p) a VH comprising the amino acid sequence of SEQ ID NO: 166 and a VL comprising the amino acid sequence of SEQ ID NO: 366;
- q) a VH comprising the amino acid sequence of SEQ ID NO: 167 and a VL comprising the amino acid sequence of SEQ ID NO: 367;
- r) a VH comprising the amino acid sequence of SEQ ID NO: 168 and a VL comprising the amino acid sequence of SEQ ID NO: 368;
- s) a VH comprising the amino acid sequence of SEQ ID NO: 169 and a VL comprising the amino acid sequence of SEQ ID NO: 369;
- t) a VH comprising the amino acid sequence of SEQ ID NO: 170 and a VL comprising the amino acid sequence of SEQ ID NO: 370;

- u) a VH comprising the amino acid sequence of SEQ ID NO: 171 and a VL comprising the amino acid sequence of SEQ ID NO: 371;
- v) a VH comprising the amino acid sequence of SEQ ID NO: 172 and a VL comprising the amino acid sequence of SEQ ID NO: 372;
- w) a VH comprising the amino acid sequence of SEQ ID NO: 173 and a VL comprising the amino acid sequence of SEQ ID NO: 373;
- x) a VH comprising the amino acid sequence of SEQ ID NO: 174 and a VL comprising the amino acid sequence of SEQ ID NO: 374;
- y) a VH comprising the amino acid sequence of SEQ ID NO: 175 and a VL comprising the amino acid sequence of SEQ ID NO: 375;
- z) a VH comprising the amino acid sequence of SEQ ID NO: 176 and a VL comprising the amino acid sequence of SEQ ID NO: 376;
- aa) a VH comprising the amino acid sequence of SEQ ID NO: 177 and a VL comprising the amino acid sequence of SEQ ID NO: 377;
- bb) a VH comprising the amino acid sequence of SEQ ID NO: 178 and a VL comprising the amino acid sequence of SEQ ID NO: 378;
- cc) a VH comprising the amino acid sequence of SEQ ID NO: 179 and a VL comprising the amino acid sequence of SEQ ID NO: 379;
- dd) a VH comprising the amino acid sequence of SEQ ID NO: 180 and a VL comprising the amino acid sequence of SEQ ID NO: 380;
- ee) a VH comprising the amino acid sequence of SEQ ID NO: 181 and a VL comprising the amino acid sequence of SEQ ID NO: 381;
- ff) a VH comprising the amino acid sequence of SEQ ID NO: 182 and a VL comprising the amino acid sequence of SEQ ID NO: 382;
- gg) a VH comprising the amino acid sequence of SEQ ID NO: 183 and a VL comprising the amino acid sequence of SEQ ID NO: 383;
- hh) a VH comprising the amino acid sequence of SEQ ID NO: 184 and a VL comprising the amino acid sequence of SEQ ID NO: 384;
- ii) a VH comprising the amino acid sequence of SEQ ID NO: 185 and a VL comprising the amino acid sequence of SEQ ID NO: 385;
- jj) a VH comprising the amino acid sequence of SEQ ID NO: 186 and a VL comprising the amino acid sequence of SEQ ID NO: 386;
- kk) a VH comprising the amino acid sequence of SEQ ID NO: 187 and a VL comprising the amino acid sequence of SEQ ID NO: 387;
- ll) a VH comprising the amino acid sequence of SEQ ID NO: 188 and a VL comprising the amino acid sequence of SEQ ID NO: 388;

- mm) a VH comprising the amino acid sequence of SEQ ID NO: 189 and a VL comprising the amino acid sequence of SEQ ID NO: 389;
- nn) a VH comprising the amino acid sequence of SEQ ID NO: 190 and a VL comprising the amino acid sequence of SEQ ID NO: 390;
- oo) a VH comprising the amino acid sequence of SEQ ID NO: 191 and a VL comprising the amino acid sequence of SEQ ID NO: 391;
- pp) a VH comprising the amino acid sequence of SEQ ID NO: 192 and a VL comprising the amino acid sequence of SEQ ID NO: 392;
- qq) a VH comprising the amino acid sequence of SEQ ID NO: 193 and a VL comprising the amino acid sequence of SEQ ID NO: 393;
- rr) a VH comprising the amino acid sequence of SEQ ID NO: 194 and a VL comprising the amino acid sequence of SEQ ID NO: 394;
- ss) a VH comprising the amino acid sequence of SEQ ID NO: 195 and a VL comprising the amino acid sequence of SEQ ID NO: 395;
- tt) a VH comprising the amino acid sequence of SEQ ID NO: 196 and a VL comprising the amino acid sequence of SEQ ID NO: 396;
- uu) a VH comprising the amino acid sequence of SEQ ID NO: 197 and a VL comprising the amino acid sequence of SEQ ID NO: 397;
- vv) a VH comprising the amino acid sequence of SEQ ID NO: 198 and a VL comprising the amino acid sequence of SEQ ID NO: 398;
- ww) a VH comprising the amino acid sequence of SEQ ID NO: 199 and a VL comprising the amino acid sequence of SEQ ID NO: 399; or
- xx) a VH comprising the amino acid sequence of SEQ ID NO: 200 and a VL comprising the amino acid sequence of SEQ ID NO: 400.

5. An antibody or antigen-binding fragment thereof that binds Sialic acid-binding immunoglobulin-like lectin 8 (SIGLEC-8), wherein the antibody or antigen-binding fragment thereof comprises:

- a) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 650 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 700;
- b) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 651 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 701;
- c) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 652 and a light chain comprising an amino

- acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 702;
- d) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 653 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 703;
 - e) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 654 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 704;
 - f) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 655 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 705;
 - g) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 656 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 706;
 - h) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 657 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 707;
 - i) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 658 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 708;
 - j) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 659 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 709;
 - k) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 660 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 710;
 - l) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 661 and a light chain comprising an amino

- acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 711;
- m) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 662 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 712;
 - n) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 663 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 713;
 - o) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 664 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 714;
 - p) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 665 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 715;
 - q) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 666 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 716;
 - r) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 667 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 717;
 - s) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 668 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 718;
 - t) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 669 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 719;
 - u) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 670 and a light chain comprising an amino

- acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 720;
- v) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 671 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 721;
 - w) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 672 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 722;
 - x) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 673 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 723;
 - y) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 674 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 724;
 - z) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 675 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 725;
 - aa) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 676 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 726;
 - bb) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 677 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 727;
 - cc) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 678 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 728;
 - dd) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 679 and a light chain comprising an amino

- acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 729;
- ee) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 680 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 730;
 - ff) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 681 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 731;
 - gg) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 682 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 732;
 - hh) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 683 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 733;
 - ii) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 684 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 734;
 - jj) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 685 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 735;
 - kk) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 686 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 736;
 - ll) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 687 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 737;
 - mm) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 688 and a light chain comprising an amino

- acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 738;
- nn) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 689 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 739;
- oo) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 690 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 740;
- pp) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 691 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 741;
- qq) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 692 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 742;
- rr) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 693 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 743;
- ss) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 694 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 744;
- tt) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 695 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 745;
- uu) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 696 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 746;
- vv) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 697 and a light chain comprising an amino

acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 747;

- ww) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 698 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 748; or
- xx) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 699 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 749.

6. The antibody or antigen-binding fragment thereof of claim 5, wherein the antibody or antigen-binding fragment thereof comprises:

- a) a heavy chain comprising the amino acid sequence of SEQ ID NO: 650 and a light chain comprising the amino acid sequence of SEQ ID NO: 700;
- b) a heavy chain comprising the amino acid sequence of SEQ ID NO: 651 and a light chain comprising the amino acid sequence of SEQ ID NO: 701;
- c) a heavy chain comprising the amino acid sequence of SEQ ID NO: 652 and a light chain comprising the amino acid sequence of SEQ ID NO: 702;
- d) a heavy chain comprising the amino acid sequence of SEQ ID NO: 653 and a light chain comprising the amino acid sequence of SEQ ID NO: 703;
- e) a heavy chain comprising the amino acid sequence of SEQ ID NO: 654 and a light chain comprising the amino acid sequence of SEQ ID NO: 704;
- f) a heavy chain comprising the amino acid sequence of SEQ ID NO: 655 and a light chain comprising the amino acid sequence of SEQ ID NO: 705;
- g) a heavy chain comprising the amino acid sequence of SEQ ID NO: 656 and a light chain comprising the amino acid sequence of SEQ ID NO: 706;
- h) a heavy chain comprising the amino acid sequence of SEQ ID NO: 657 and a light chain comprising the amino acid sequence of SEQ ID NO: 707;
- i) a heavy chain comprising the amino acid sequence of SEQ ID NO: 658 and a light chain comprising the amino acid sequence of SEQ ID NO: 708;
- j) a heavy chain comprising the amino acid sequence of SEQ ID NO: 659 and a light chain comprising the amino acid sequence of SEQ ID NO: 709;
- k) a heavy chain comprising the amino acid sequence of SEQ ID NO: 660 and a light chain comprising the amino acid sequence of SEQ ID NO: 710;
- l) a heavy chain comprising the amino acid sequence of SEQ ID NO: 661 and a light chain comprising the amino acid sequence of SEQ ID NO: 711;

- m) a heavy chain comprising the amino acid sequence of SEQ ID NO: 662 and a light chain comprising the amino acid sequence of SEQ ID NO: 712;
- n) a heavy chain comprising the amino acid sequence of SEQ ID NO: 663 and a light chain comprising the amino acid sequence of SEQ ID NO: 713;
- o) a heavy chain comprising the amino acid sequence of SEQ ID NO: 664 and a light chain comprising the amino acid sequence of SEQ ID NO: 714;
- p) a heavy chain comprising the amino acid sequence of SEQ ID NO: 665 and a light chain comprising the amino acid sequence of SEQ ID NO: 715;
- q) a heavy chain comprising the amino acid sequence of SEQ ID NO: 666 and a light chain comprising the amino acid sequence of SEQ ID NO: 716;
- r) a heavy chain comprising the amino acid sequence of SEQ ID NO: 667 and a light chain comprising the amino acid sequence of SEQ ID NO: 717;
- s) a heavy chain comprising the amino acid sequence of SEQ ID NO: 668 and a light chain comprising the amino acid sequence of SEQ ID NO: 718;
- t) a heavy chain comprising the amino acid sequence of SEQ ID NO: 669 and a light chain comprising the amino acid sequence of SEQ ID NO: 719;
- u) a heavy chain comprising the amino acid sequence of SEQ ID NO: 670 and a light chain comprising the amino acid sequence of SEQ ID NO: 720;
- v) a heavy chain comprising the amino acid sequence of SEQ ID NO: 671 and a light chain comprising the amino acid sequence of SEQ ID NO: 721;
- w) a heavy chain comprising the amino acid sequence of SEQ ID NO: 672 and a light chain comprising the amino acid sequence of SEQ ID NO: 722;
- x) a heavy chain comprising the amino acid sequence of SEQ ID NO: 673 and a light chain comprising the amino acid sequence of SEQ ID NO: 723;
- y) a heavy chain comprising the amino acid sequence of SEQ ID NO: 674 and a light chain comprising the amino acid sequence of SEQ ID NO: 724;
- z) a heavy chain comprising the amino acid sequence of SEQ ID NO: 675 and a light chain comprising the amino acid sequence of SEQ ID NO: 725;
- aa) a heavy chain comprising the amino acid sequence of SEQ ID NO: 676 and a light chain comprising the amino acid sequence of SEQ ID NO: 726;
- bb) a heavy chain comprising the amino acid sequence of SEQ ID NO: 677 and a light chain comprising the amino acid sequence of SEQ ID NO: 727;
- cc) a heavy chain comprising the amino acid sequence of SEQ ID NO: 678 and a light chain comprising the amino acid sequence of SEQ ID NO: 728;
- dd) a heavy chain comprising the amino acid sequence of SEQ ID NO: 679 and a light chain comprising the amino acid sequence of SEQ ID NO: 729;

- ee) a heavy chain comprising the amino acid sequence of SEQ ID NO: 680 and a light chain comprising the amino acid sequence of SEQ ID NO: 730;
- ff) a heavy chain comprising the amino acid sequence of SEQ ID NO: 681 and a light chain comprising the amino acid sequence of SEQ ID NO: 731;
- gg) a heavy chain comprising the amino acid sequence of SEQ ID NO: 682 and a light chain comprising the amino acid sequence of SEQ ID NO: 732;
- hh) a heavy chain comprising the amino acid sequence of SEQ ID NO: 683 and a light chain comprising the amino acid sequence of SEQ ID NO: 733;
- ii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 684 and a light chain comprising the amino acid sequence of SEQ ID NO: 734;
- jj) a heavy chain comprising the amino acid sequence of SEQ ID NO: 685 and a light chain comprising the amino acid sequence of SEQ ID NO: 735;
- kk) a heavy chain comprising the amino acid sequence of SEQ ID NO: 686 and a light chain comprising the amino acid sequence of SEQ ID NO: 736;
- ll) a heavy chain comprising the amino acid sequence of SEQ ID NO: 687 and a light chain comprising the amino acid sequence of SEQ ID NO: 737;
- mm) a heavy chain comprising the amino acid sequence of SEQ ID NO: 688 and a light chain comprising the amino acid sequence of SEQ ID NO: 738;
- nn) a heavy chain comprising the amino acid sequence of SEQ ID NO: 689 and a light chain comprising the amino acid sequence of SEQ ID NO: 739;
- oo) a heavy chain comprising the amino acid sequence of SEQ ID NO: 690 and a light chain comprising the amino acid sequence of SEQ ID NO: 740;
- pp) a heavy chain comprising the amino acid sequence of SEQ ID NO: 691 and a light chain comprising the amino acid sequence of SEQ ID NO: 741;
- qq) a heavy chain comprising the amino acid sequence of SEQ ID NO: 692 and a light chain comprising the amino acid sequence of SEQ ID NO: 742;
- rr) a heavy chain comprising the amino acid sequence of SEQ ID NO: 693 and a light chain comprising the amino acid sequence of SEQ ID NO: 743;
- ss) a heavy chain comprising the amino acid sequence of SEQ ID NO: 694 and a light chain comprising the amino acid sequence of SEQ ID NO: 744;
- tt) a heavy chain comprising the amino acid sequence of SEQ ID NO: 695 and a light chain comprising the amino acid sequence of SEQ ID NO: 745;
- uu) a heavy chain comprising the amino acid sequence of SEQ ID NO: 696 and a light chain comprising the amino acid sequence of SEQ ID NO: 746;
- vv) a heavy chain comprising the amino acid sequence of SEQ ID NO: 697 and a light chain comprising the amino acid sequence of SEQ ID NO: 747;

- ww) a heavy chain comprising the amino acid sequence of SEQ ID NO: 698 and a light chain comprising the amino acid sequence of SEQ ID NO: 748; or
- xx) a heavy chain comprising the amino acid sequence of SEQ ID NO: 699 and a light chain comprising the amino acid sequence of SEQ ID NO: 749.

7. The antibody or antigen-binding fragment thereof of any one of claims 1-6, that is a monoclonal antibody or an antigen-binding fragment thereof.

8. The antibody or antigen-binding fragment thereof of any one of claims 1-7, wherein the antibody is a monospecific antibody, a bispecific antibody, or a multispecific antibody; or wherein the antigen-binding fragment thereof is a single-chain Fv (scFv), a disulfide-linked Fv (sdFv), a Fab fragment, or a F(ab')₂ fragment.

9. The antibody or antigen-binding fragment thereof of any one of claims 1-8, wherein the SIGLEC-8 is human SIGLEC-8.

10. The antibody or antigen-binding fragment thereof of any one of claims 1-9, wherein the antibody or antigen-binding fragment thereof binds to SIGLEC-8 with a K_D of less than 75 nM, less than 50 nM, less than 25 nM, or less than 10 nM.

11. An isolated nucleic acid that encodes the antibody or antigen-binding fragment thereof of any one of claims 1-10.

12. An expression vector comprising the nucleic acid of claim 11.

13. An isolated host cell comprising the nucleic acid of claim 11 or the expression vector of claim 12.

14. An isolated host cell that expresses the antibody or antigen-binding fragment thereof of any one of claims 1-10.

15. A method of producing an antibody or antigen-binding fragment thereof that binds SIGLEC-8, comprising incubating the host cell of claim 13 or claim 14 under conditions suitable for producing the antibody or antigen-binding fragment thereof.

16. The method of claim 15, further comprising isolating the antibody or antigen-binding fragment thereof.

17. An antibody or antigen-binding fragment thereof that binds cluster of differentiation 117 (CD117), wherein the antibody or antigen-binding fragment thereof comprises:

- a) a heavy chain complementary determining region 1 (HCDR1) comprising the amino acid sequence of SEQ ID NO: 451 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 451, a heavy chain complementary determining region 2 (HCDR2) comprising the amino acid sequence of SEQ ID NO: 472 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 472, a heavy chain complementary determining region 3 (HCDR3) comprising the amino acid sequence of SEQ ID NO: 493 or a functional variant thereof having one or two amino

- acid substitutions with respect to the amino acid sequence of SEQ ID NO: 493, a light chain complementary determining region 1 (LCDR1) comprising the amino acid sequence of SEQ ID NO: 535 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 535, a light chain complementary determining region 2 (LCDR2) comprising the amino acid sequence of SEQ ID NO: 556 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 556, and a light chain complementary determining region 3 (LCDR3) comprising the amino acid sequence of SEQ ID NO: 577 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 577;
- b) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 452 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 452, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 473 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 473, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 494 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 494, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 536 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 536, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 557 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 557, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 578 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 578;
- c) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 453 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 453, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 474 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 474, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 495 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 495, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 537 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 537, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 558 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 558, and an

- LCDR3 comprising the amino acid sequence of SEQ ID NO: 579 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 579;
- d) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 454 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 454, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 475 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 475, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 496 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 496, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 538 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 538, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 559 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 559, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 580 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 580;
- e) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 455 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 455, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 476 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 476, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 497 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 497, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 539 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 539, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 560 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 560, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 581 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 581;
- f) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 456 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 456, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 477 or a functional variant thereof having one or two amino acid

substitutions with respect to the amino acid sequence of SEQ ID NO: 477, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 498 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 498, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 540 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 540, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 561 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 561, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 582 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 582;

- g) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 457 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 457, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 478 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 478, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 499 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 499, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 541 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 541, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 562 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 562, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 583 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 583;
- h) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 458 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 458, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 479 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 479, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 500 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 500, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 542 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 542, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 563 or a functional variant thereof having one or two amino

- acid substitutions with respect to the amino acid sequence of SEQ ID NO: 563, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 584 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 584;
- i) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 459 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 459, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 480 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 480, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 501 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 501, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 543 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 543, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 564 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 564, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 585 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 585;
- j) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 460 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 460, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 481 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 481, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 502 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 502, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 544 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 544, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 565 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 565, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 586 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 586;
- k) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 461 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 461, an HCDR2 comprising the amino acid sequence of

SEQ ID NO: 482 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 482, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 503 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 503, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 545 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 545, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 566 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 566, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 587 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 587;

- l) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 462 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 462, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 483 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 483, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 504 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 504, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 546 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 546, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 567 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 567, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 588 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 588;
- m) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 463 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 463, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 484 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 484, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 505 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 505, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 547 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 547, an LCDR2 comprising the amino acid

- sequence of SEQ ID NO: 568 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 568, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 589 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 589;
- n) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 464 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 464, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 485 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 485, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 506 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 506, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 548 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 548, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 569 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 569, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 590 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 590;
- o) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 465 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 465, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 486 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 486, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 507 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 507, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 549 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 549, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 570 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 570, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 591 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 591;
- p) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 466 or a functional variant thereof having one or two amino acid substitutions with respect to the amino

acid sequence of SEQ ID NO: 466, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 487 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 487, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 508 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 508, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 550 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 550, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 571 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 571, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 592 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 592;

- q) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 467 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 467, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 488 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 488, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 509 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 509, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 551 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 551, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 572 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 572, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 593 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 593;
- r) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 468 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 468, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 489 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 489, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 510 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 510, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 552 or a functional variant thereof having one or two amino acid substitutions with respect

- to the amino acid sequence of SEQ ID NO: 552, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 573 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 573, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 594 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 594;
- s) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 469 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 469, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 490 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 490, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 511 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 511, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 553 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 553, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 574 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 574, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 595 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 595;
- t) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 470 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 470, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 491 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 491, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 512 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 512, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 554 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 554, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 575 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 575, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 596 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 596; or

- u) an HCDR1 comprising the amino acid sequence of SEQ ID NO: 471 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 471, an HCDR2 comprising the amino acid sequence of SEQ ID NO: 492 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 492, an HCDR3 comprising the amino acid sequence of SEQ ID NO: 513 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 513, an LCDR1 comprising the amino acid sequence of SEQ ID NO: 555 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 555, an LCDR2 comprising the amino acid sequence of SEQ ID NO: 576 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 576, and an LCDR3 comprising the amino acid sequence of SEQ ID NO: 597 or a functional variant thereof having one or two amino acid substitutions with respect to the amino acid sequence of SEQ ID NO: 597.

18. An antibody or antigen-binding fragment thereof that binds cluster of differentiation 117 (CD117), wherein the antibody or antigen-binding fragment thereof comprises:

- a) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 514 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 598;
- b) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 515 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 599;
- c) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 516 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 600;
- d) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 517 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 601;
- e) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 518 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 602;
- f) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 519 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 603;

- [illegible]

- s) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 532 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 616;
- t) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 533 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 617;
or
- u) a VH comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 534 and a VL comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 618.

19. The antibody or antigen-binding fragment thereof of claim 17 or claim 18, wherein the antibody or antigen-binding fragment thereof is a humanized or chimeric antibody, or an antigen-binding fragment thereof.

20. The antibody or antigen-binding fragment thereof of claim 18, wherein the antigen or antigen-binding fragment thereof comprises:

- a) a VH comprising the amino acid sequence of SEQ ID NO: 514 and a VL comprising the amino acid sequence of SEQ ID NO: 598;
- b) a VH comprising the amino acid sequence of SEQ ID NO: 515 and a VL comprising the amino acid sequence of SEQ ID NO: 599;
- c) a VH comprising the amino acid sequence of SEQ ID NO: 516 and a VL comprising the amino acid sequence of SEQ ID NO: 600;
- d) a VH comprising the amino acid sequence of SEQ ID NO: 517 and a VL comprising the amino acid sequence of SEQ ID NO: 601;
- e) a VH comprising the amino acid sequence of SEQ ID NO: 518 and a VL comprising the amino acid sequence of SEQ ID NO: 602;
- f) a VH comprising the amino acid sequence of SEQ ID NO: 519 and a VL comprising the amino acid sequence of SEQ ID NO: 603;
- g) a VH comprising the amino acid sequence of SEQ ID NO: 520 and a VL comprising the amino acid sequence of SEQ ID NO: 604;
- h) a VH comprising the amino acid sequence of SEQ ID NO: 521 and a VL comprising the amino acid sequence of SEQ ID NO: 605;
- i) a VH comprising the amino acid sequence of SEQ ID NO: 522 and a VL comprising the amino acid sequence of SEQ ID NO: 606;
- j) a VH comprising the amino acid sequence of SEQ ID NO: 523 and a VL comprising the amino acid sequence of SEQ ID NO: 607;
- k) a VH comprising the amino acid sequence of SEQ ID NO: 524 and a VL comprising the amino acid sequence of SEQ ID NO: 608;

- l) a VH comprising the amino acid sequence of SEQ ID NO: 525 and a VL comprising the amino acid sequence of SEQ ID NO: 609;
- m) a VH comprising the amino acid sequence of SEQ ID NO: 526 and a VL comprising the amino acid sequence of SEQ ID NO: 610;
- n) a VH comprising the amino acid sequence of SEQ ID NO: 527 and a VL comprising the amino acid sequence of SEQ ID NO: 611;
- o) a VH comprising the amino acid sequence of SEQ ID NO: 528 and a VL comprising the amino acid sequence of SEQ ID NO: 612;
- p) a VH comprising the amino acid sequence of SEQ ID NO: 529 and a VL comprising the amino acid sequence of SEQ ID NO: 613;
- q) a VH comprising the amino acid sequence of SEQ ID NO: 530 and a VL comprising the amino acid sequence of SEQ ID NO: 614;
- r) a VH comprising the amino acid sequence of SEQ ID NO: 531 and a VL comprising the amino acid sequence of SEQ ID NO: 615;
- s) a VH comprising the amino acid sequence of SEQ ID NO: 532 and a VL comprising the amino acid sequence of SEQ ID NO: 616;
- t) a VH comprising the amino acid sequence of SEQ ID NO: 533 and a VL comprising the amino acid sequence of SEQ ID NO: 617; or
- u) a VH comprising the amino acid sequence of SEQ ID NO: 534 and a VL comprising the amino acid sequence of SEQ ID NO: 618.

21. An antibody or antigen-binding fragment thereof that binds cluster of differentiation 117 (CD117), wherein the antibody or antigen-binding fragment thereof comprises:

- a) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 750 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 771;
- b) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 751 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 772;
- c) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 752 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 773;
- d) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 753 and a light chain comprising an amino

- acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 774;
- e) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 754 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 775;
 - f) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 755 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 776;
 - g) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 756 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 777;
 - h) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 757 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 778;
 - i) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 758 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 779;
 - j) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 759 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 780;
 - k) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 760 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 781;
 - l) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 761 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 782;
 - m) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 762 and a light chain comprising an amino

- acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 783;
- n) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 763 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 784;
 - o) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 764 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 785;
 - p) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 765 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 786;
 - q) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 766 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 787;
 - r) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 767 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 788;
 - s) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 768 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 789;
 - t) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 769 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 790; or
 - u) a heavy chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 770 and a light chain comprising an amino acid sequence at least 90% or at least 95% identical to the amino acid sequence of SEQ ID NO: 791.

22. The antibody or antigen-binding fragment thereof of claim 21, wherein the antibody or antigen-binding fragment thereof comprises:

- a) a heavy chain comprising the amino acid sequence of SEQ ID NO: 750 and a light chain comprising the amino acid sequence of SEQ ID NO: 771;
- b) a heavy chain comprising the amino acid sequence of SEQ ID NO: 751 and a light chain comprising the amino acid sequence of SEQ ID NO: 772;
- c) a heavy chain comprising the amino acid sequence of SEQ ID NO: 752 and a light chain comprising the amino acid sequence of SEQ ID NO: 773;
- d) a heavy chain comprising the amino acid sequence of SEQ ID NO: 753 and a light chain comprising the amino acid sequence of SEQ ID NO: 774;
- e) a heavy chain comprising the amino acid sequence of SEQ ID NO: 754 and a light chain comprising the amino acid sequence of SEQ ID NO: 775;
- f) a heavy chain comprising the amino acid sequence of SEQ ID NO: 755 and a light chain comprising the amino acid sequence of SEQ ID NO: 776;
- g) a heavy chain comprising the amino acid sequence of SEQ ID NO: 756 and a light chain comprising the amino acid sequence of SEQ ID NO: 777;
- h) a heavy chain comprising the amino acid sequence of SEQ ID NO: 757 and a light chain comprising the amino acid sequence of SEQ ID NO: 778;
- i) a heavy chain comprising the amino acid sequence of SEQ ID NO: 758 and a light chain comprising the amino acid sequence of SEQ ID NO: 779;
- j) a heavy chain comprising the amino acid sequence of SEQ ID NO: 759 and a light chain comprising the amino acid sequence of SEQ ID NO: 780;
- k) a heavy chain comprising the amino acid sequence of SEQ ID NO: 760 and a light chain comprising the amino acid sequence of SEQ ID NO: 781;
- l) a heavy chain comprising the amino acid sequence of SEQ ID NO: 761 and a light chain comprising the amino acid sequence of SEQ ID NO: 782;
- m) a heavy chain comprising the amino acid sequence of SEQ ID NO: 762 and a light chain comprising the amino acid sequence of SEQ ID NO: 783;
- n) a heavy chain comprising the amino acid sequence of SEQ ID NO: 763 and a light chain comprising the amino acid sequence of SEQ ID NO: 784;
- o) a heavy chain comprising the amino acid sequence of SEQ ID NO: 764 and a light chain comprising the amino acid sequence of SEQ ID NO: 785;
- p) a heavy chain comprising the amino acid sequence of SEQ ID NO: 765 and a light chain comprising the amino acid sequence of SEQ ID NO: 786;
- q) a heavy chain comprising the amino acid sequence of SEQ ID NO: 766 and a light chain comprising the amino acid sequence of SEQ ID NO: 787;
- r) a heavy chain comprising the amino acid sequence of SEQ ID NO: 767 and a light chain comprising the amino acid sequence of SEQ ID NO: 788;

- s) a heavy chain comprising the amino acid sequence of SEQ ID NO: 768 and a light chain comprising the amino acid sequence of SEQ ID NO: 789;
- t) a heavy chain comprising the amino acid sequence of SEQ ID NO: 769 and a light chain comprising the amino acid sequence of SEQ ID NO: 790; or
- u) a heavy chain comprising the amino acid sequence of SEQ ID NO: 770 and a light chain comprising the amino acid sequence of SEQ ID NO: 791.

23. The antibody or antigen-binding fragment thereof of any one of claims 17-22, that is a monoclonal antibody or an antigen-binding fragment thereof.

24. The antibody or antigen-binding fragment thereof of any one of claims 17-23, wherein the antibody is a monospecific antibody, a bispecific antibody, or a multispecific antibody; or wherein the antigen-binding fragment thereof is a single-chain Fv (scFv), a disulfide-linked Fv (sdFv), a Fab fragment, or a F(ab')₂ fragment.

25. The antibody or antigen-binding fragment thereof of any one of claims 17-24, wherein the CD117 is human CD177.

26. The antibody or antigen-binding fragment thereof of any one of claims 17-25, wherein the antibody or antigen-binding fragment thereof binds to CD117 with a K_D of less than 75 nM, less than 50 nM, less than 25 nM, or less than 10 nM.

27. An isolated nucleic acid that encodes the antibody or antigen-binding fragment thereof of any one of claims 17-26.

28. An expression vector comprising the nucleic acid of claim 27.

29. An isolated host cell comprising the nucleic acid of claim 27 or the expression vector of claim 28.

30. An isolated host cell that expresses the antibody or antigen-binding fragment thereof of any one of claims 17-26.

31. A method of producing an antibody or antigen-binding fragment thereof that binds CD117, comprising incubating the host cell of claim 29 or claim 30 under conditions suitable for producing the antibody or antigen-binding fragment thereof.

32. The method of claim 31, further comprising isolating the antibody or antigen-binding fragment thereof.

33. A method of treating a disease or disorder associated with SIGLEC-8 expression in a subject in need thereof, the method comprising administering to the subject an effective amount of the antibody or antigen-binding fragment thereof of any one of claims 1-10.

34. The method of claim 33, wherein the disease or disorder is a mast cell disease.

35. The method of claim 34, wherein the mast cell disease is systemic mastocytosis, mast cell activation syndrome, or hereditary alpha-tryptasemia.

36. The method of claim 33, wherein the disease or disorder is an immune disease.

37. The method of claim 33, wherein the disease or disorder is a cancer.

38. The method of claim 37, wherein the cancer is chronic eosinophilic leukemia, hypereosinophilic syndrome, or chronic myeloid leukemia.
39. The method of claim 33, wherein the disease or disorder is asthma, an allergy, chronic urticaria, atopic dermatitis, or asthma.
40. The method of claim 33, wherein the disease or disorder is eosinophilic esophagitis, eosinophilic gastroenteritis, or duodenitis.
41. A method of treating a disease or disorder associated with CD117 expression in a subject in need thereof, the method comprising administering to the subject an effective amount of the antibody or antigen-binding fragment thereof of any one of claims 17-26.
42. The method of claim 41, wherein the disease or disorder is a cancer.
43. The method of claim 42, wherein the cancer is an ovarian carcinoma, a seminoma, a glioma, a glioblastoma, a mast cell tumor, a melanoma, or a gastrointestinal tumor.
44. The method of claim 41, wherein the disease or disorder is chronic urticaria, prurigo nodularis, severe combined immunodeficiency, or a retinopathy.
45. The method of claim 44, wherein the retinopathy is diabetic retinopathy, retinopathy of prematurity, or wet macular degeneration.

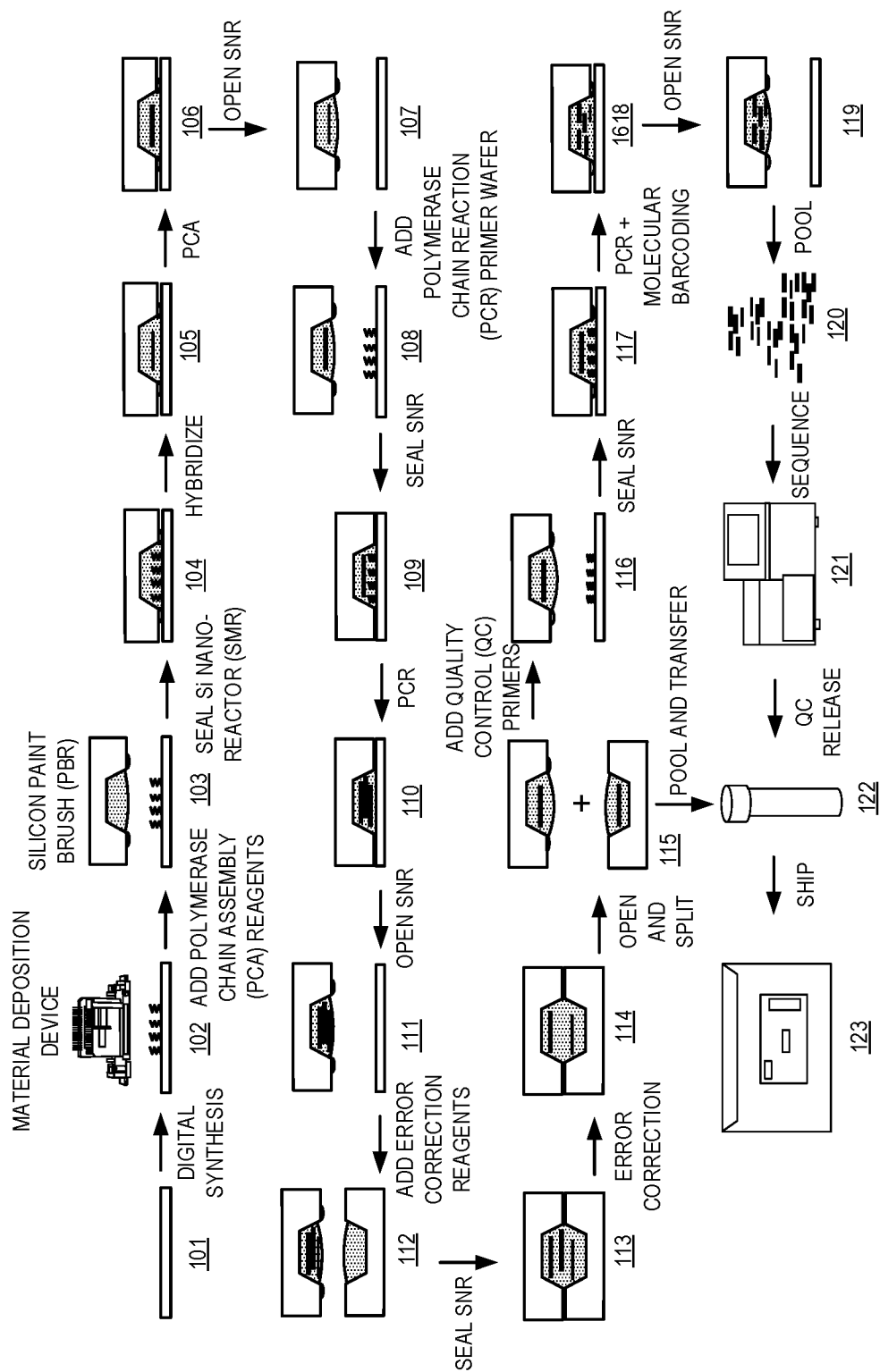


FIG. 1

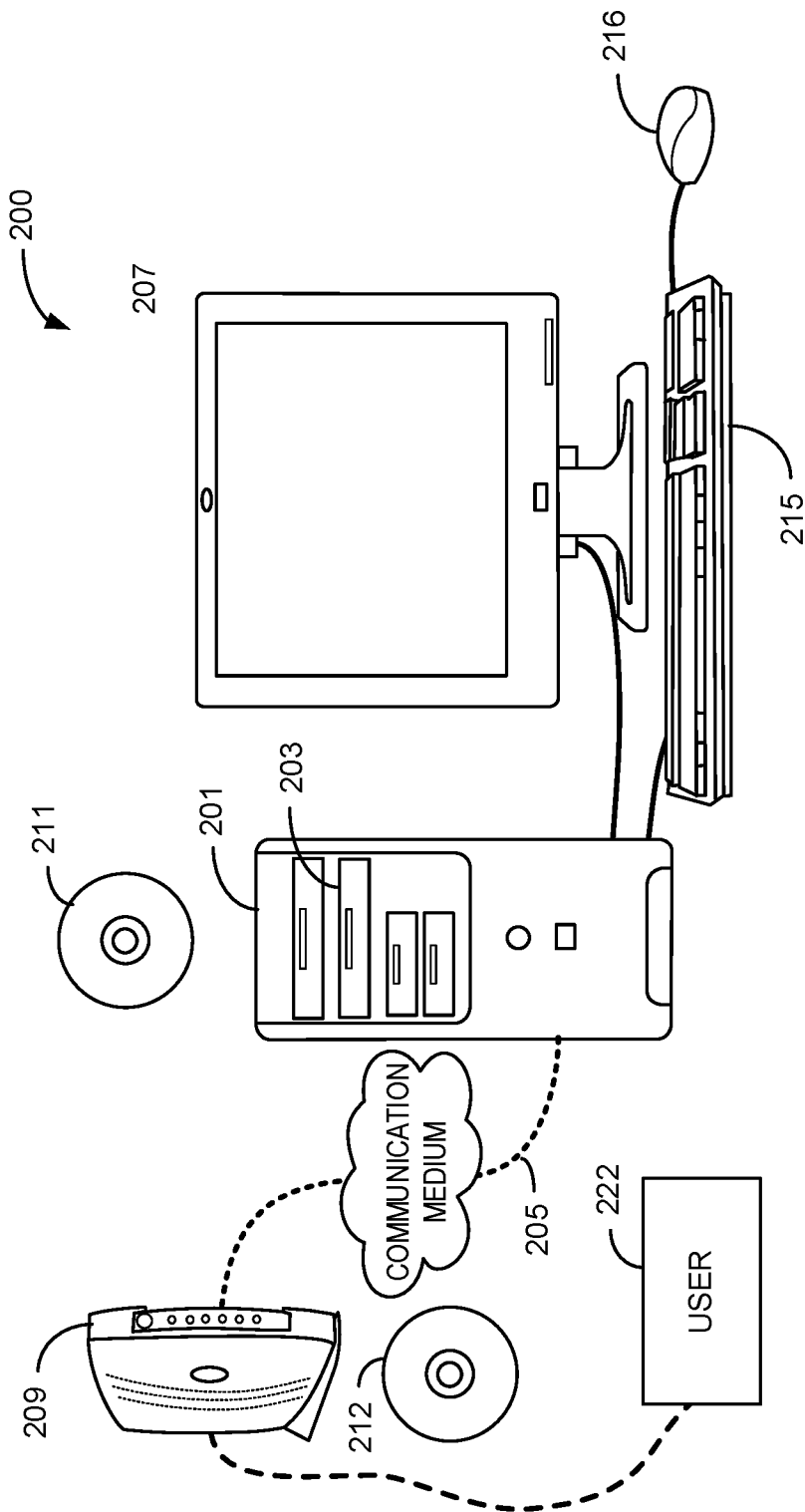


FIG. 2

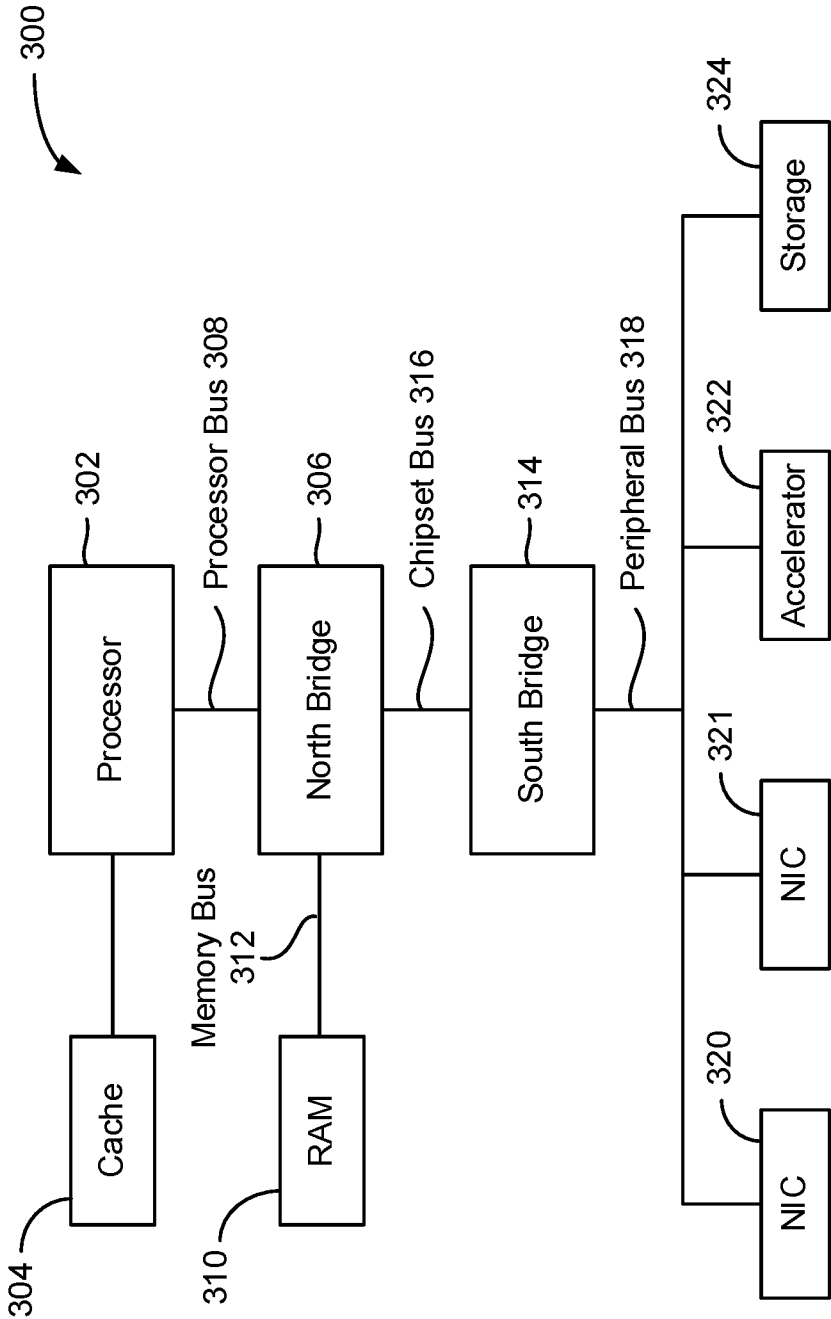


FIG. 3

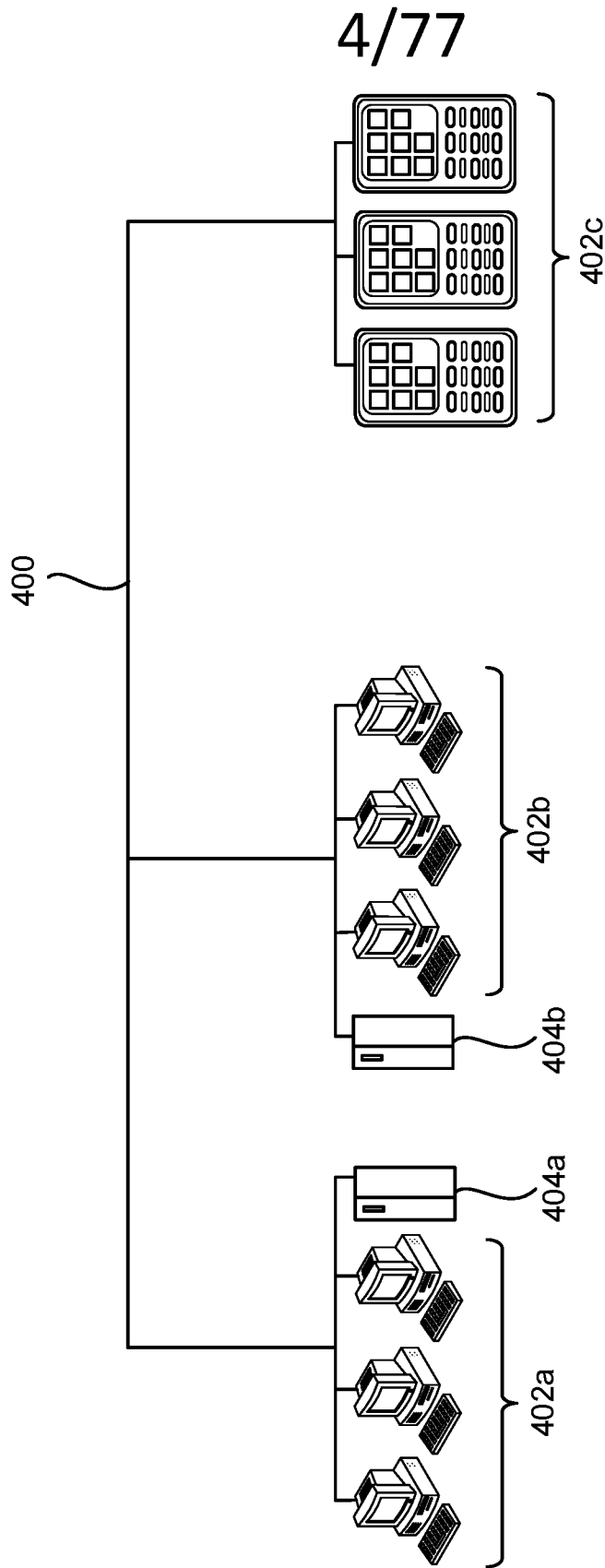
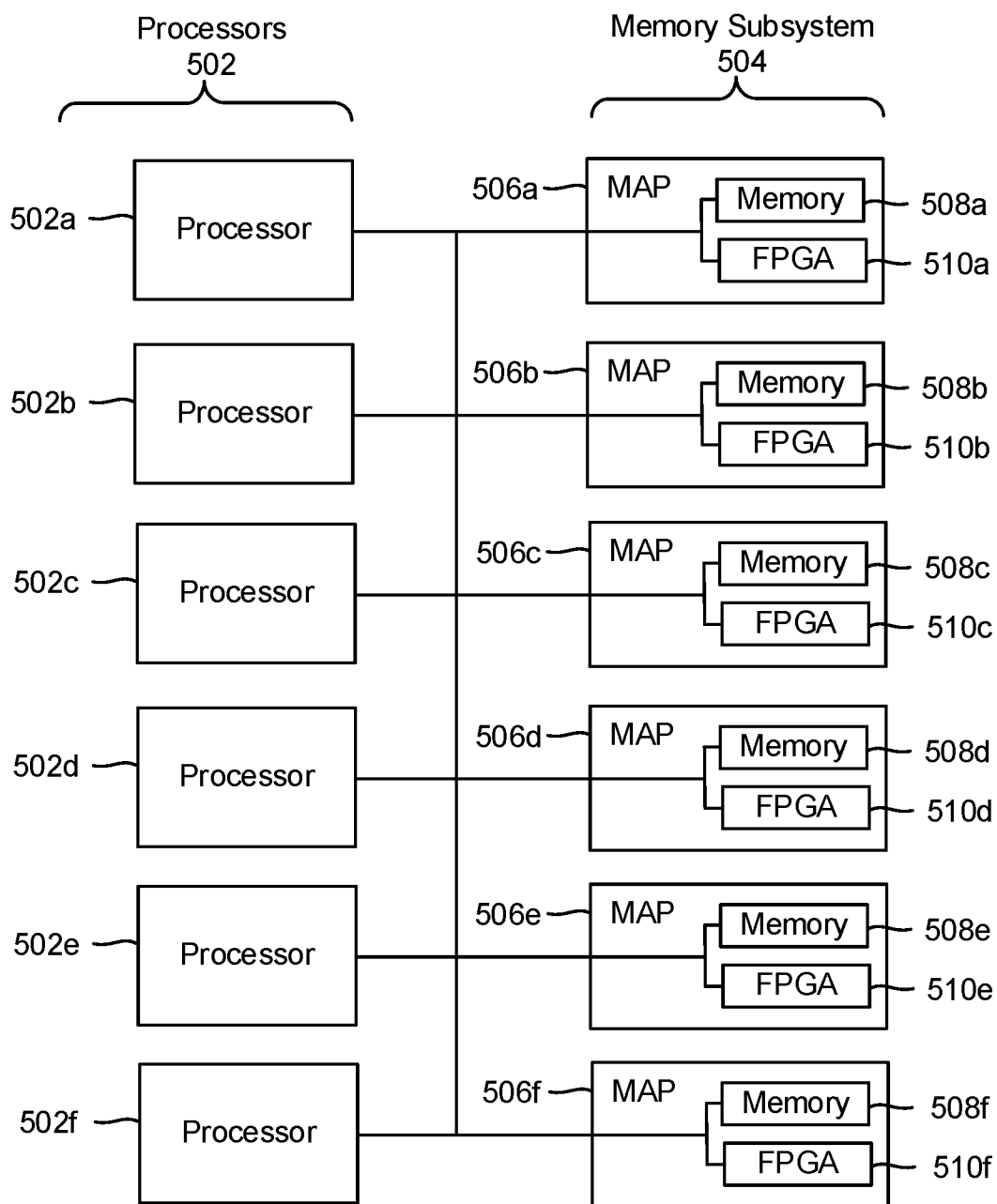


FIG. 4

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**FIG. 5**

pTT5-SIGLEC-8 P2A mVenus

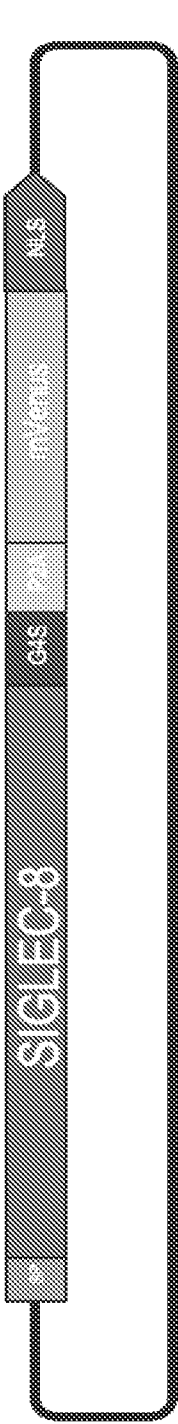


FIG. 6A

pTT5-SIGLEC-8 mVenus

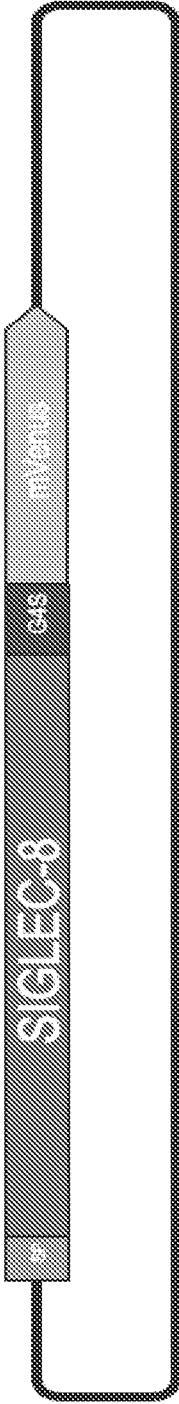


FIG. 6B

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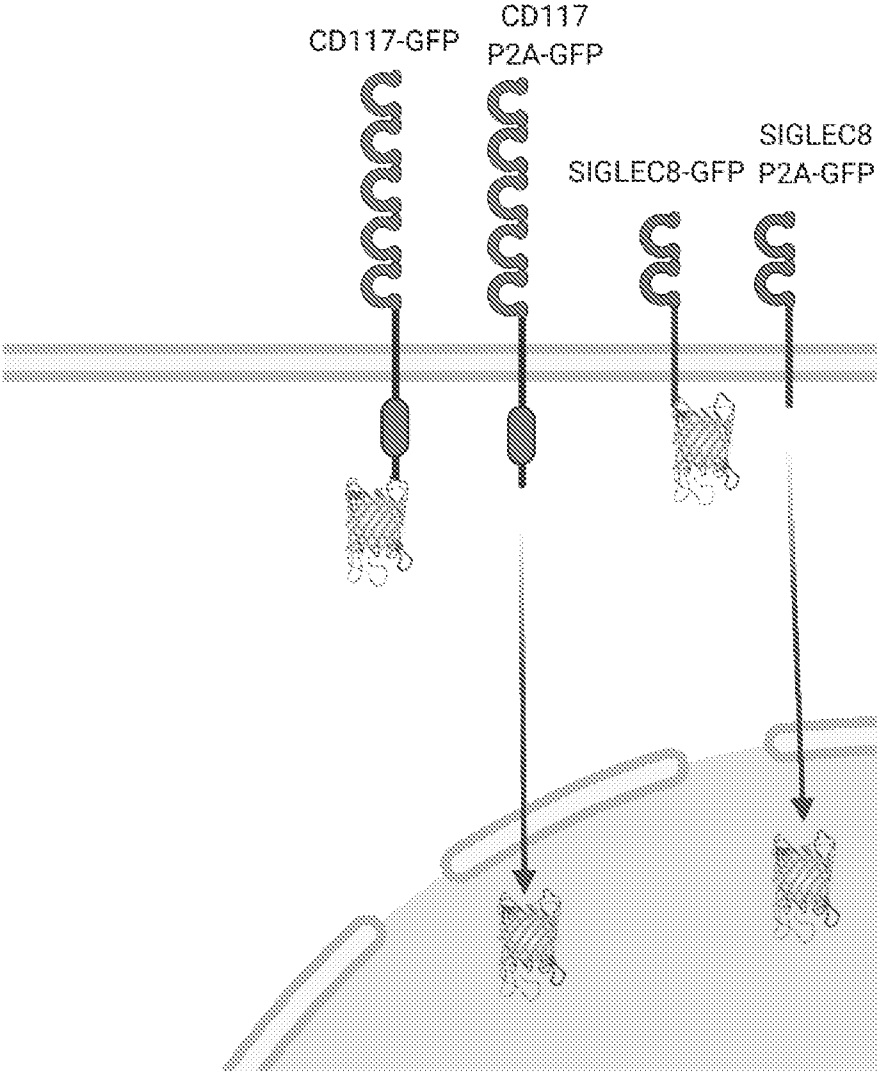


FIG. 6C

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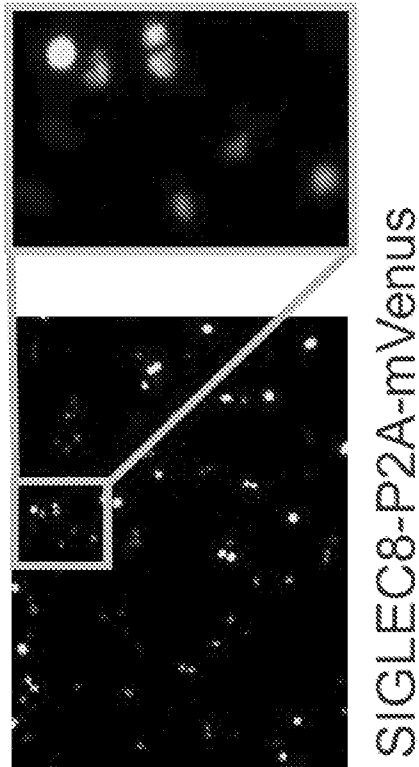


FIG. 6E

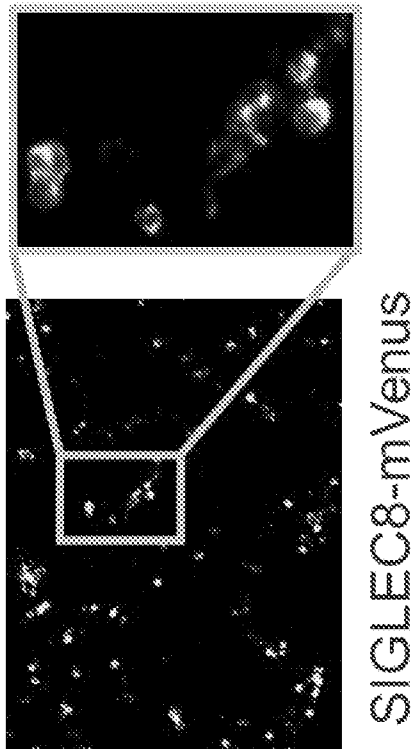


FIG. 6D

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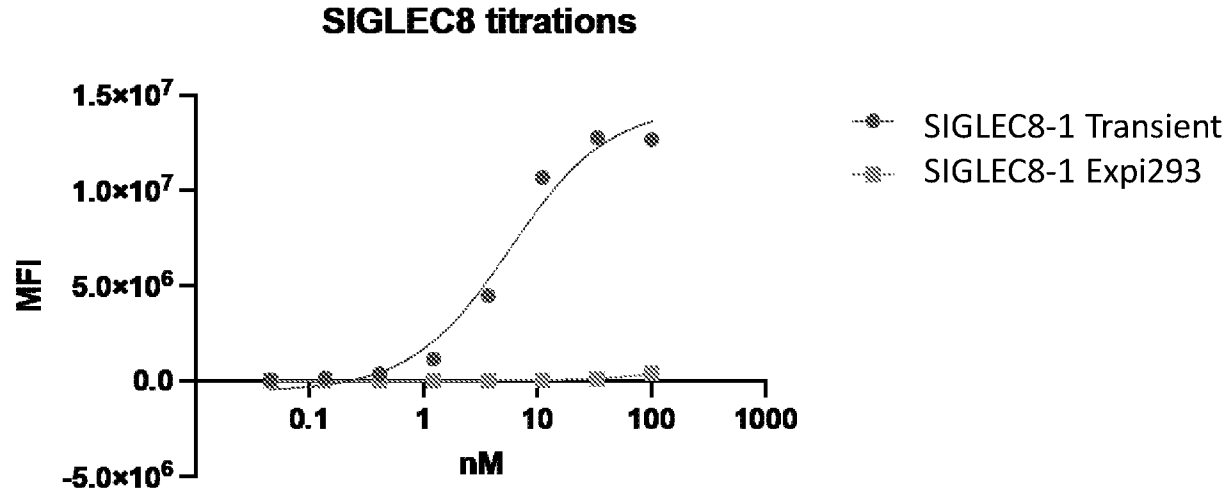
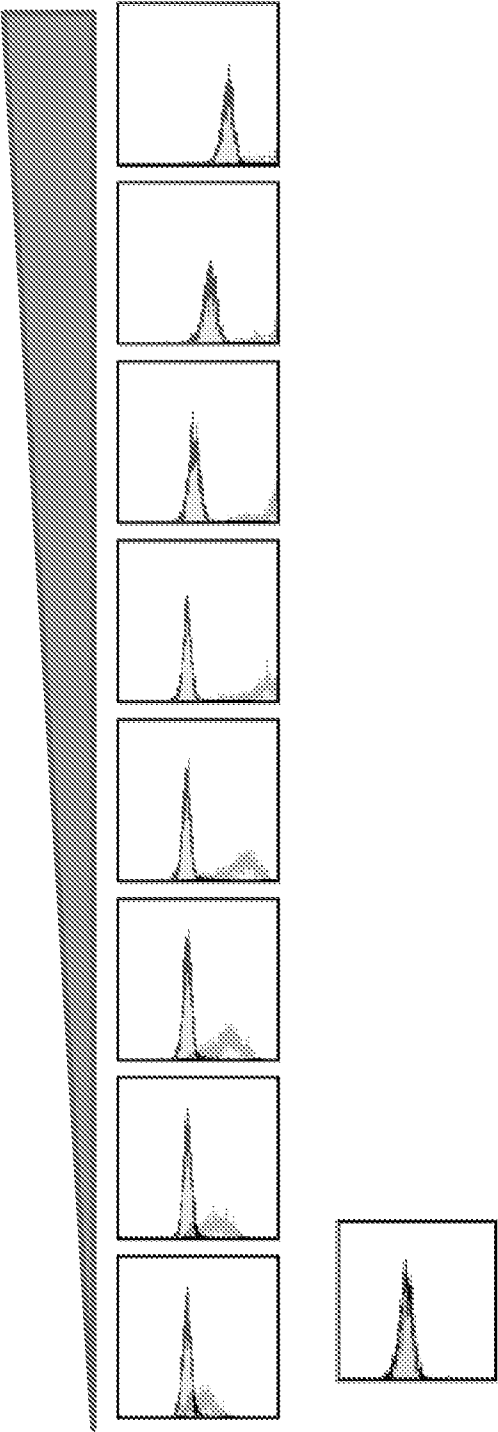


FIG. 6F

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SIGLEC8-1



SIGLEC8-1
Hu 2 only

FIG. 6G

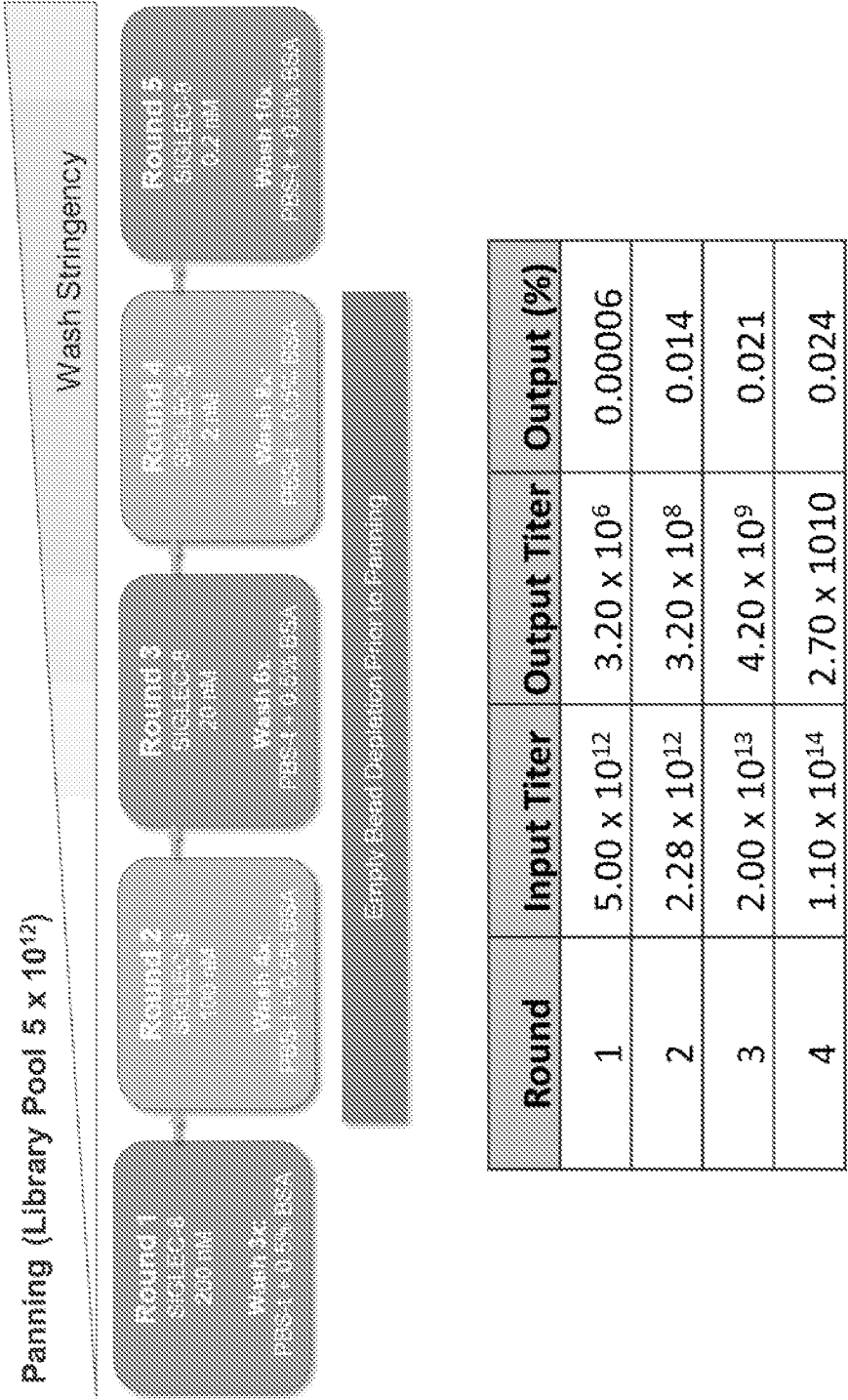
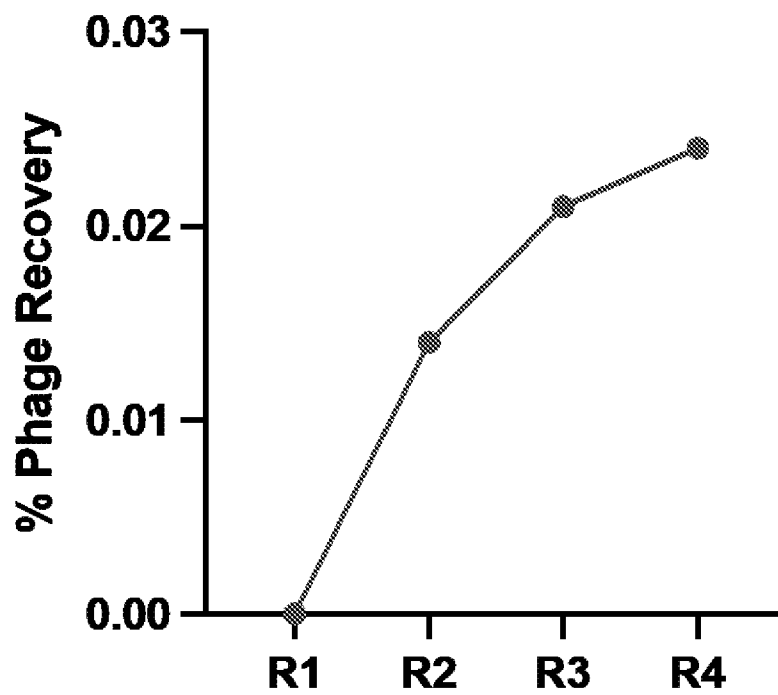
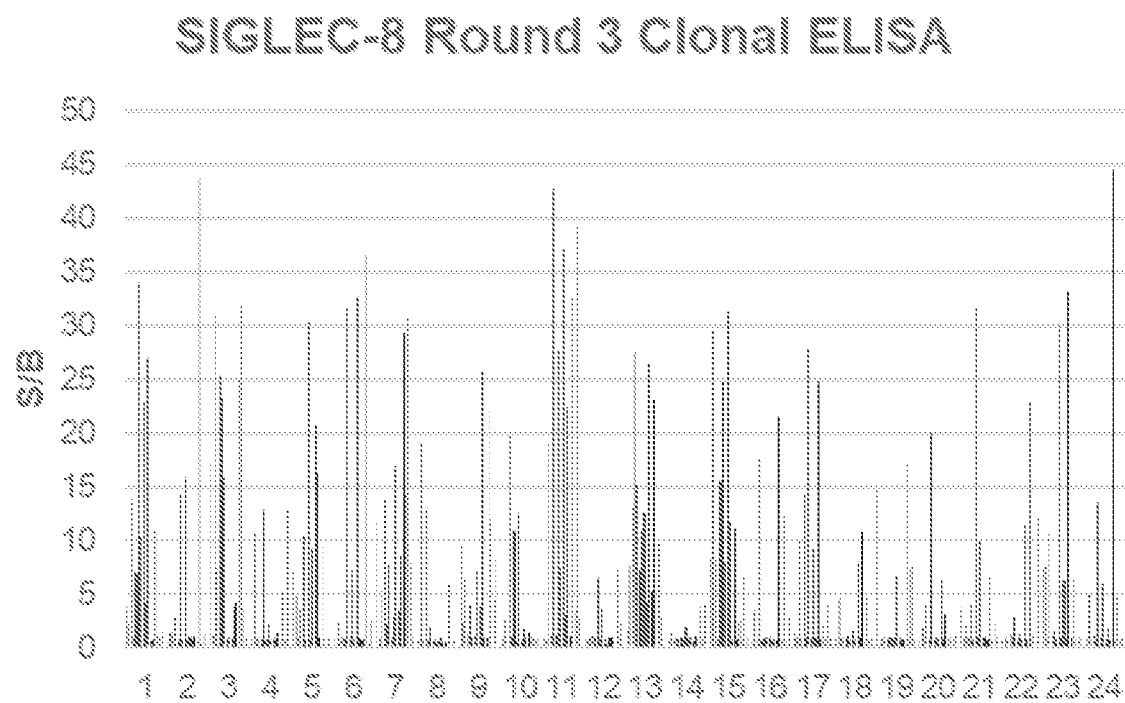


FIG. 7A

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SIGLEC-8 Panning Phage Recovery**FIG. 7B**

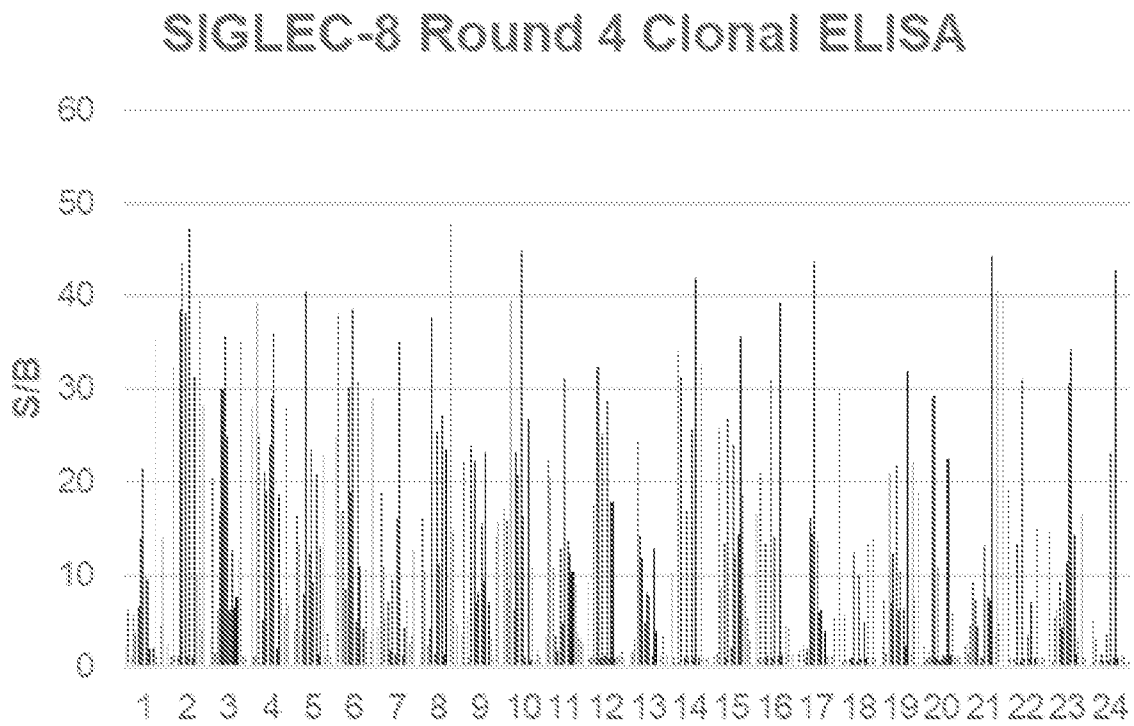
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S/B	# of Hits
3.00	136
10.00	76

FIG. 8A

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S/B	# of Hits
3.00	243
10.00	153

FIG. 8B

Round	Number of Clones Screened	Number of Unique Clones	Clonotypes
R3	380	49	52
R4	380	12	

FIG. 8C

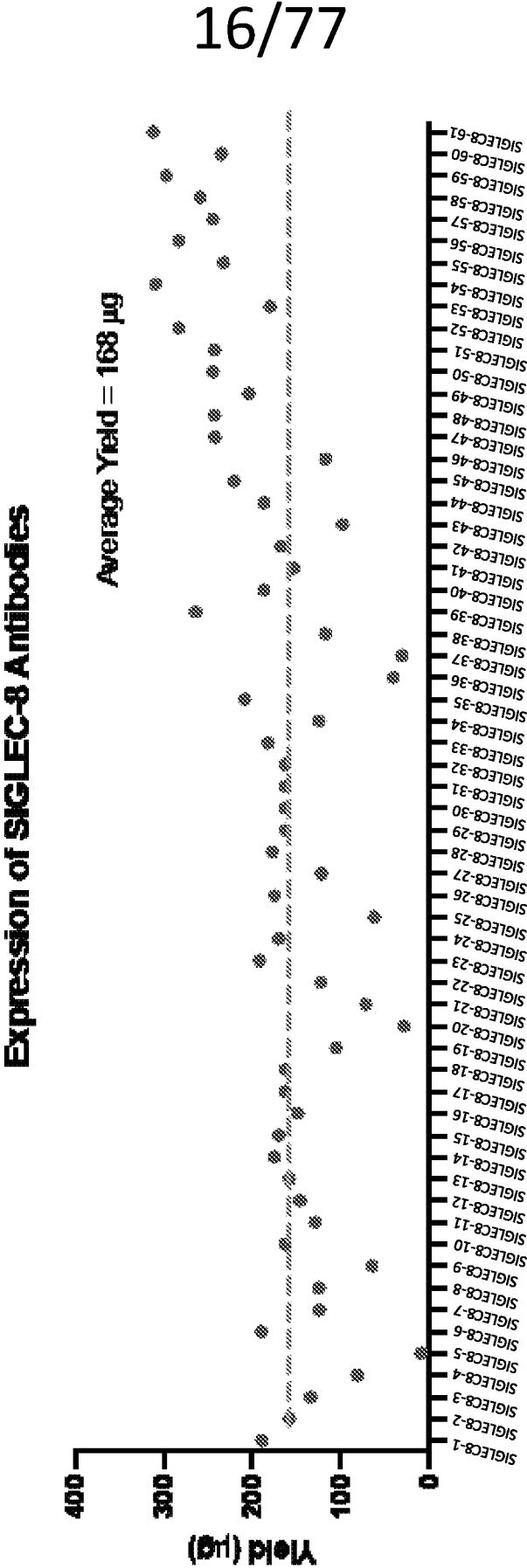
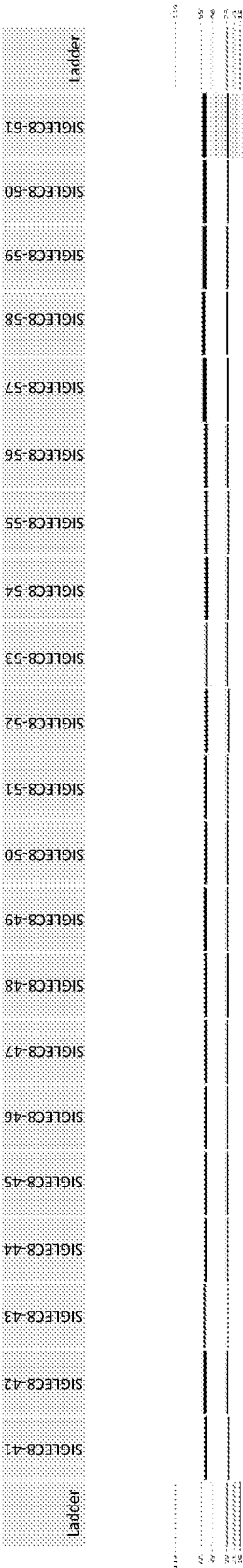
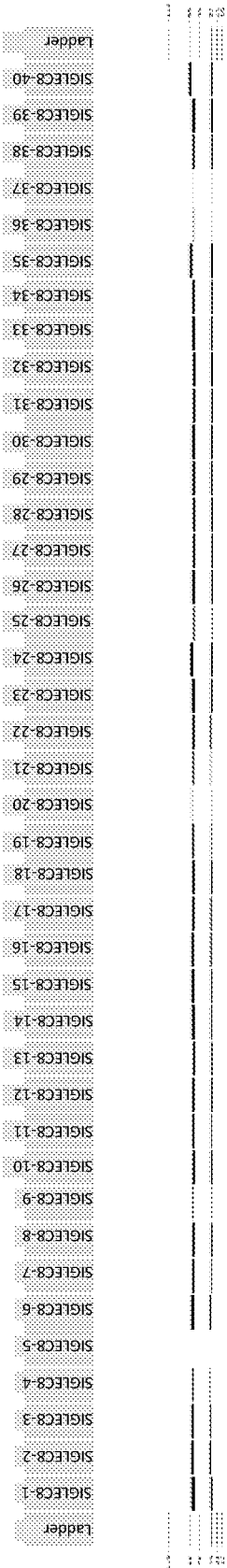


FIG. 9A



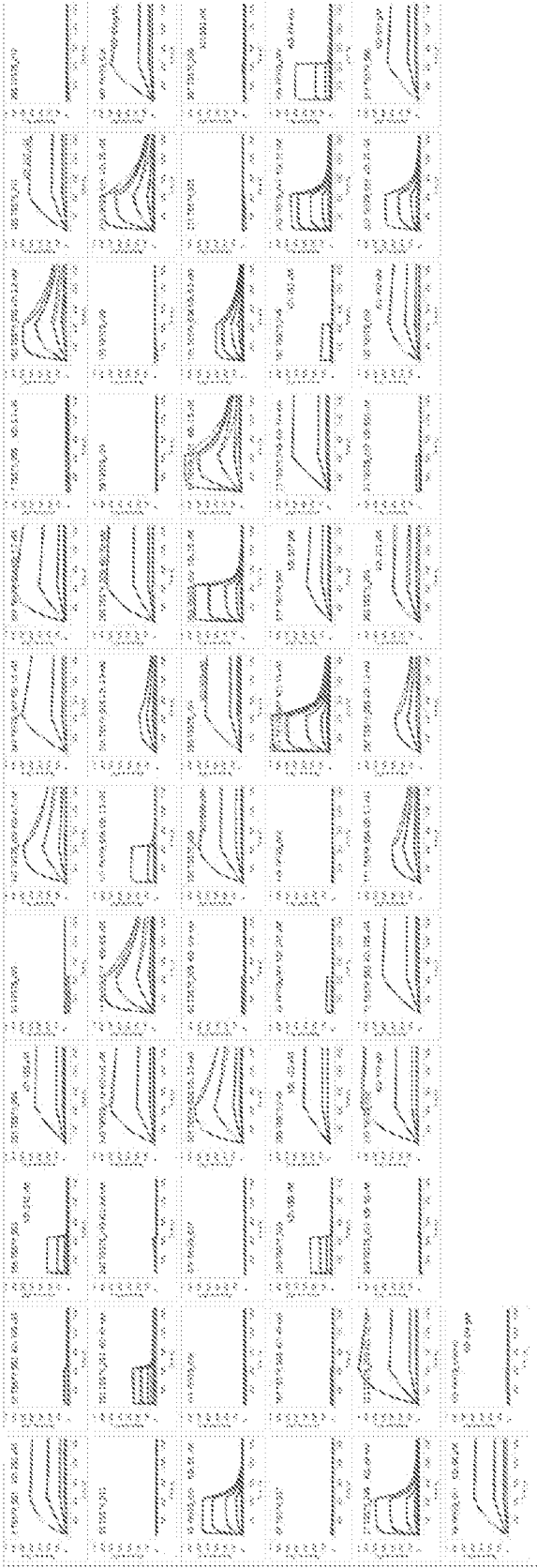
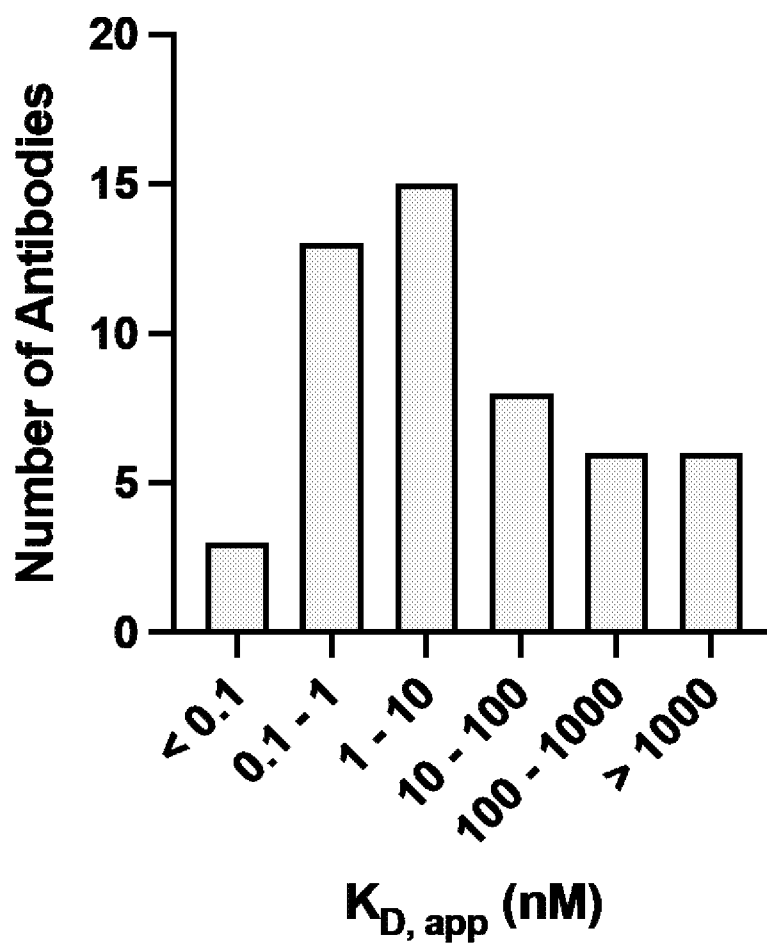


FIG. 10A

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Summary of Carterra Kinetic Data

**FIG. 10B**

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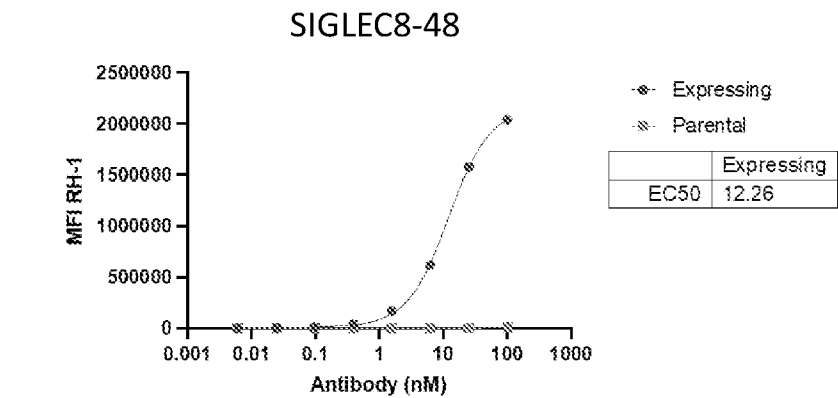


FIG. 11A

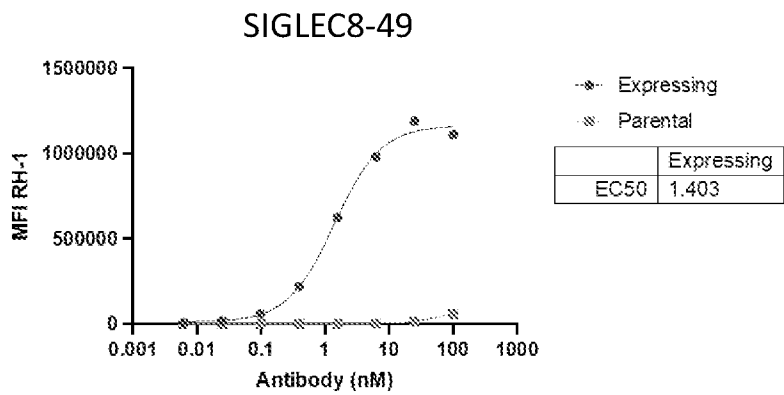


FIG. 11B

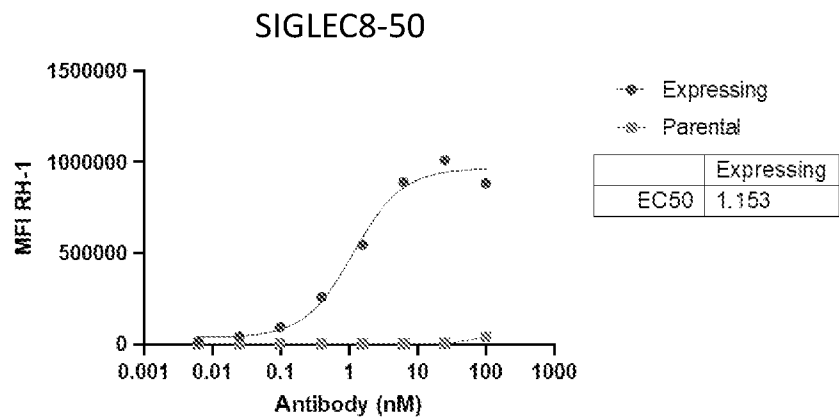


FIG. 11C

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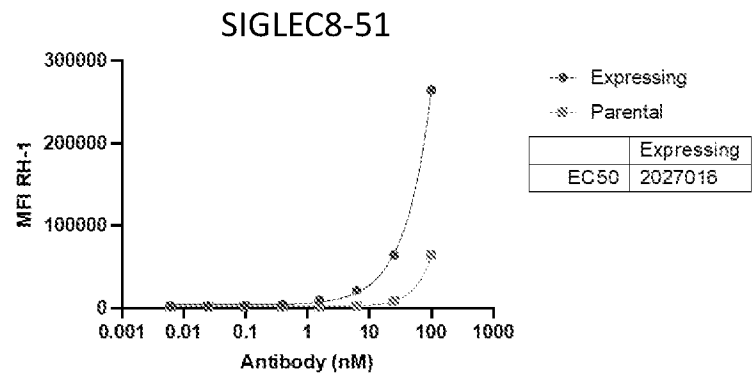


FIG. 11D

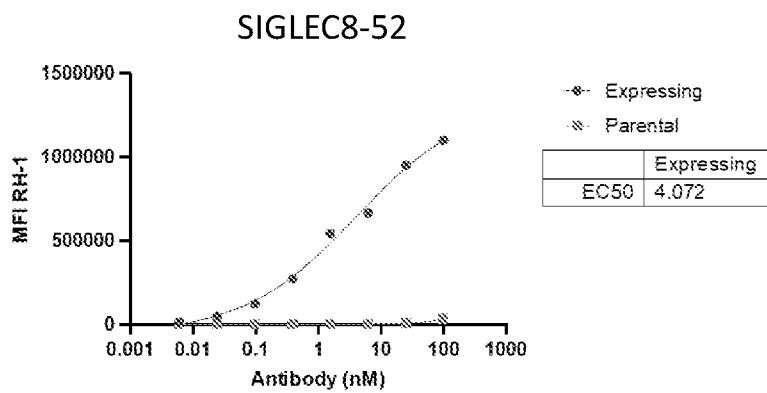


FIG. 11E

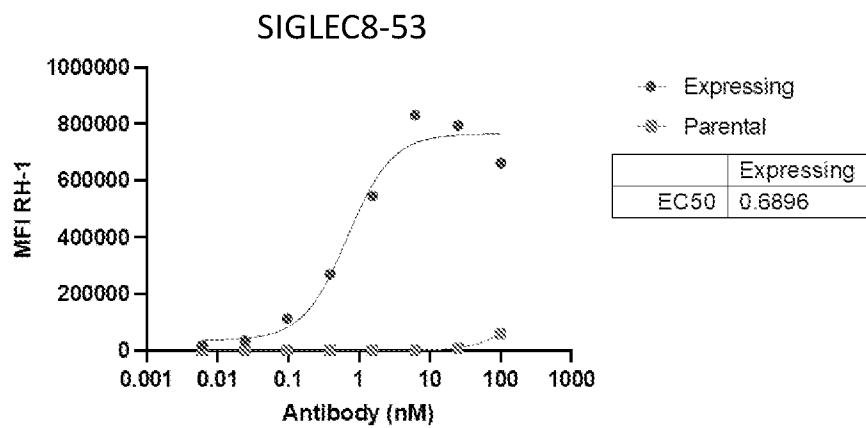


FIG. 11F

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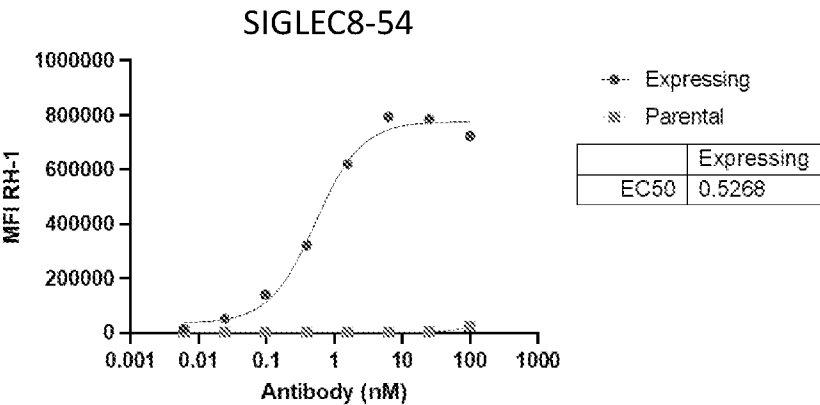


FIG. 11G

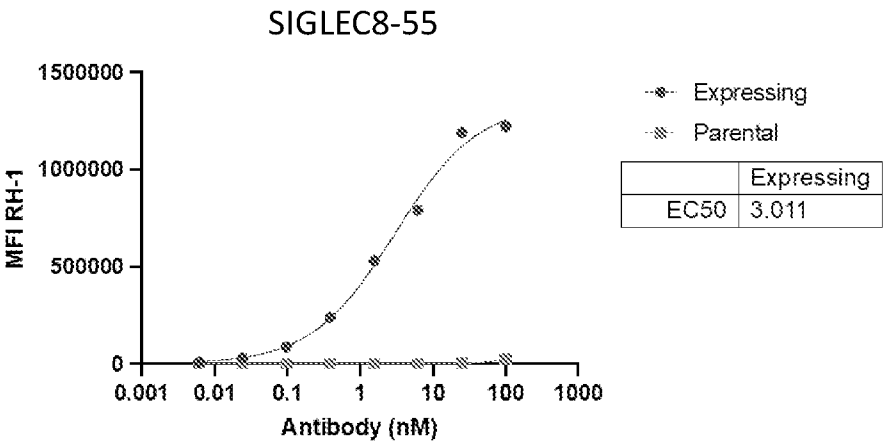


FIG. 11H

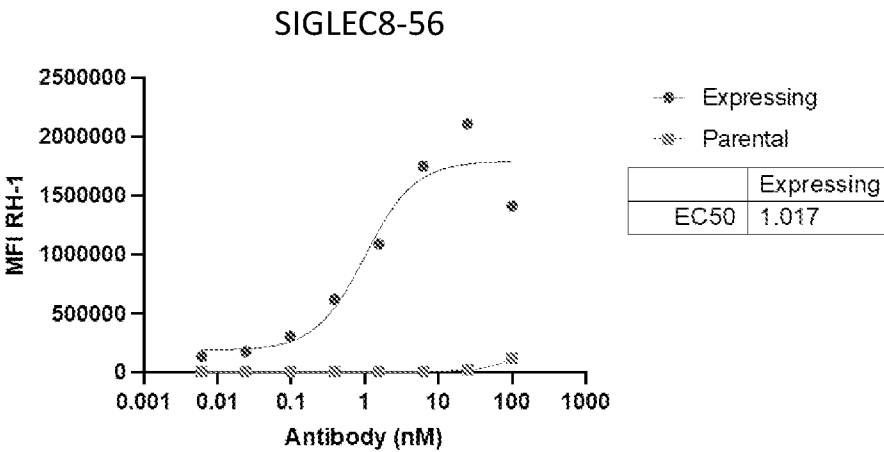


FIG. 11I

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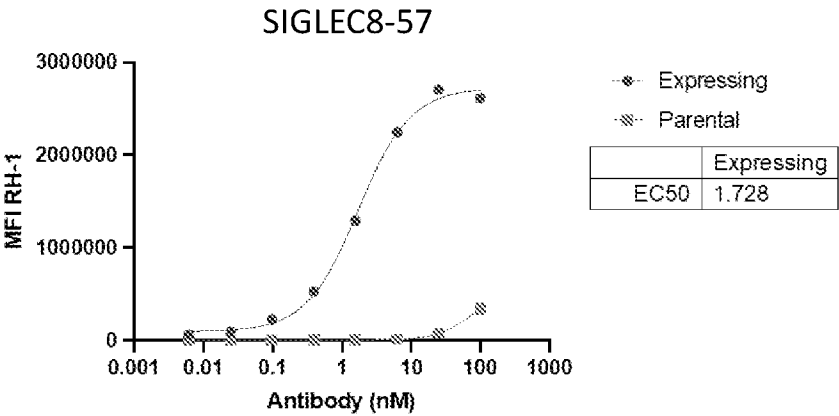


FIG. 11J

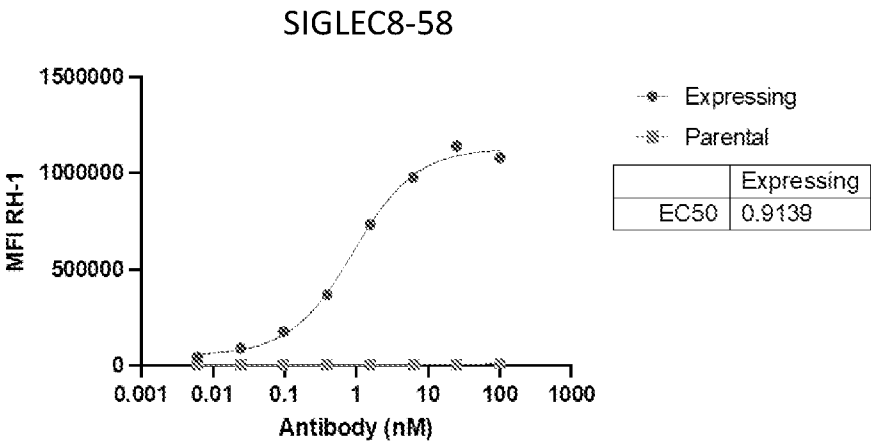


FIG. 11K

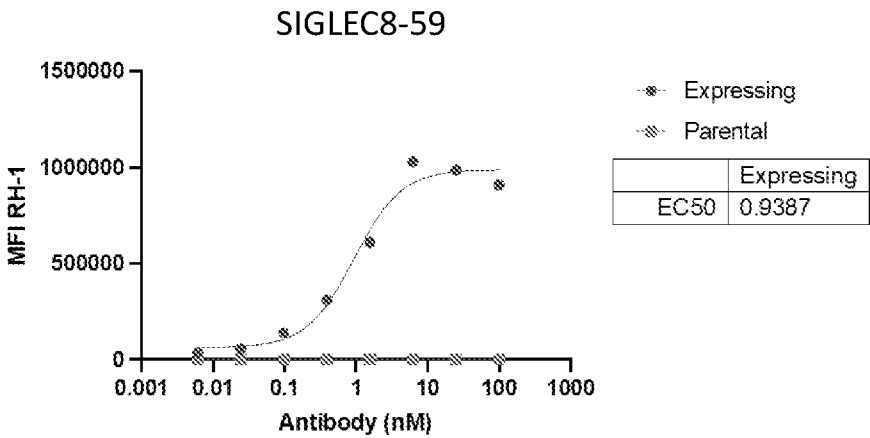


FIG. 11L

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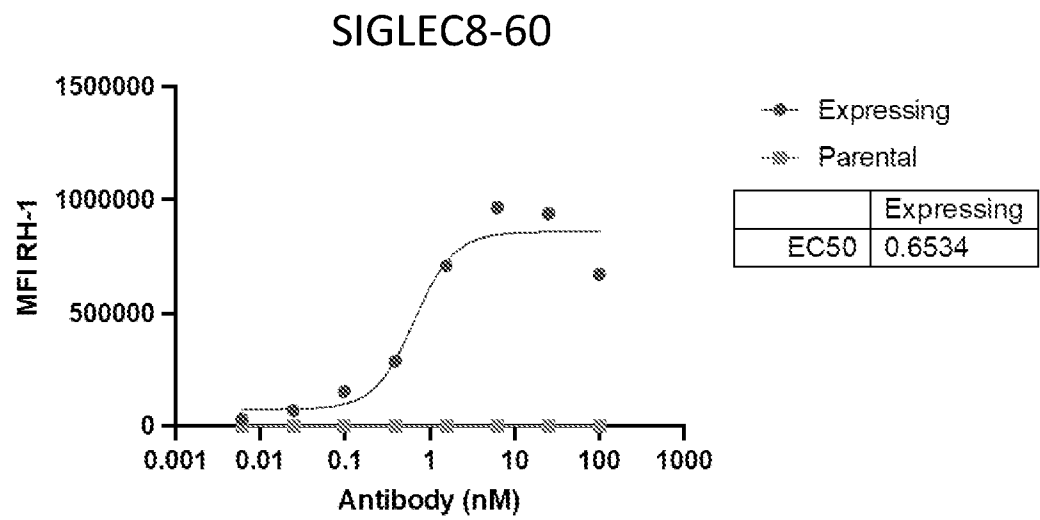


FIG. 11M

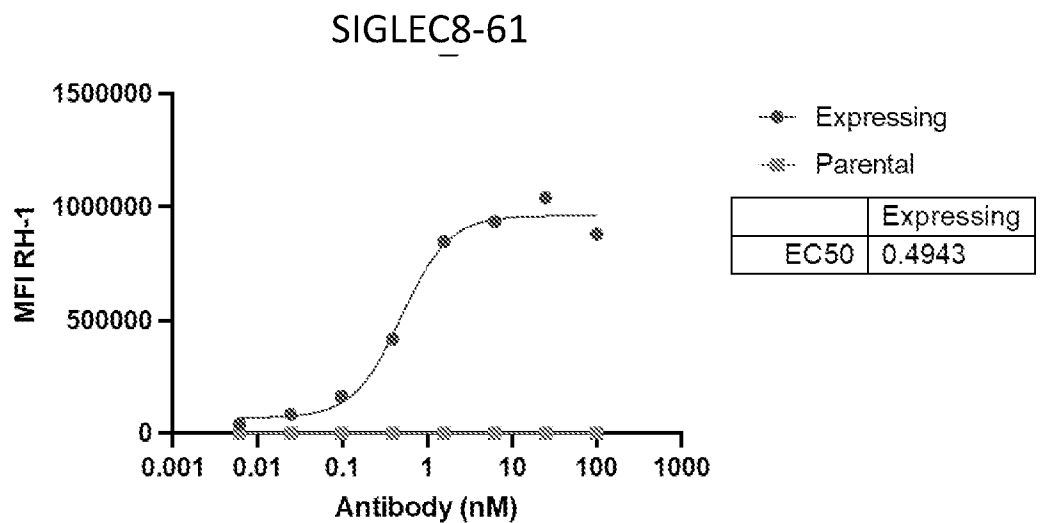
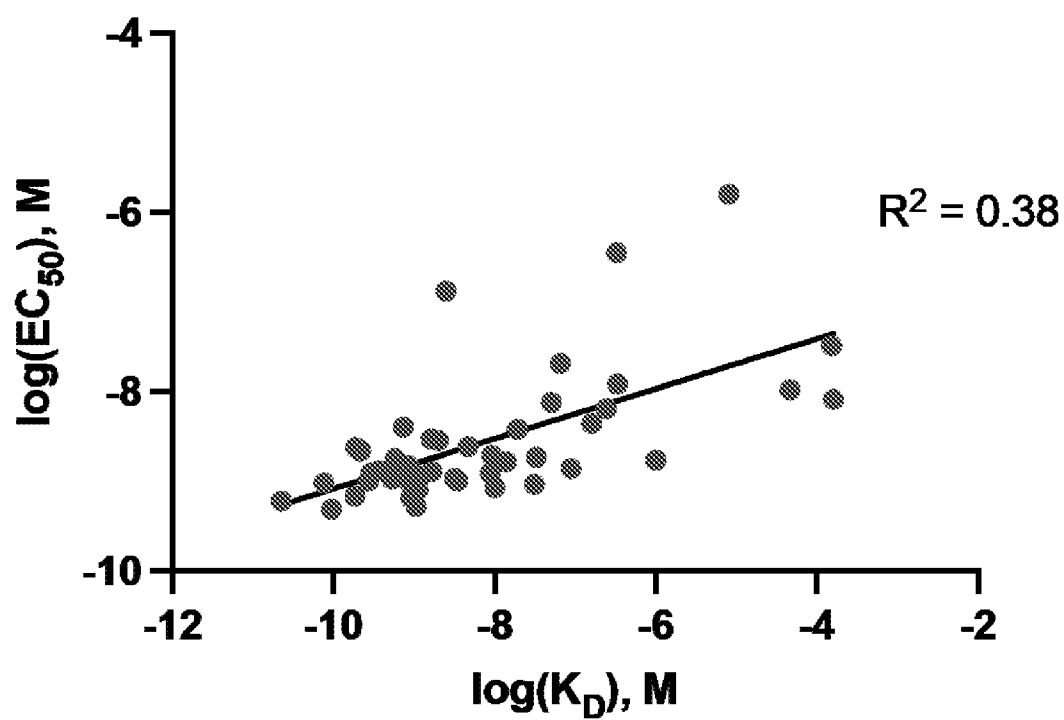


FIG. 11N

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 K_D vs EC_{50} Regression for SIGLEC-8 Antibodies

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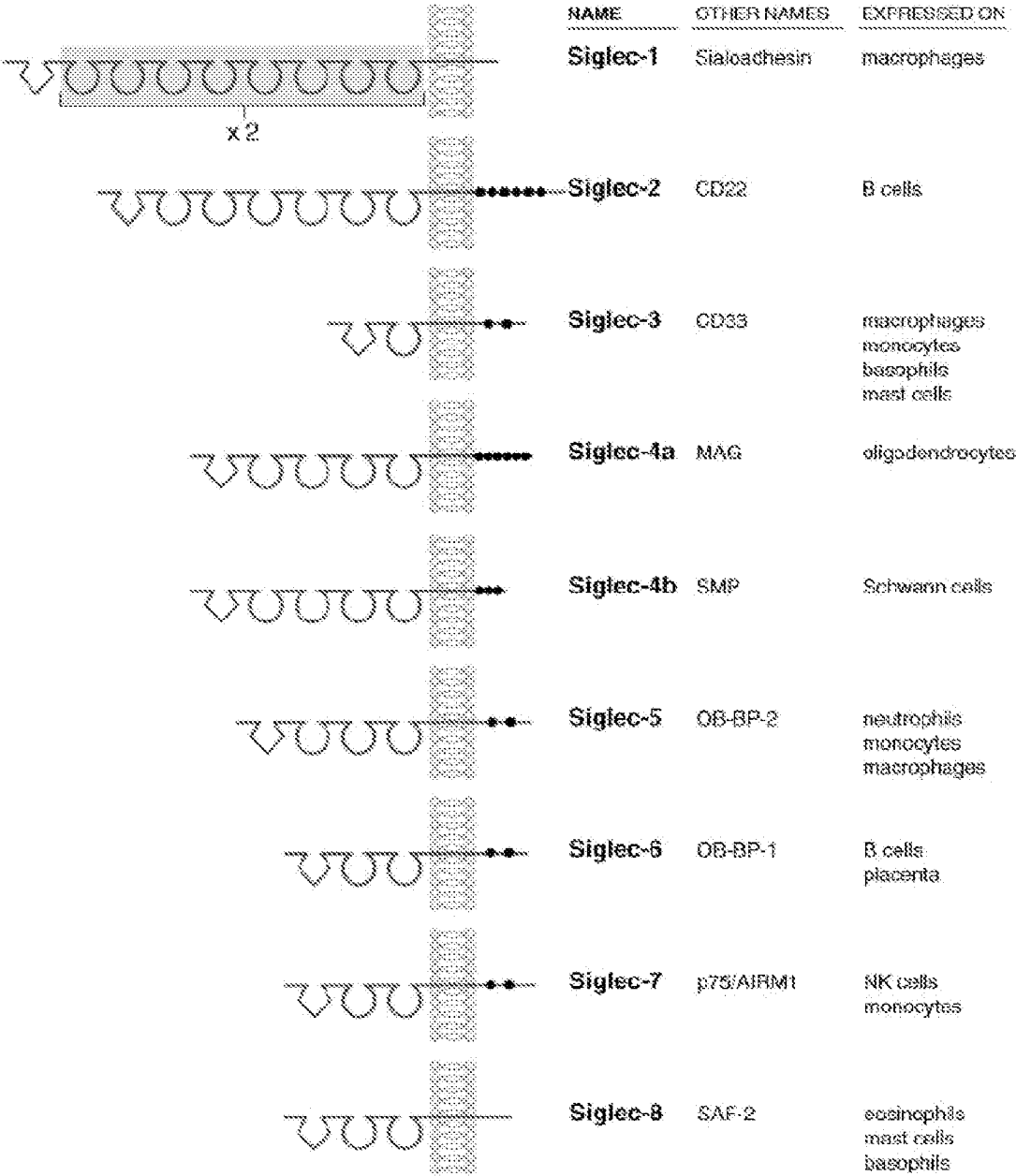


FIG. 12A

[illegible]

SIGLEC-8 = SEQ ID NO: 644
 SIGLEC-7= SEQ ID NO: 645
 OBBP-Like= SEQ ID NO: 646
 SIGLEC-5= SEQ ID NO: 647
 CD33= SEQ ID NO: 648
 SIGLEC-6= SEQ ID NO: 649

FIG. 12B

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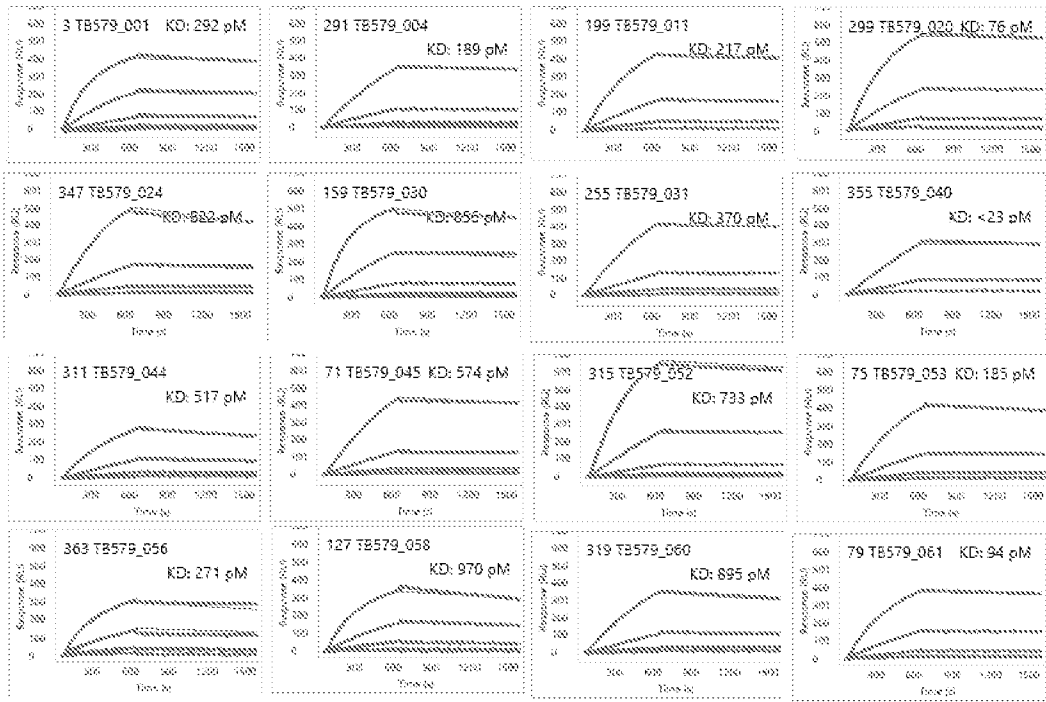


FIG. 13A

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Name	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	K_D (nM)
SIGLEC8-1	1.50E+05	4.38E-05	0.29
SIGLEC8-4	1.65E+05	3.12E-05	0.19
SIGLEC8-11	3.34E+05	7.23E-05	0.22
SIGLEC8-20	4.45E+05	3.40E-05	0.08
SIGLEC8-24	2.36E+05	1.94E-04	0.82
SIGLEC8-30	1.45E+05	1.24E-04	0.86
SIGLEC8-31	1.52E+05	5.63E-05	0.37
SIGLEC8-40	4.44E+05	1.00E-05	0.02
SIGLEC8-44	2.67E+05	1.38E-04	0.52
SIGLEC8-45	1.46E+05	8.37E-05	0.57
SIGLEC8-52	8.49E+04	6.22E-05	0.73
SIGLEC8-53	2.59E+05	4.78E-05	0.18
SIGLEC8-56	5.76E+05	1.56E-04	0.27
SIGLEC8-58	1.31E+05	1.27E-04	0.97
SIGLEC8-60	1.29E+05	1.16E-04	0.89
SIGLEC8-61	3.90E+05	3.67E-05	0.09

FIG. 13B

	SIGLEC-8	SIGLEC-2	SIGLEC-3	SIGLEC-5	SIGLEC-6	SIGLEC-7
	K_D (nM)	K_D (nM)	K_D (nM)	K_D (nM)	K_D (nM)	K_D (nM)
Control	0.031	N/A	N/A	N/A	N/A	N/A
SIGLEC8-1	0.29	196	135	5.8	7.0	5240
SIGLEC8-7	1.1	N/A	N/A	123	N/A	N/A
SIGLEC8-8	1.7	4300	N/A	39.3	5290	N/A
SIGLEC8-10	3.2	755	N/A	N/A	N/A	N/A
SIGLEC8-11	0.22	N/A	N/A	29.7	N/A	N/A
SIGLEC8-17	8.9	836	N/A	N/A	N/A	N/A
SIGLEC8-19	4.9	N/A	N/A	14.5	1070	N/A
SIGLEC8-24	0.82	21100	N/A	33.7	N/A	N/A
SIGLEC8-32	19	128	104	4.2	5.3	17.4
SIGLEC8-34	9.2	208	62.2	5.5	6.9	N/A
SIGLEC8-44	0.52	N/A	N/A	6.7	35.2	N/A
SIGLEC8-48	336	629	N/A	N/A	N/A	N/A
SIGLEC8-54	1.1	N/A	N/A	19.9	12.0	N/A
SIGLEC8-56	0.27	43.2	60.5	3.4	5.0	18.0
SIGLEC8-57	990	N/A	N/A	28.3	9.6	N/A
SIGLEC8-58	0.97	N/A	N/A	169	N/A	N/A

FIG. 13C

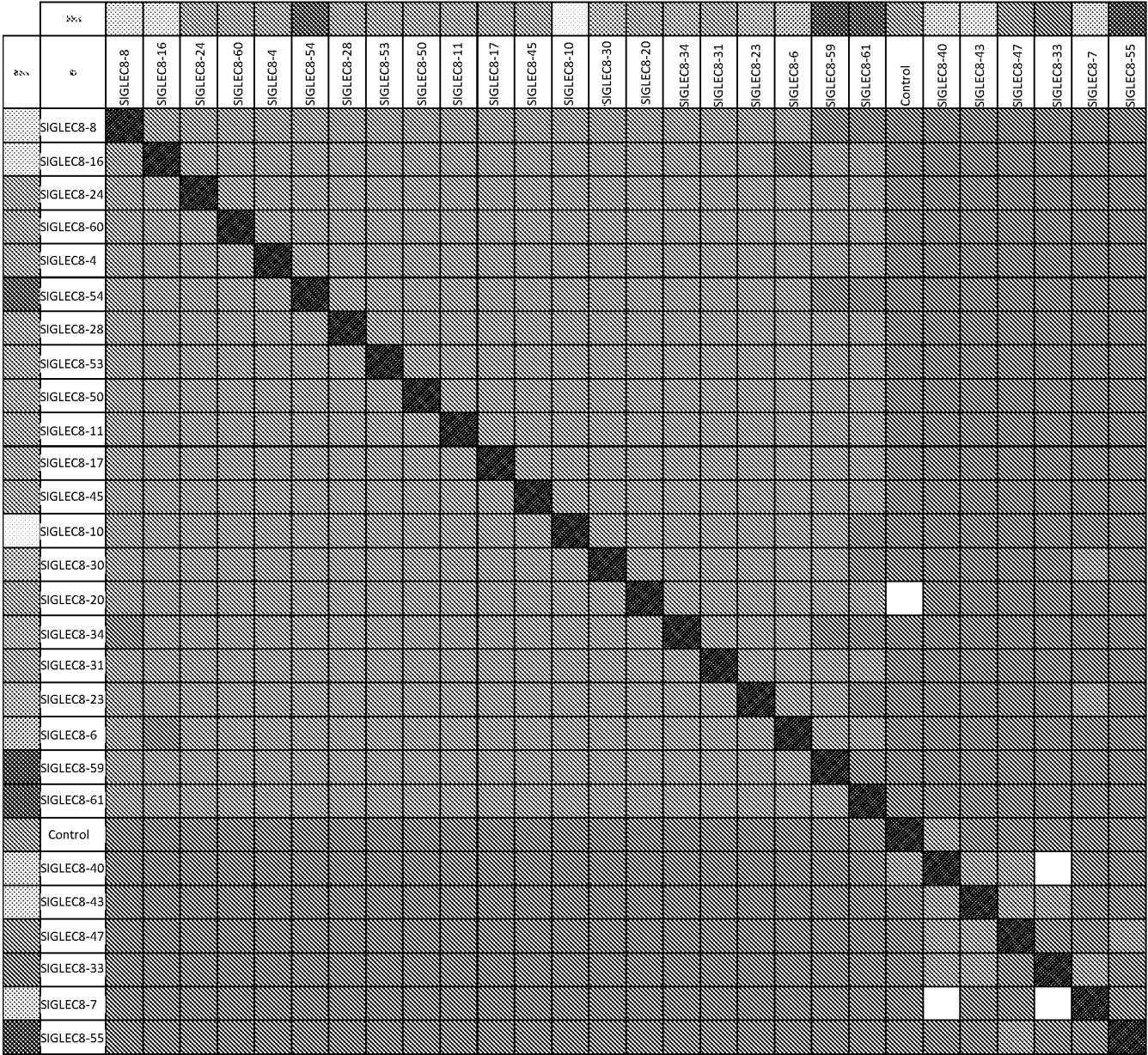


FIG. 14A

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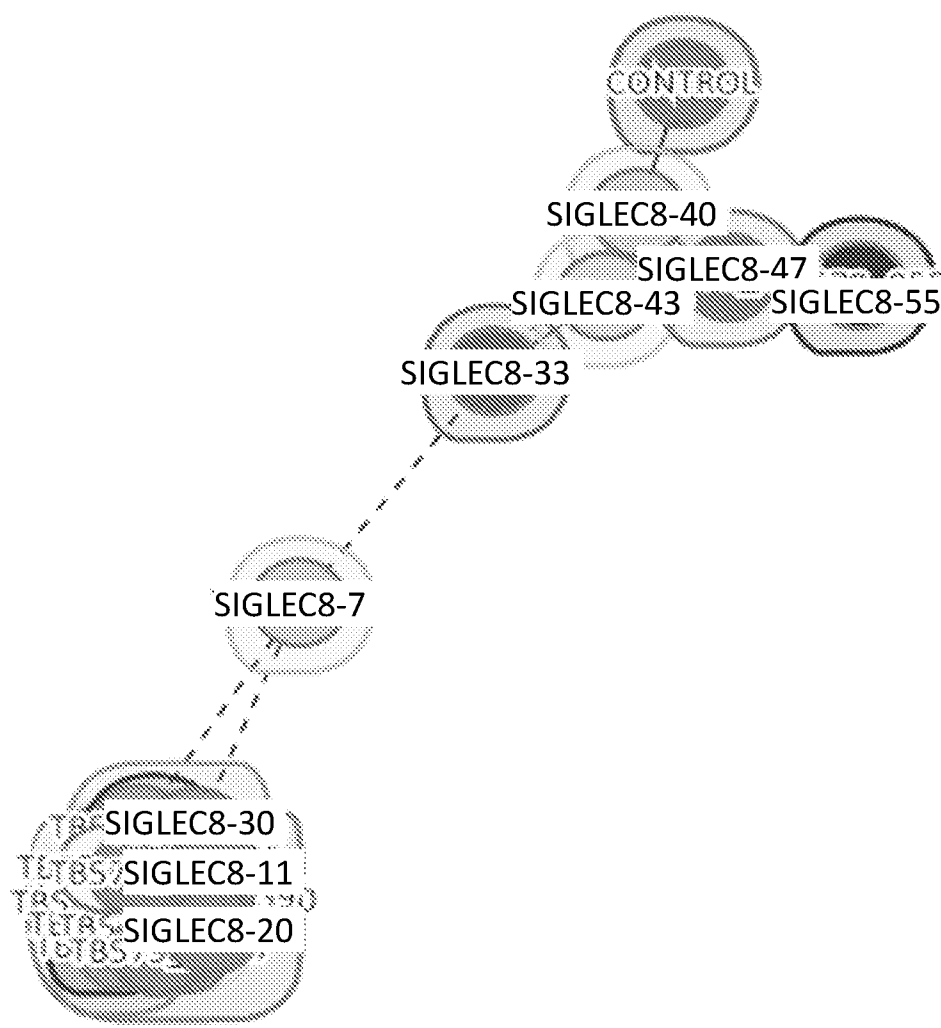


FIG. 14B

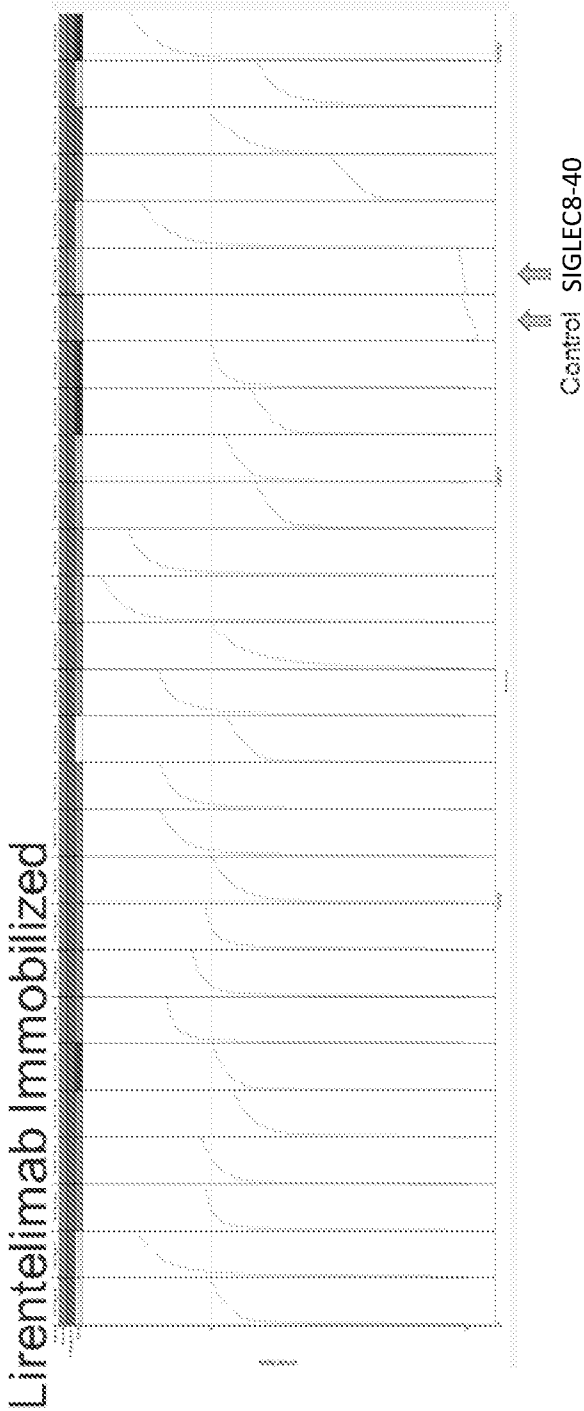


FIG. 15A

SIGLEC8-40 Immobilized

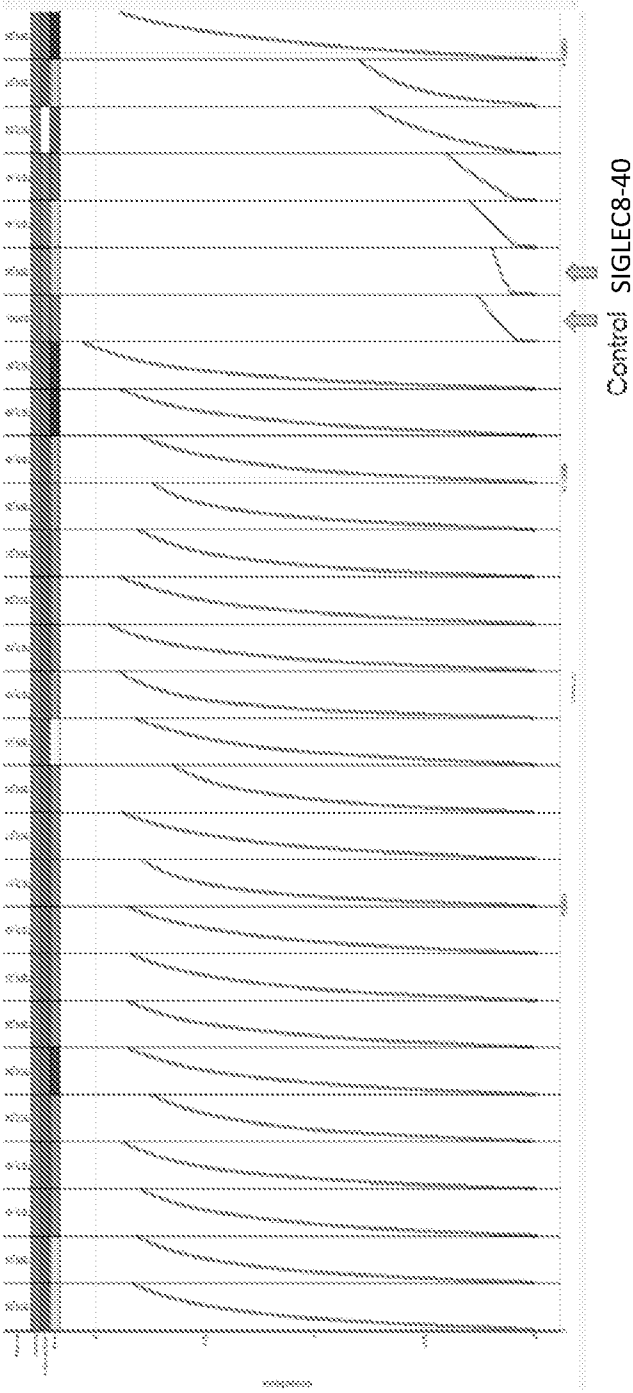


FIG. 15B

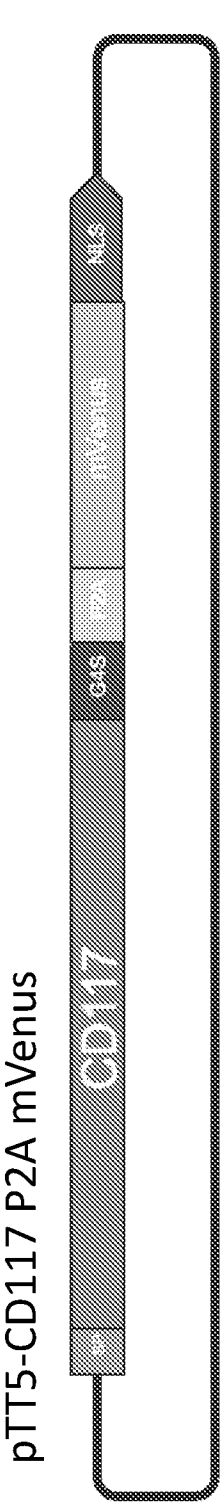


FIG. 16A

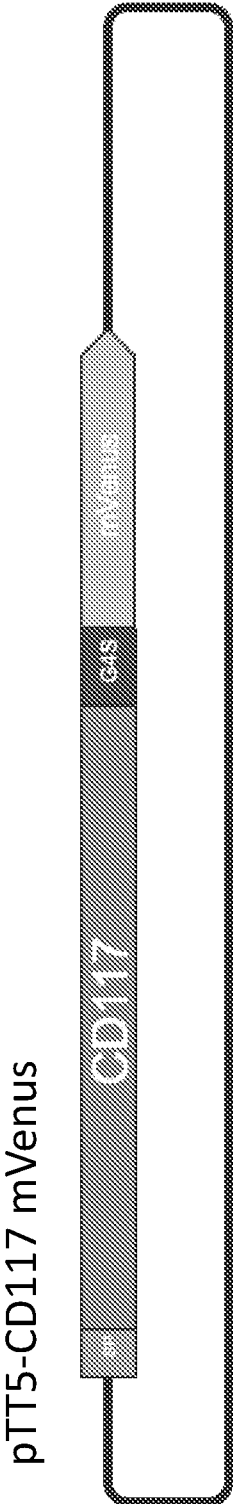
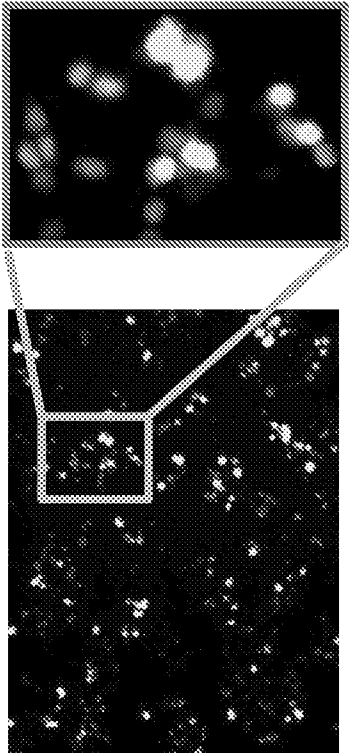


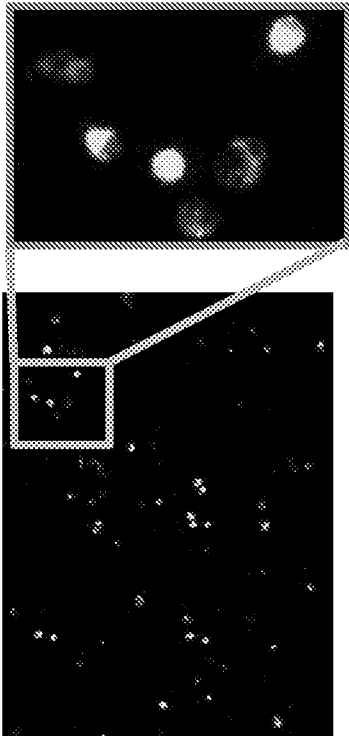
FIG. 16B

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CD117-P2A-mVenus

FIG. 16D



CD117-mVenus

GFP

FIG. 16C

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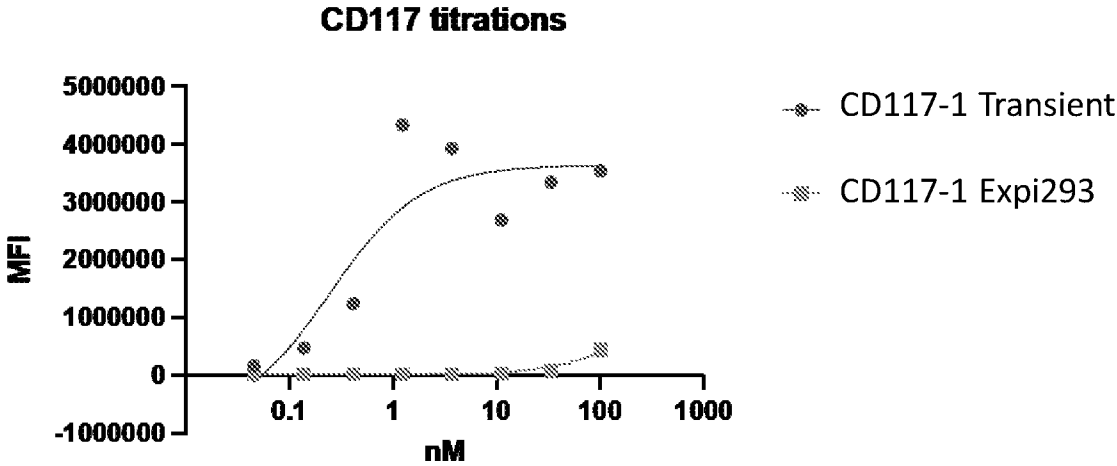


FIG. 17A

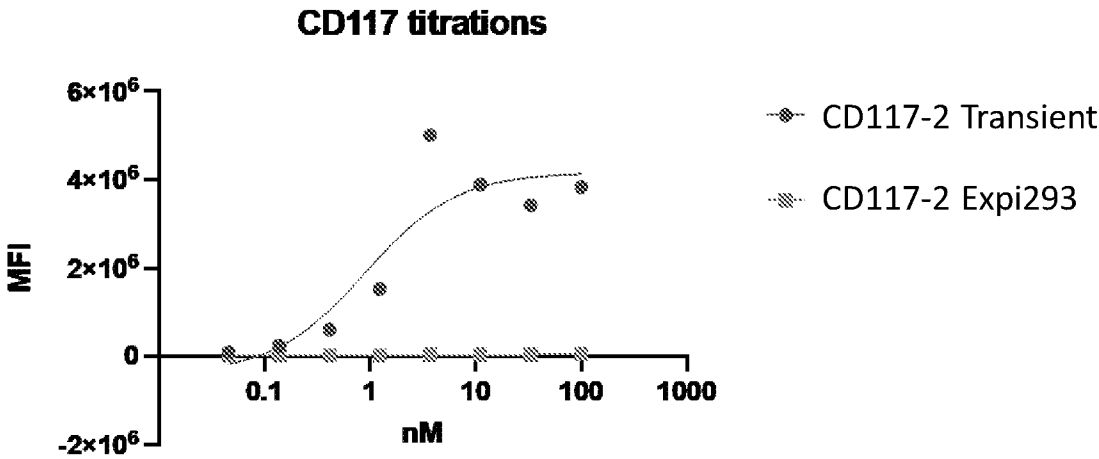


FIG. 17B

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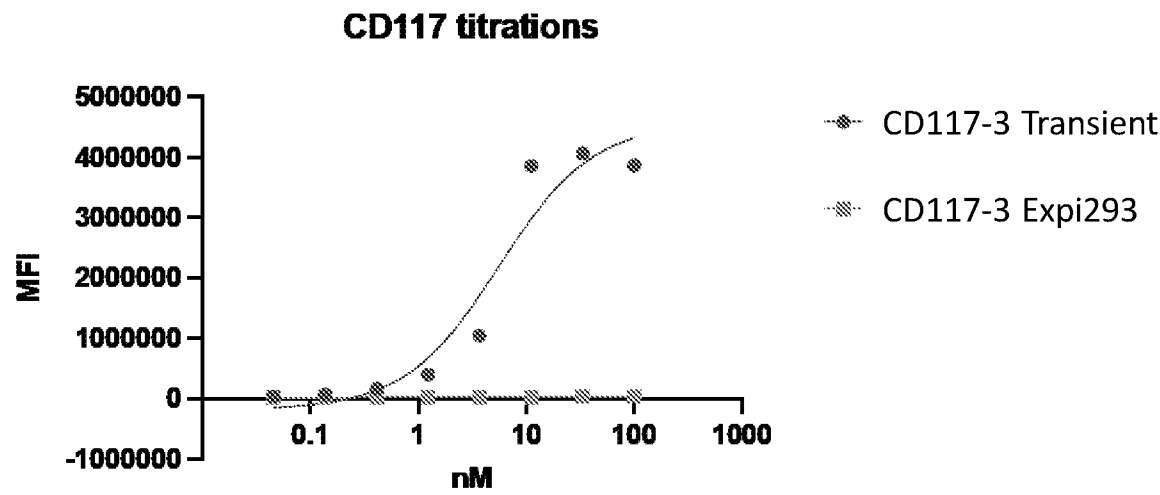


FIG. 17C

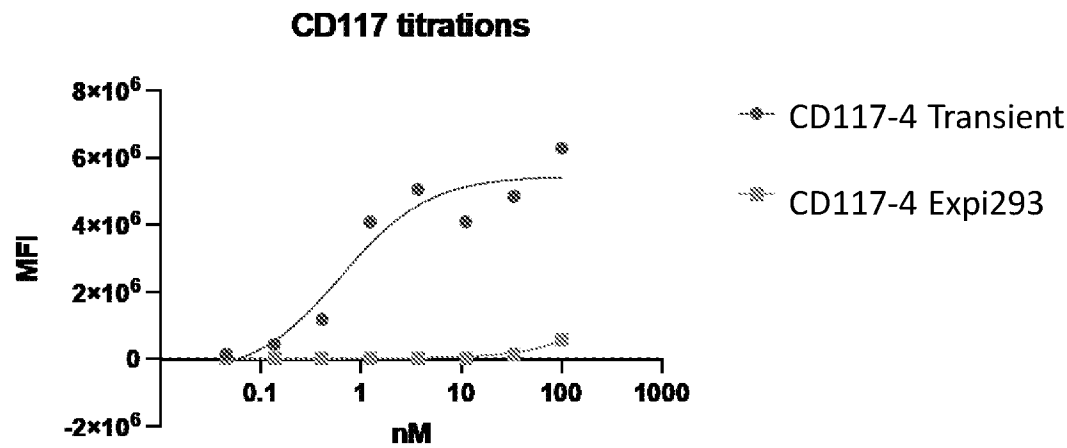


FIG. 17D

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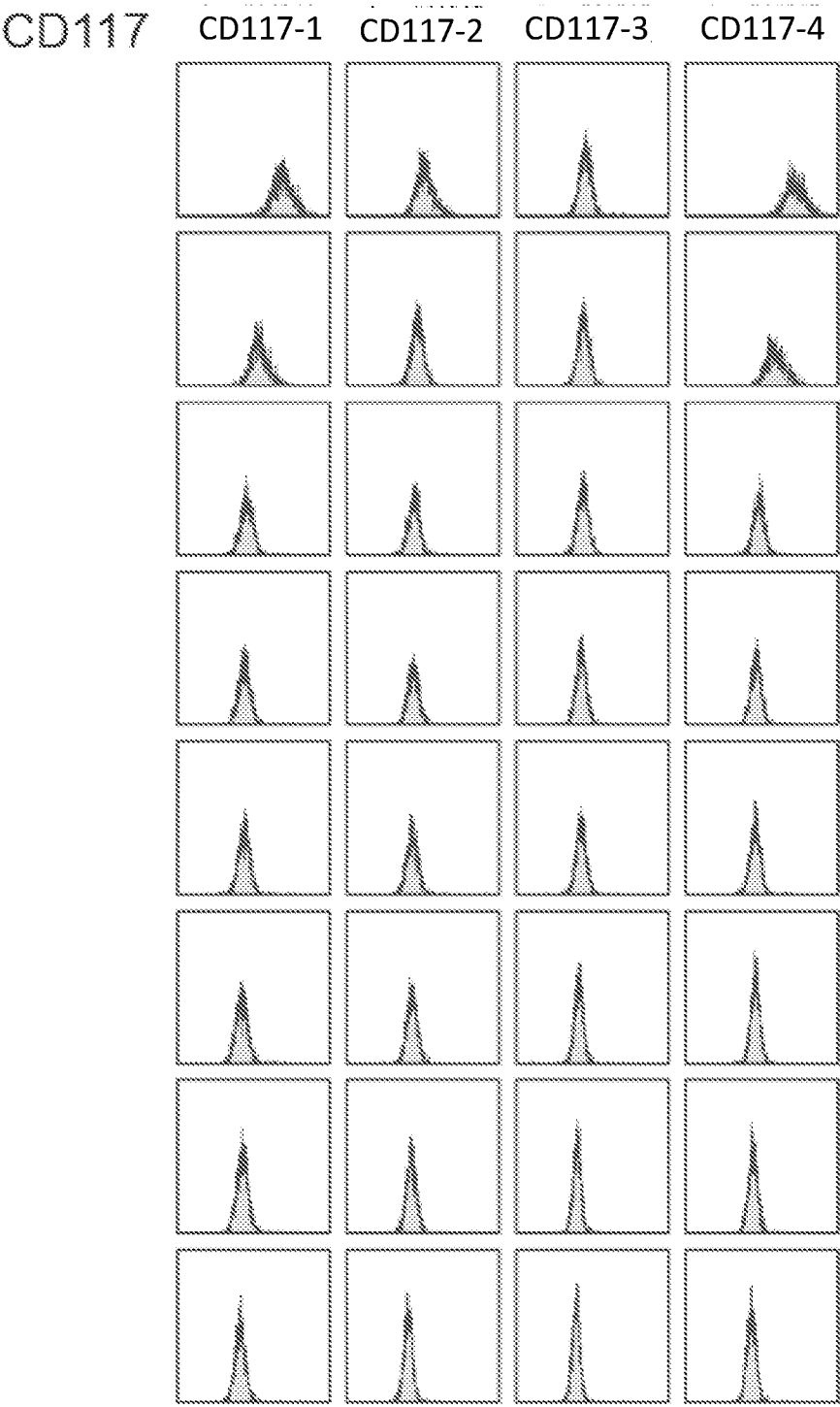


FIG. 17E

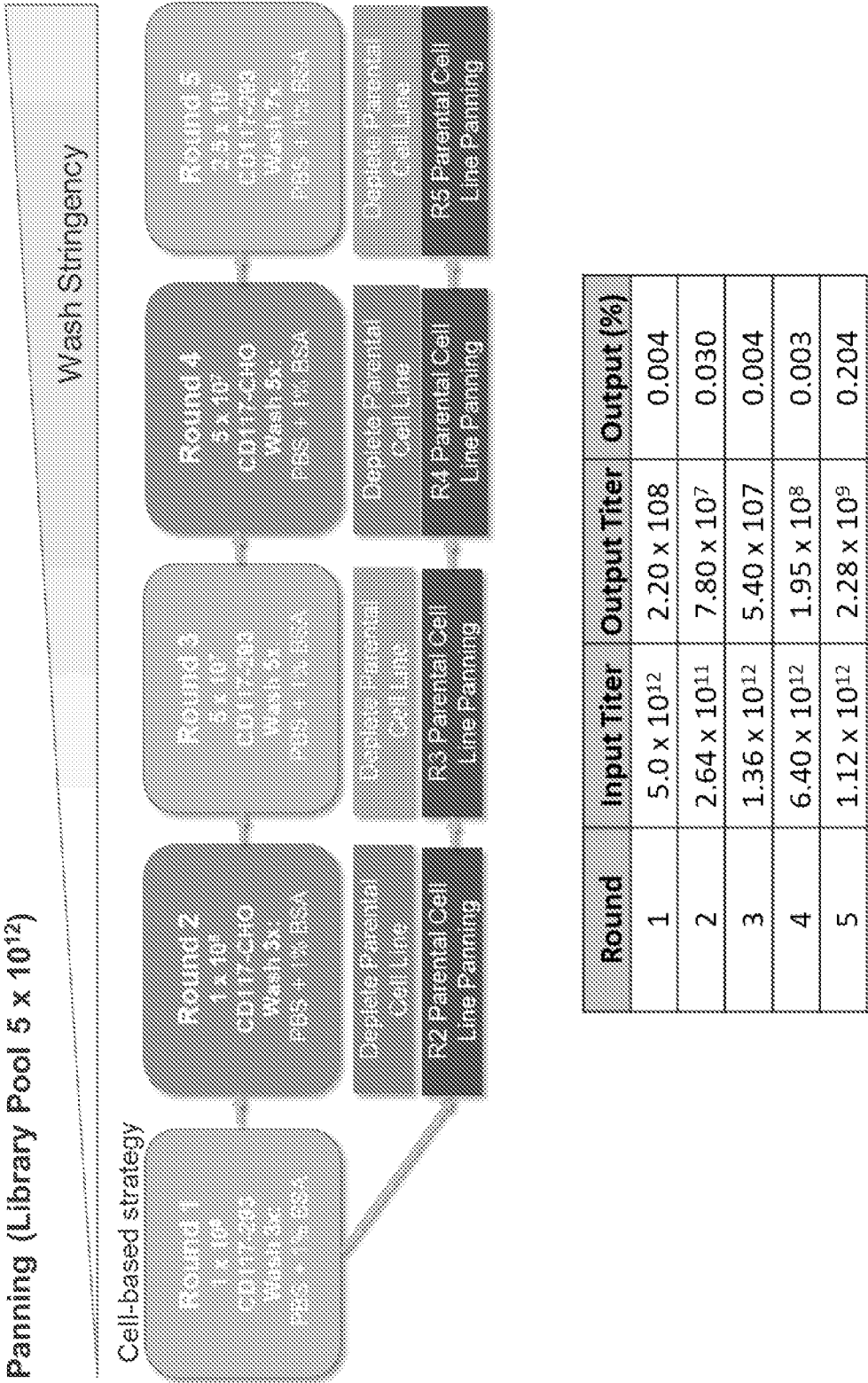
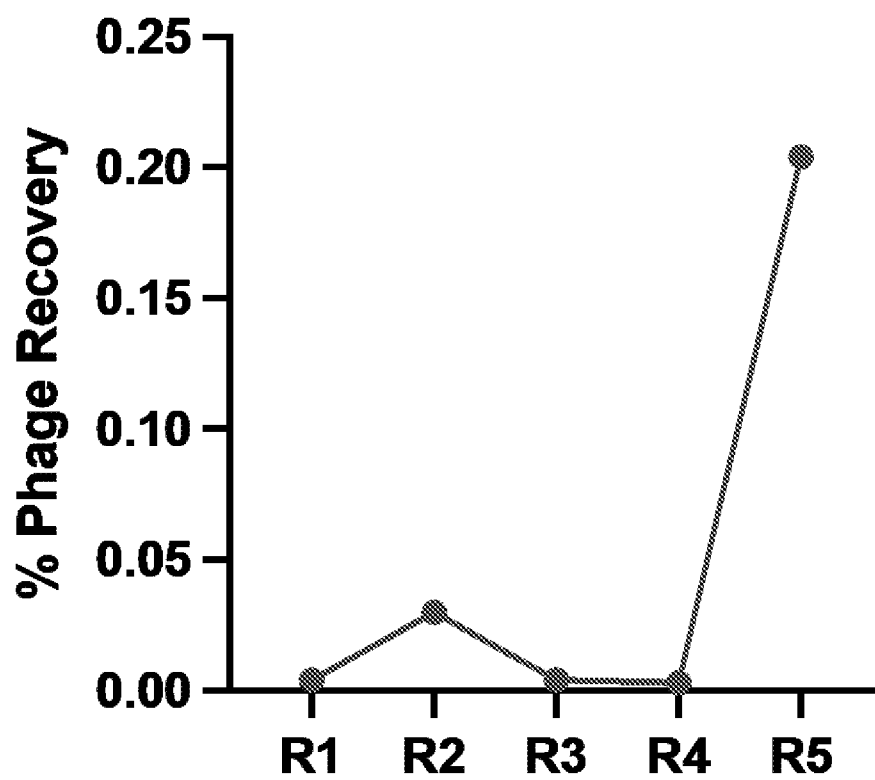


FIG. 18A

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CD117 Panning Phage Recovery**FIG. 18B**

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Top 100 Clusters Grouped by cdr1-cdr2-cdr3_len both , Dist by cdr1-cdr2-cdr3 both, dist cutoff: 5 aa, , linkage average_21.195 k sample

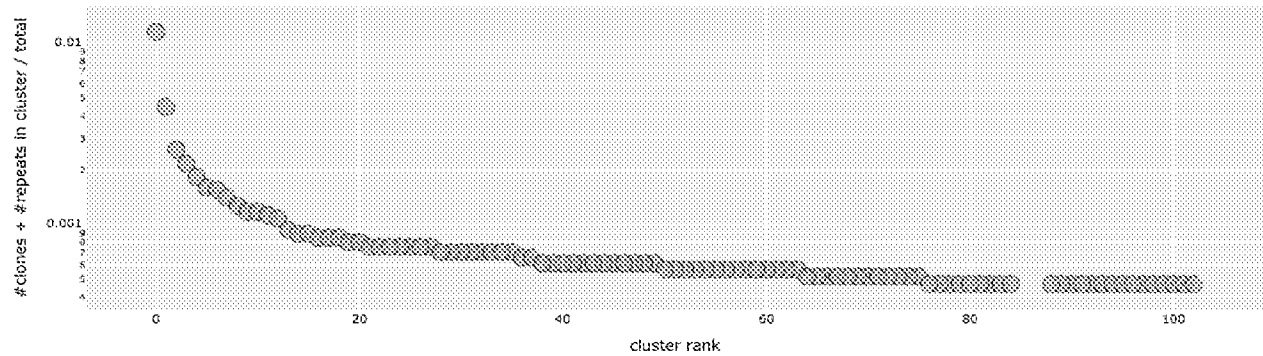


FIG. 19A

Top 100 Clusters Grouped by cdr1-cdr2-cdr3_len both , Dist by cdr1-cdr2-cdr3 both, dist cutoff: 5 aa, , linkage average_25.202 k sample

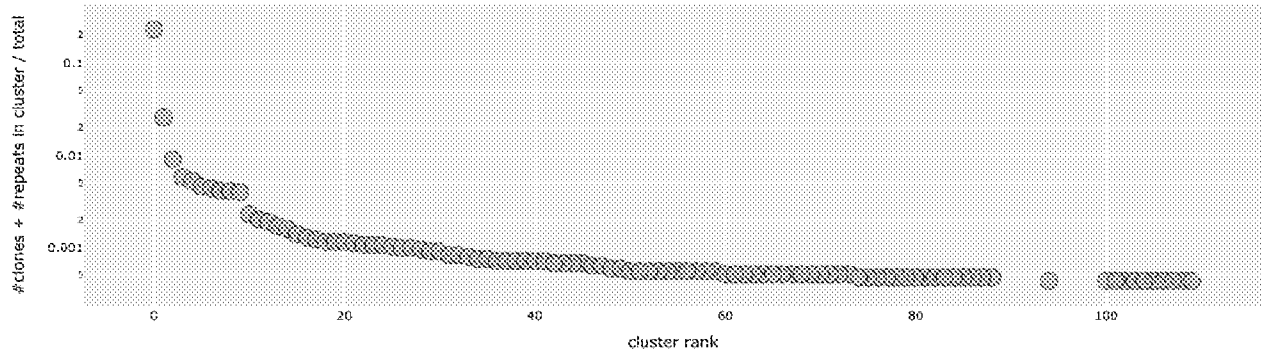


FIG. 19B

Overlap of Unique Sequences by cdr3_aa Between Rounds

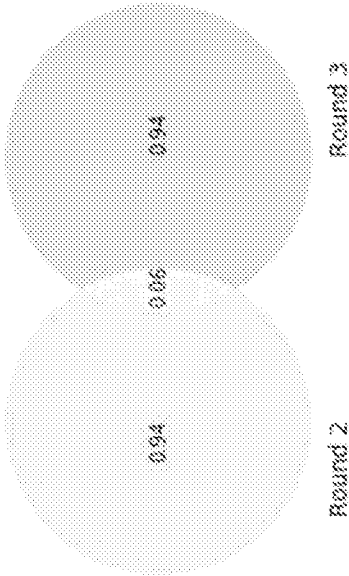


FIG. 19C

Overlap of Unique Sequences by cdr3_aa Between Rounds

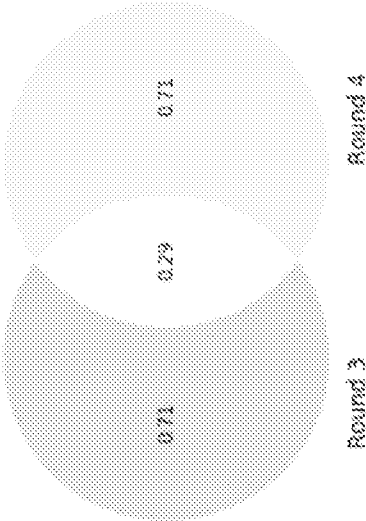


FIG. 19D

Overlap of Unique Sequences by cdr3_aa Between Rounds

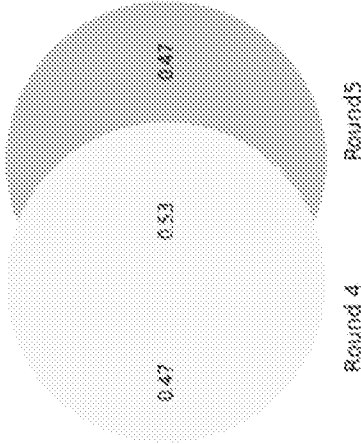


FIG. 19E

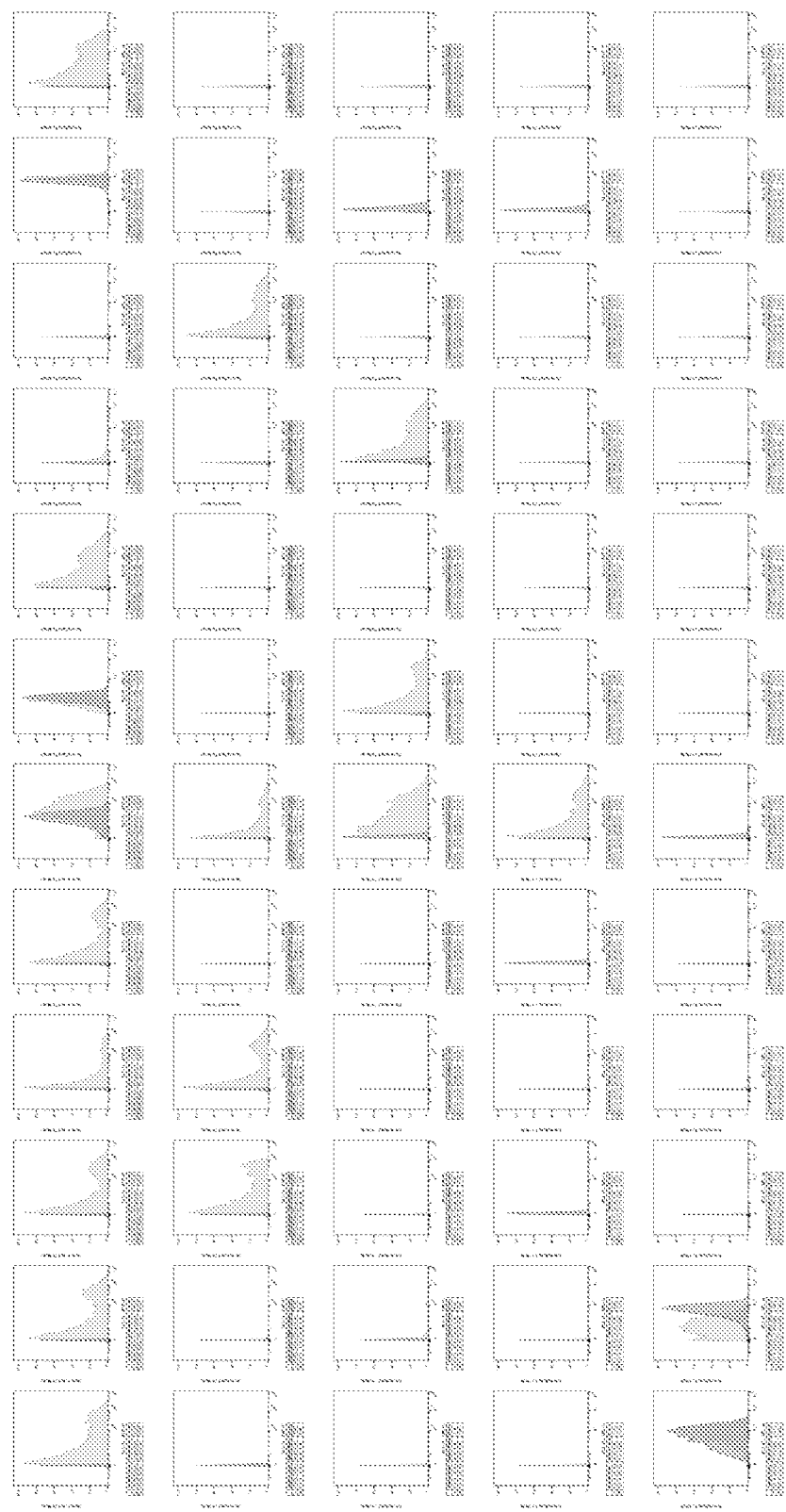


FIG. 20A

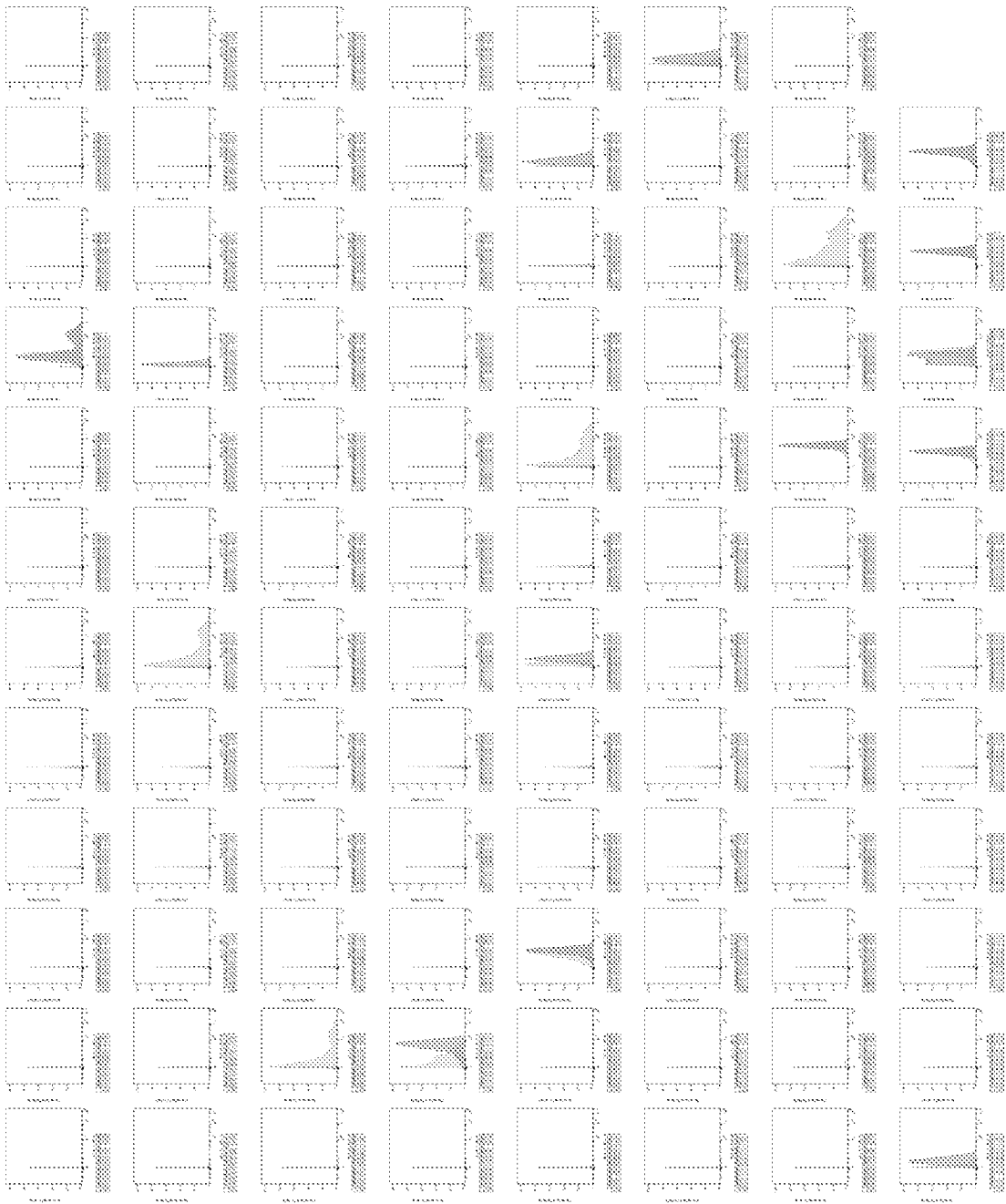


FIG. 20B

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	Expressing	Parental	MFI Ratio	Concentration (ug/uL)
CD117-2	1357	44.2	30.701	0.0607
CD117-9	1730	59.5	29.076	0.3737
CD117-1	1401	52.7	26.584	0.3527
CD117-7	1524	69.7	21.865	1.2278
CD117-3	1051	49.3	21.318	0.0859
CD117-5	977	45.9	21.285	0.052
CD117-21	1517	71.4	21.246	0.0107
CD117-10	1262	59.5	21.210	0.0133
CD117-17	1096	54.4	20.147	0.41
CD117-15	1022	54.4	18.787	0.233
CD117-13	1076	57.8	18.616	1.148
CD117-11	788	45.9	17.168	0.0942
CD117-18	883	54.4	16.232	0.39
CD117-20	879	61.2	14.363	0.91
CD117-19	744	57.8	12.872	0.74
CD117-14	2145	176	12.189	1.8201
CD117-12	633	59.5	10.639	0.0075
CD117-4	806	57.8	10.484	0.9278
CD117-16	1444	172	8.395	0.05
CD117-8	224	52.7	4.250	0.2009

FIG. 20C

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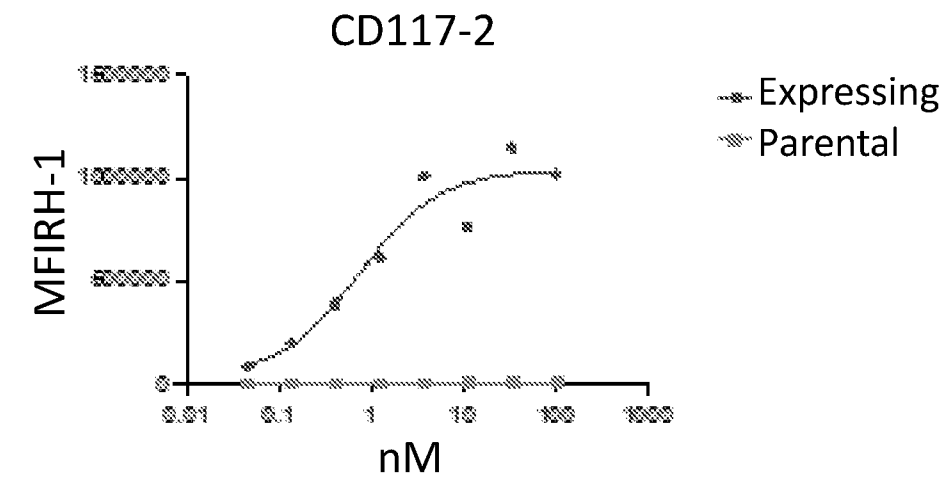


FIG. 21A

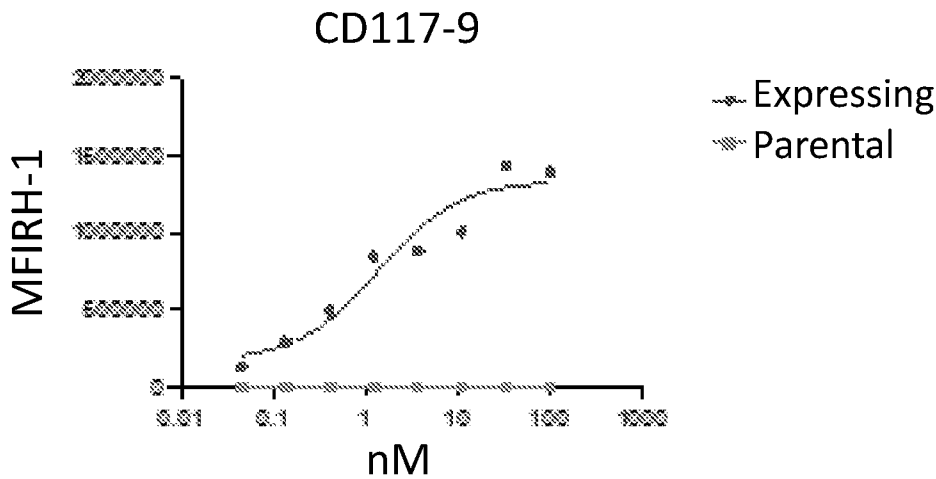


FIG. 21B

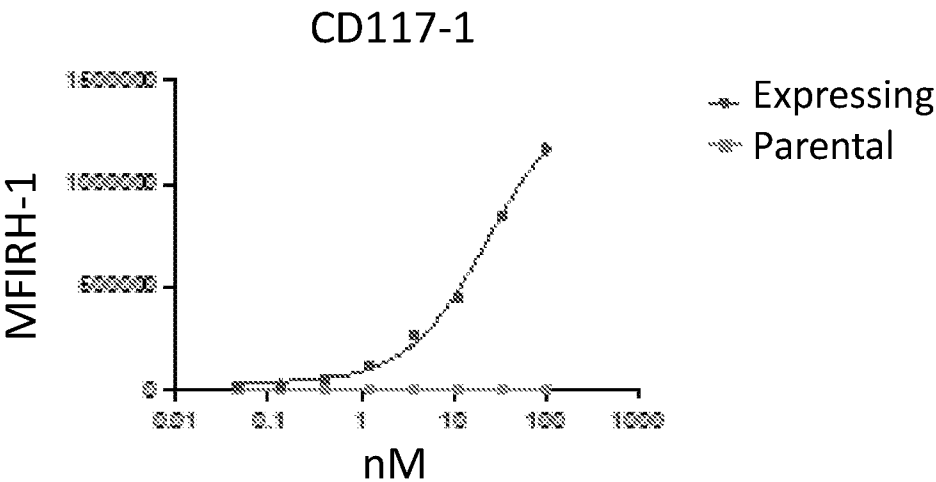


FIG. 21C

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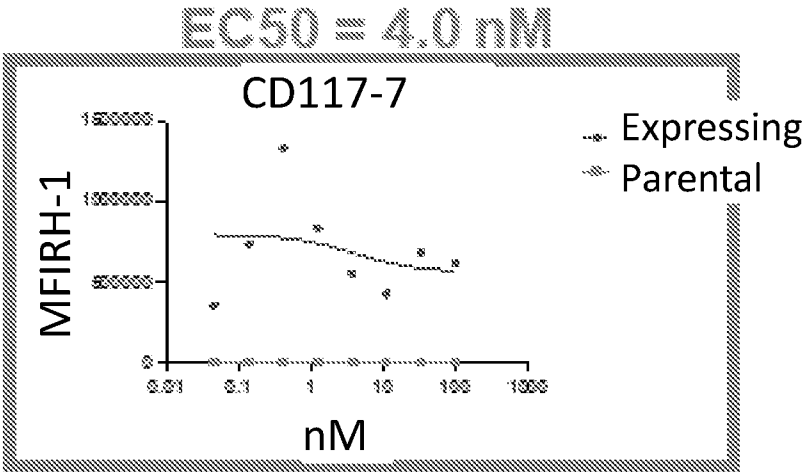


FIG. 21D

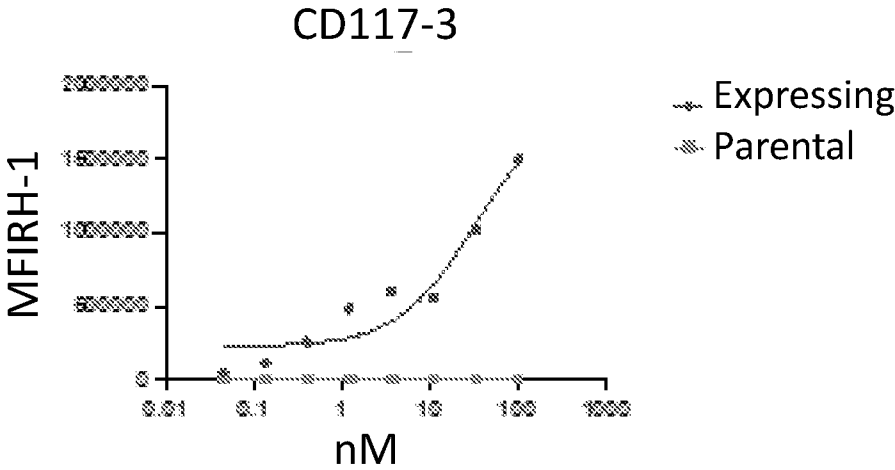


FIG. 21E

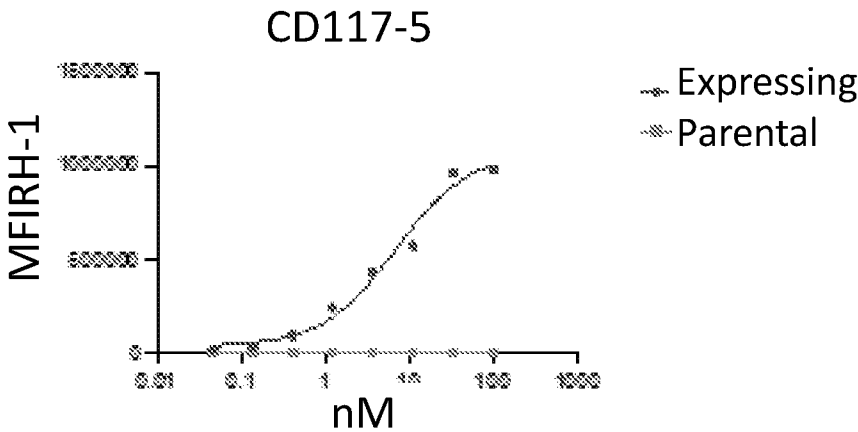


FIG. 21F

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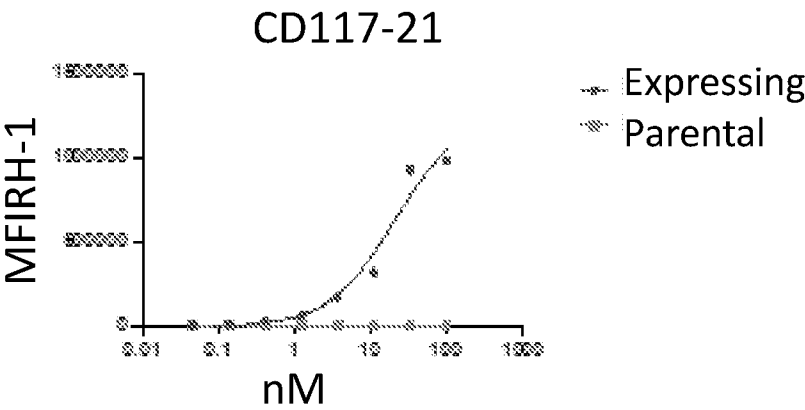


FIG. 21G

EC50= 91.28 nM

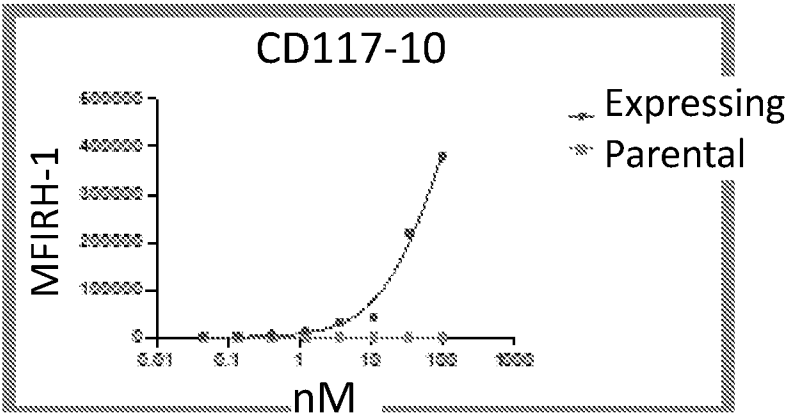


FIG. 21H

EC50 = 7.6 nM

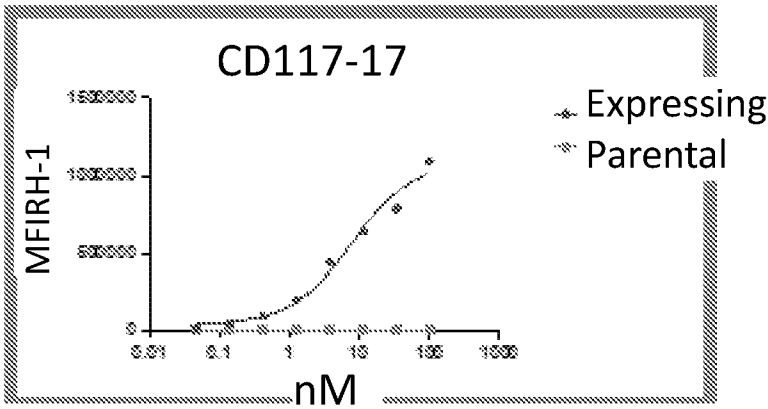


FIG. 21I

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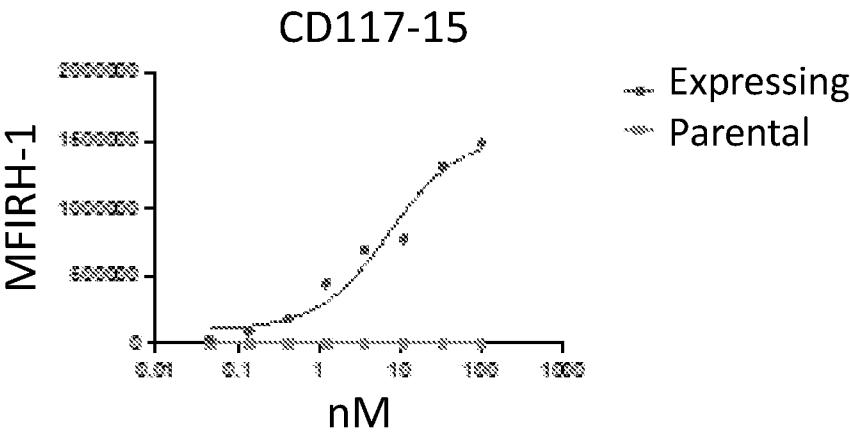


FIG. 21J

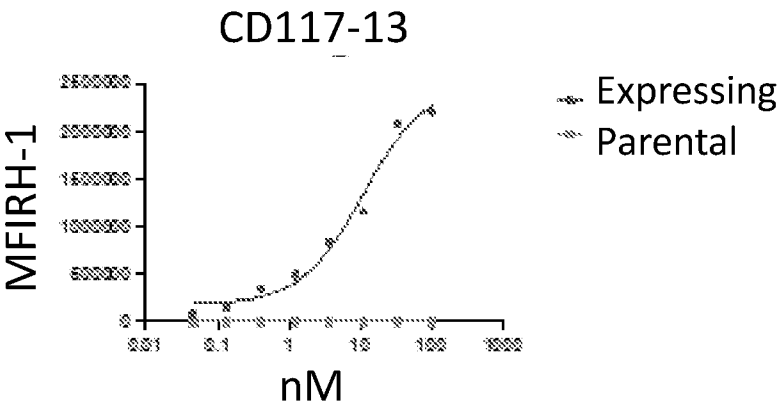


FIG. 21K

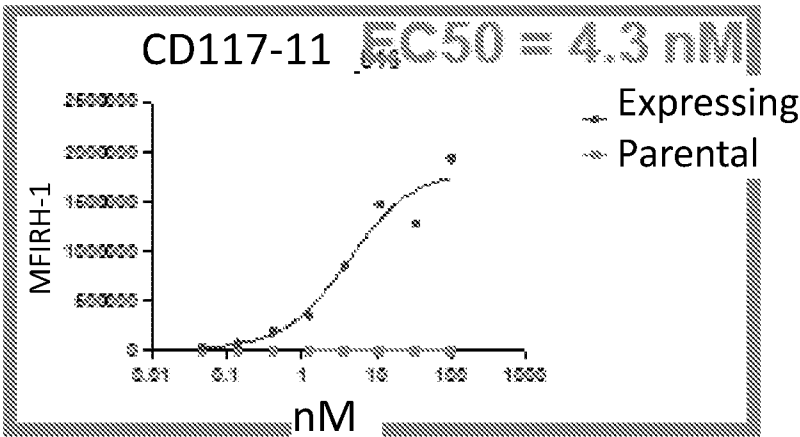


FIG. 21L

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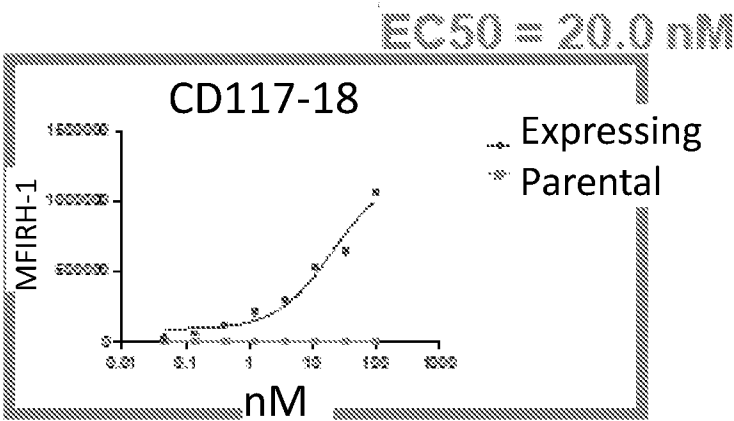


FIG. 21M

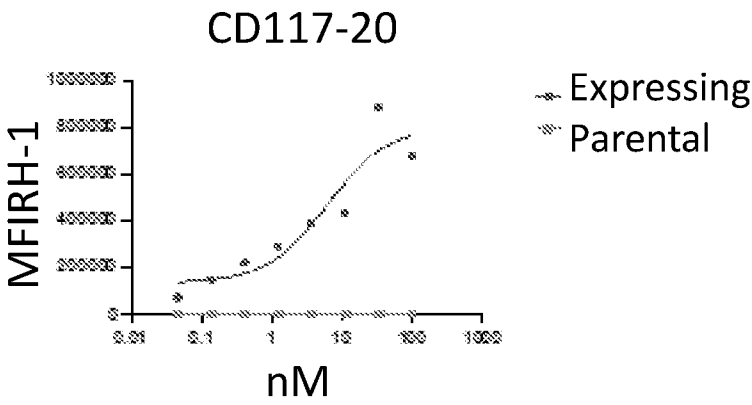


FIG. 21N

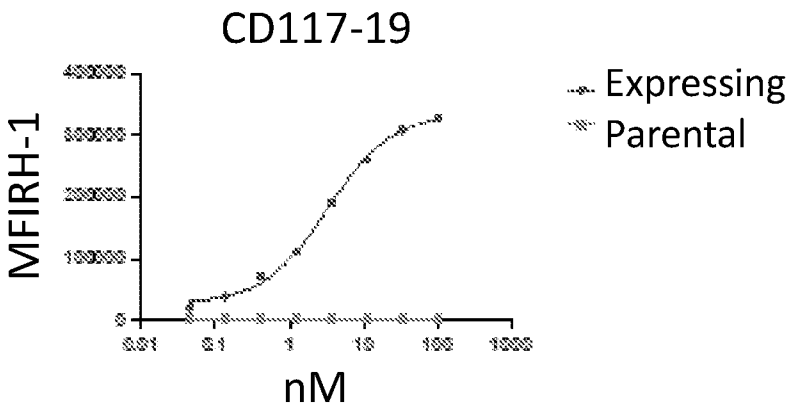


FIG. 21O

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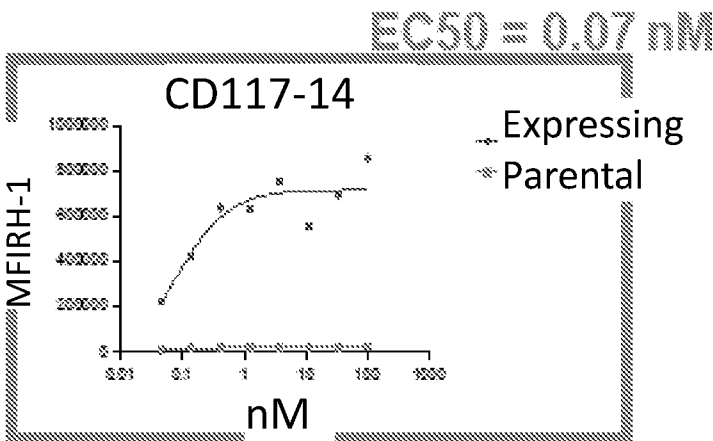


FIG. 21P

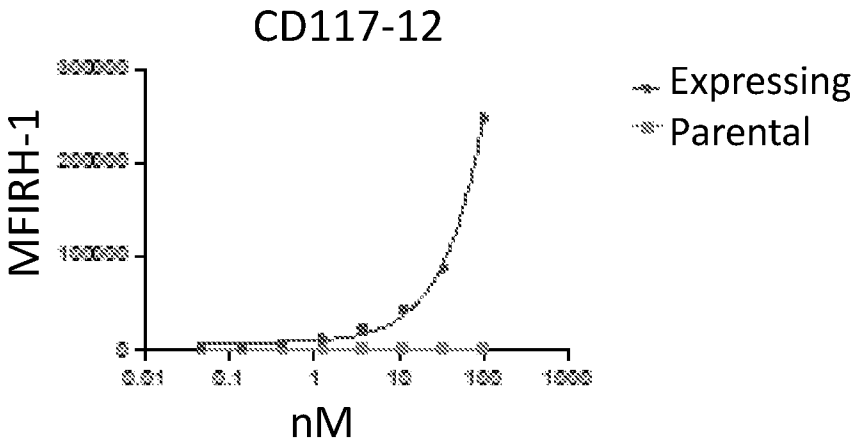


FIG. 21Q

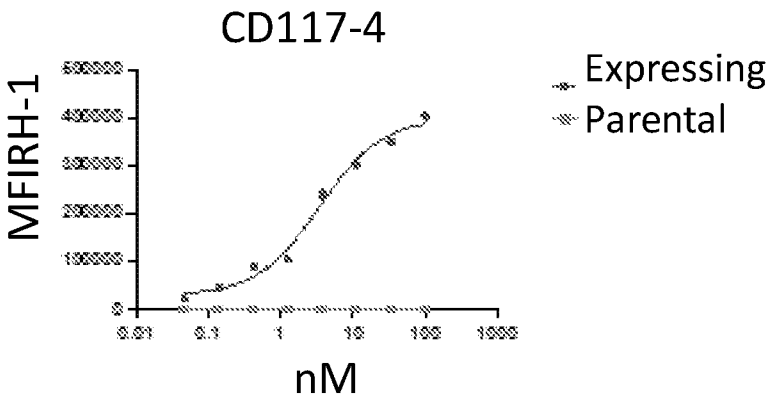


FIG. 21R

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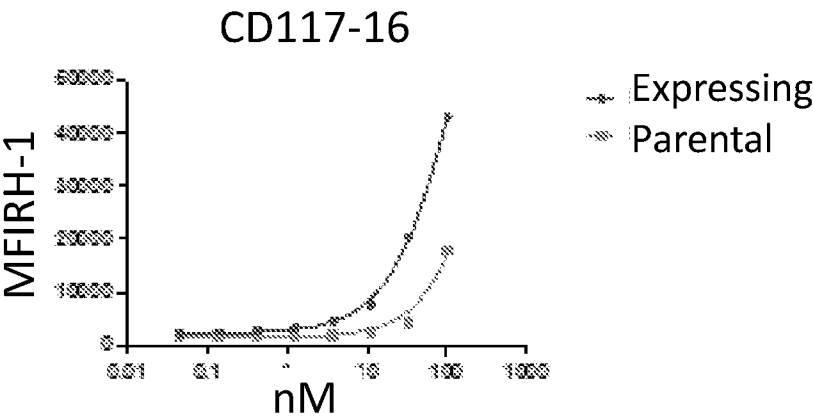


FIG. 21S

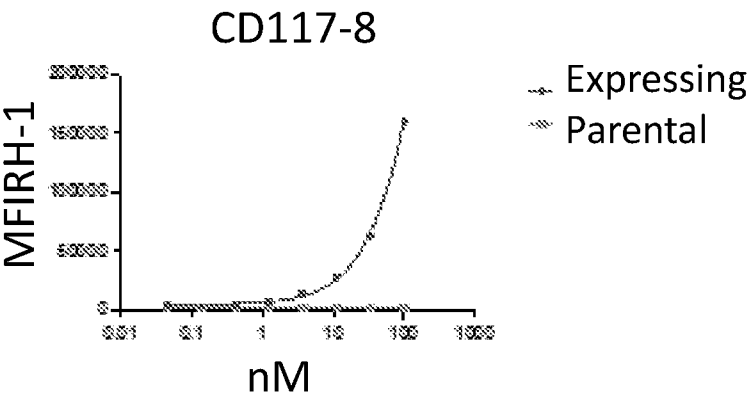


FIG. 21T

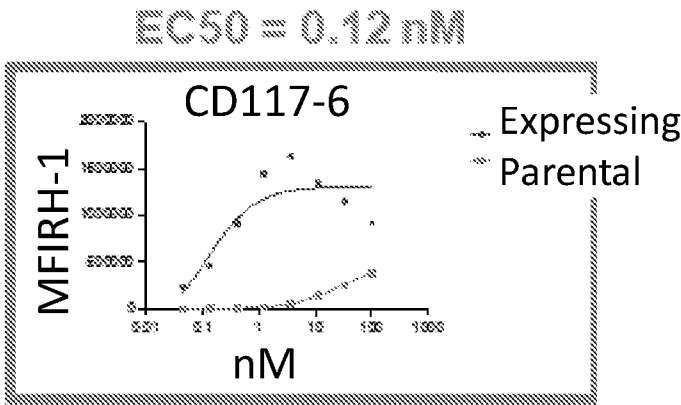


FIG. 21U

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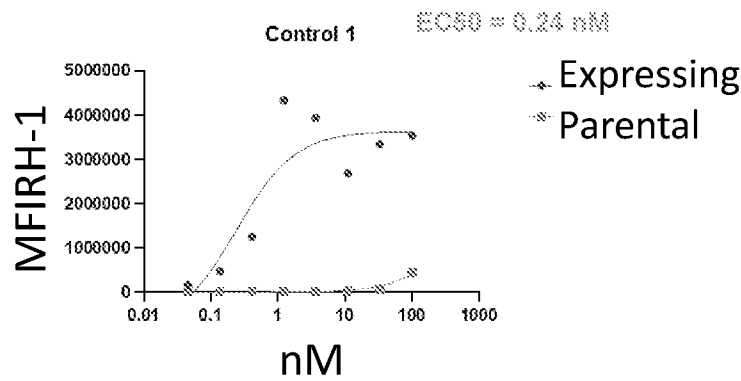


FIG. 21V

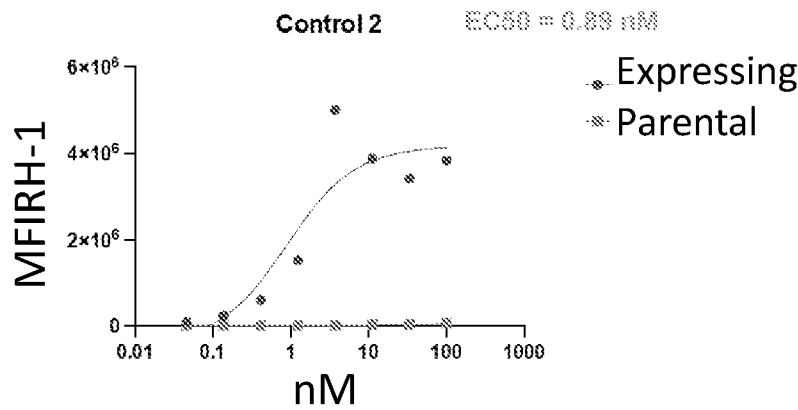


FIG. 21W

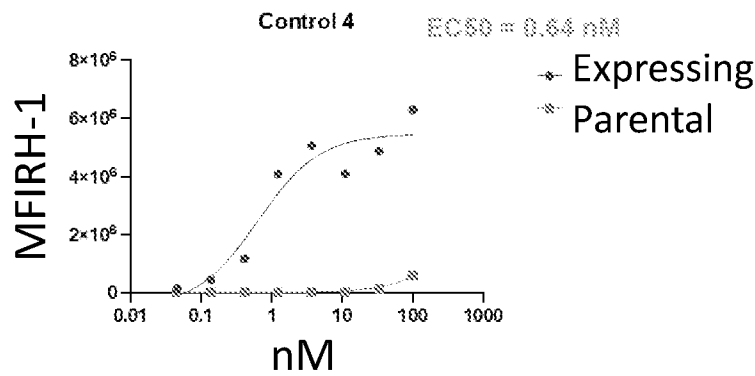


FIG. 21X

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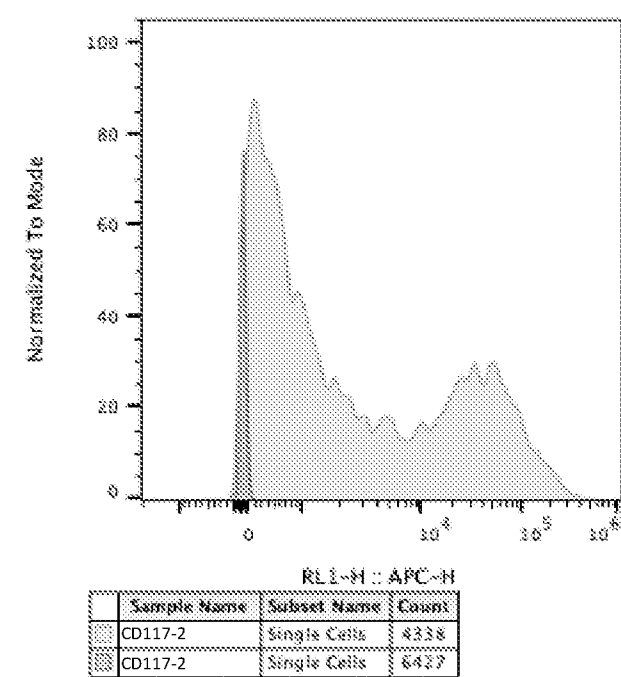


FIG. 22A

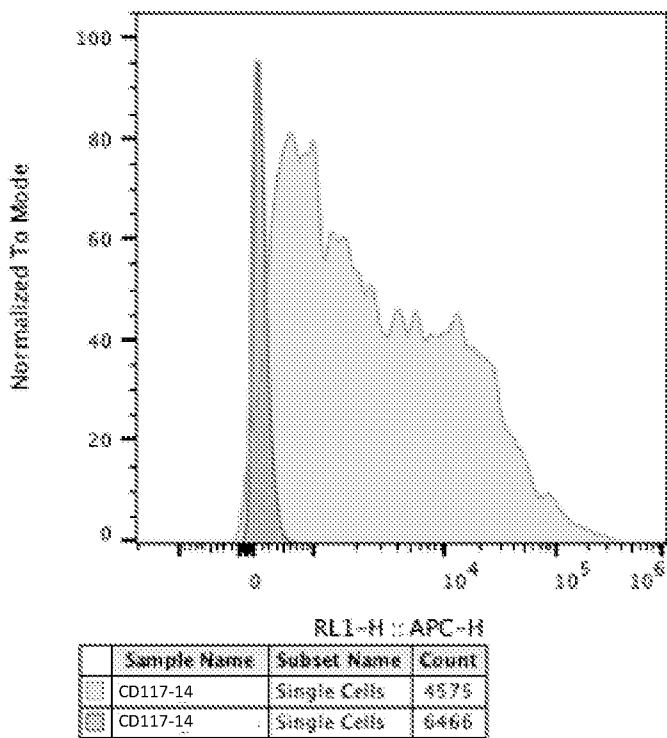


FIG. 22B

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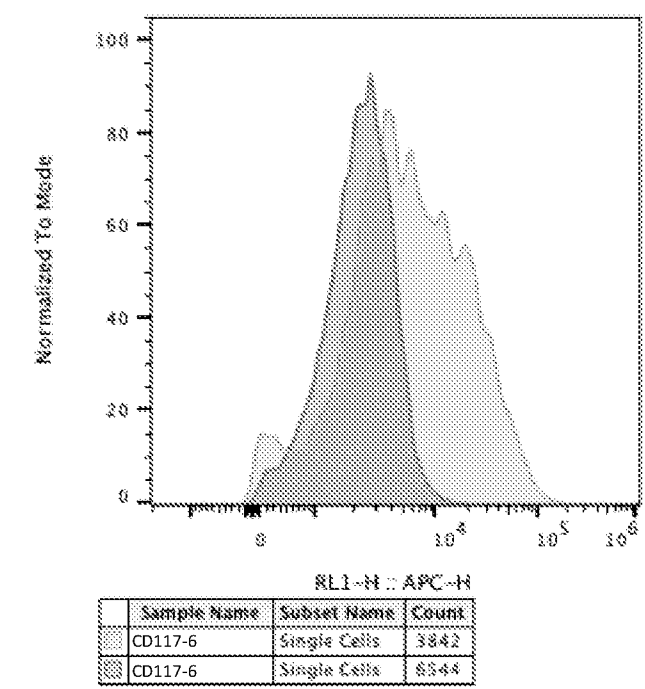


FIG. 22C

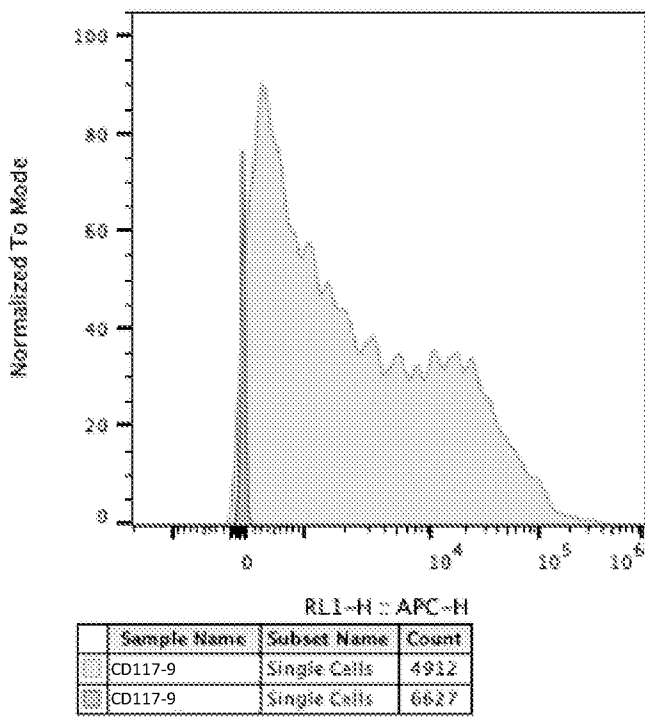


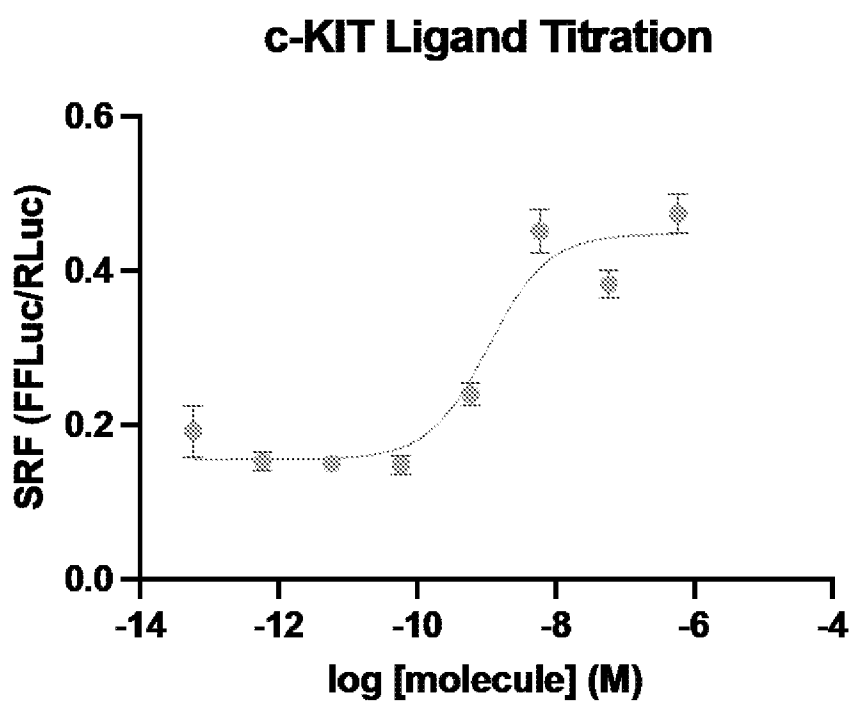
FIG. 22D

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Clone	EC50
CD117-2	0.7420
CD117-14	0.07182
CD117-6	0.1162
CD117-9	1.386
Control 1	0.2446
Control 2	0.8929
Control 3	5.576
Control 4	0.6412

FIG. 22E

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**FIG. 23**

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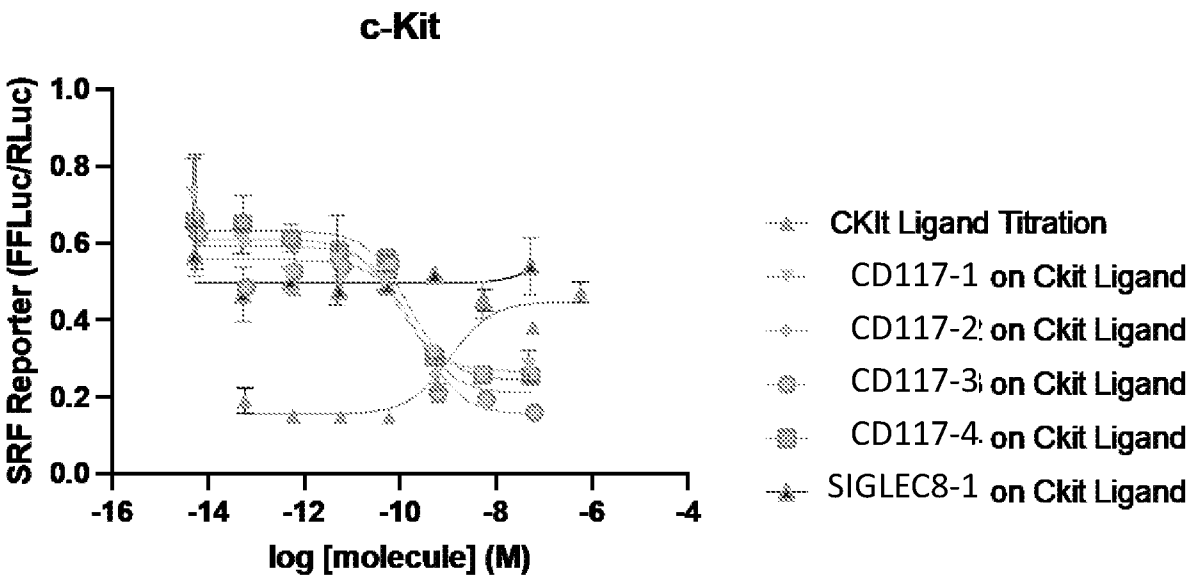


FIG. 24A

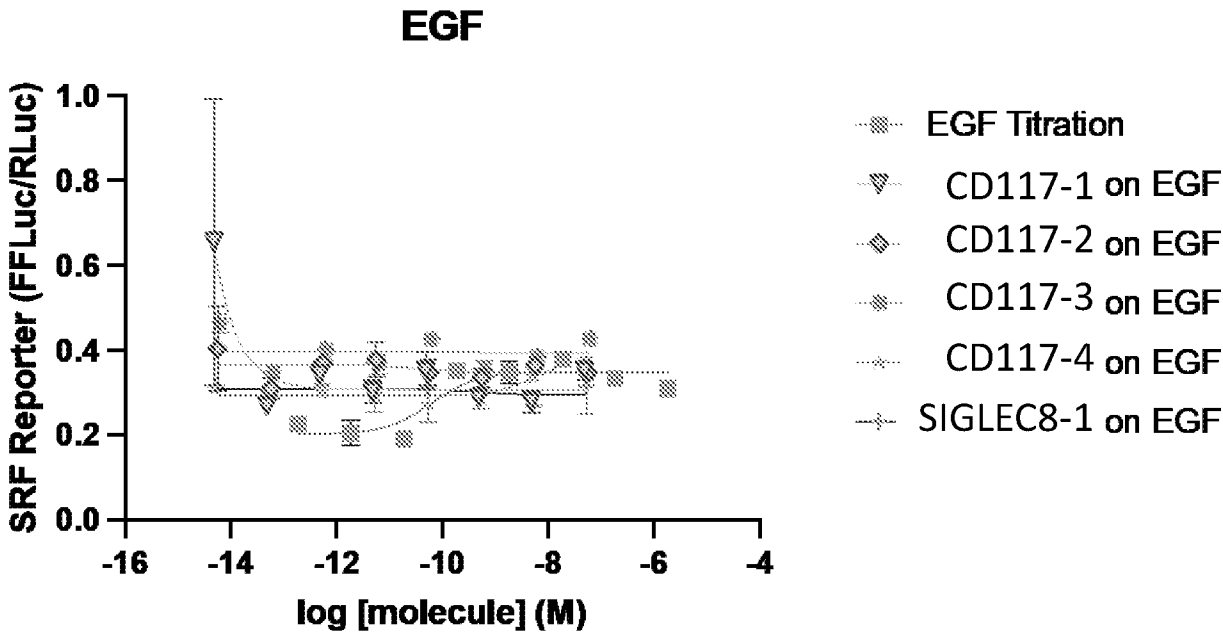


FIG. 24B

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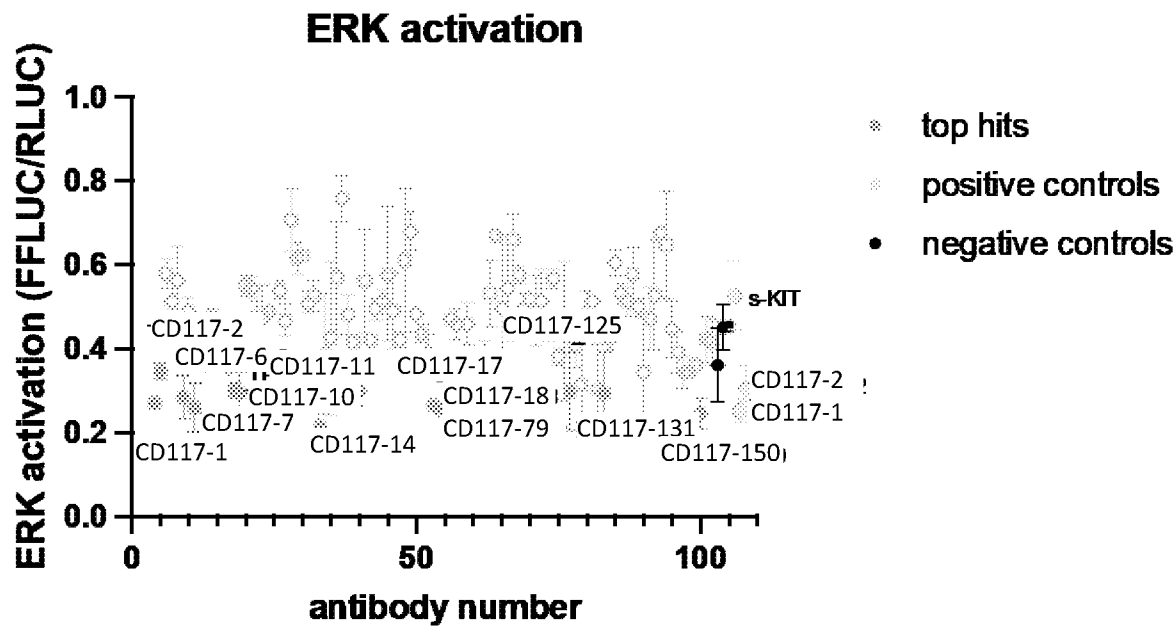


FIG. 25A

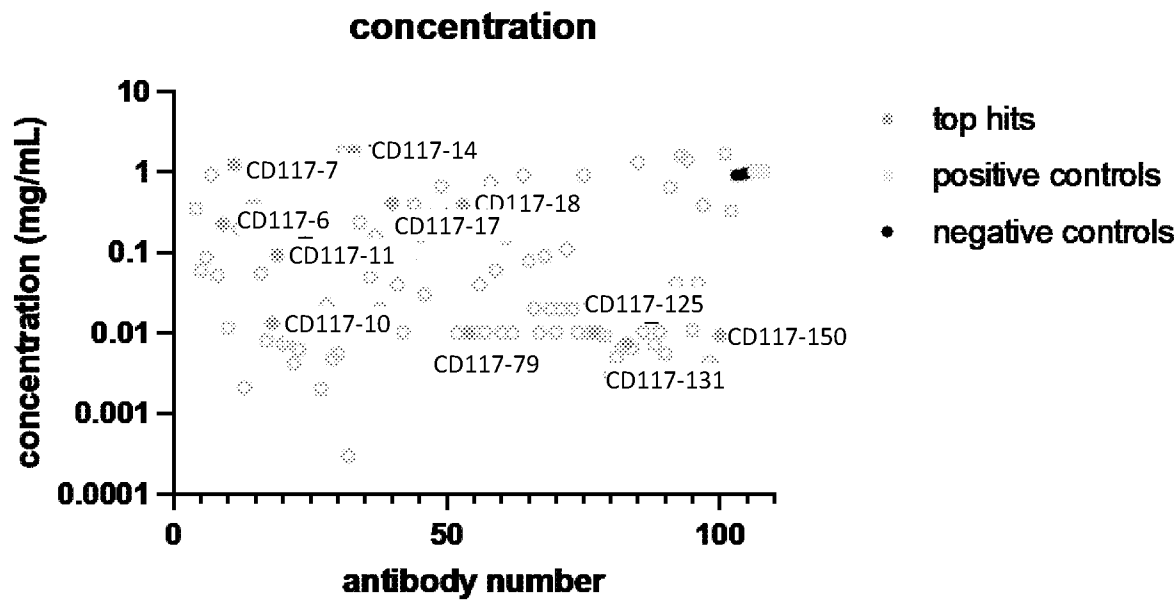


FIG. 25B

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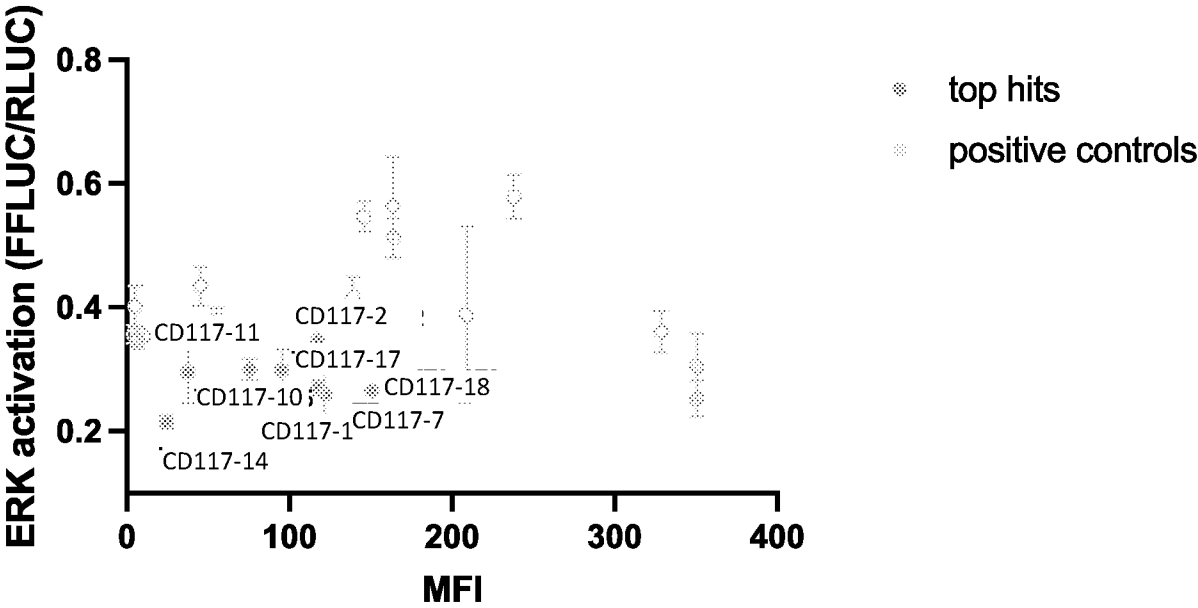


FIG. 25C

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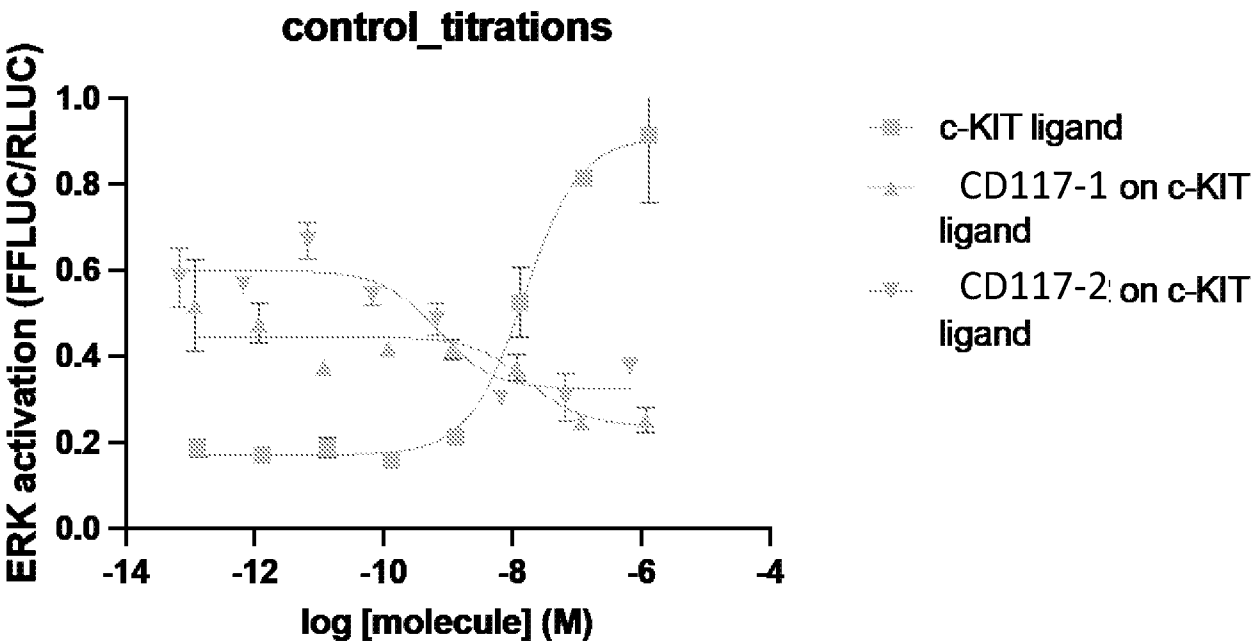


FIG. 26A

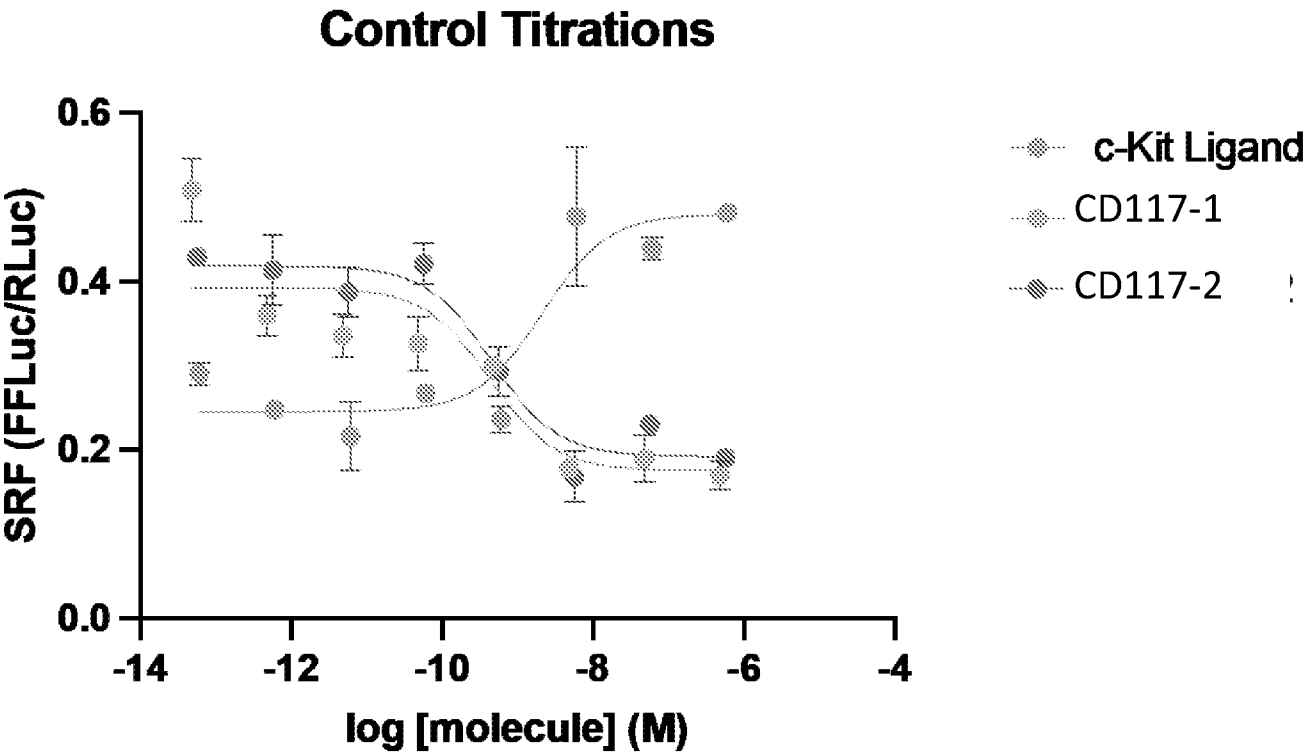


FIG. 26B

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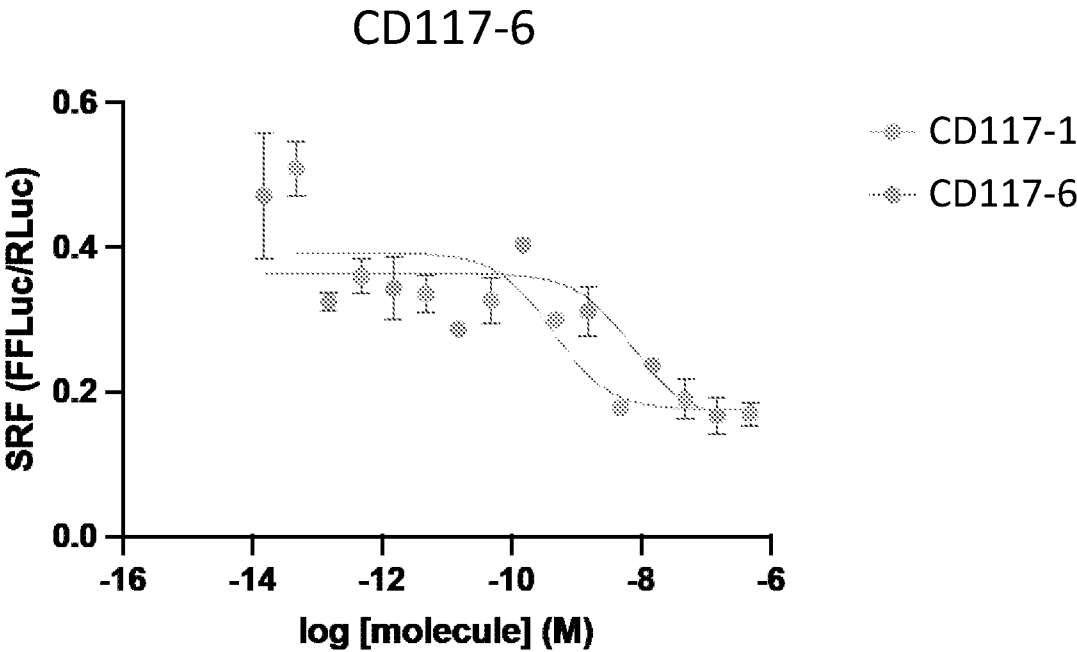


FIG. 27A

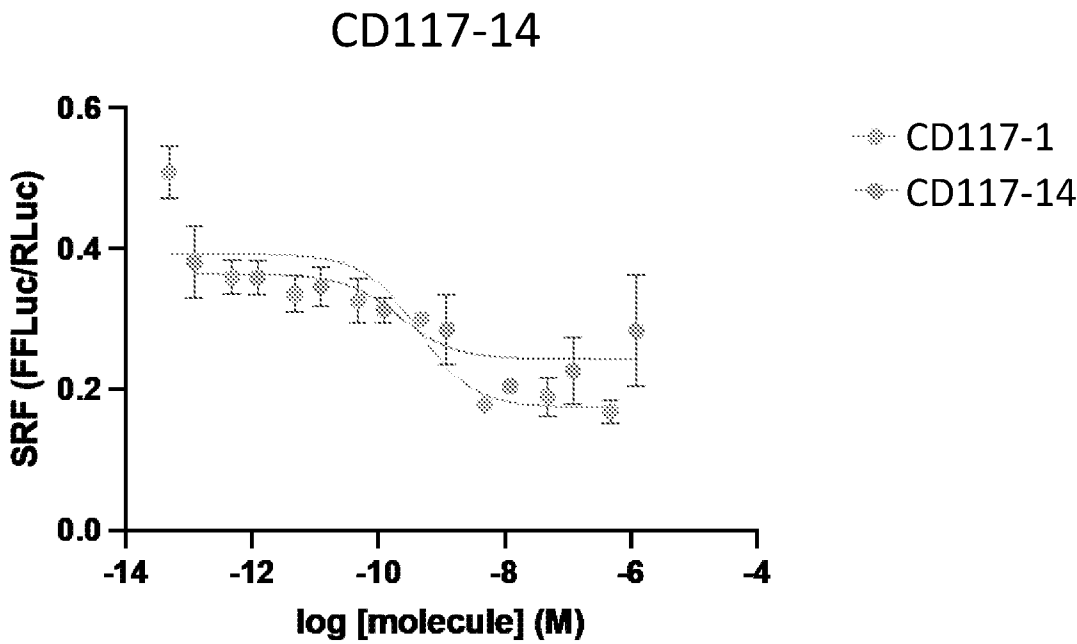


FIG. 27B

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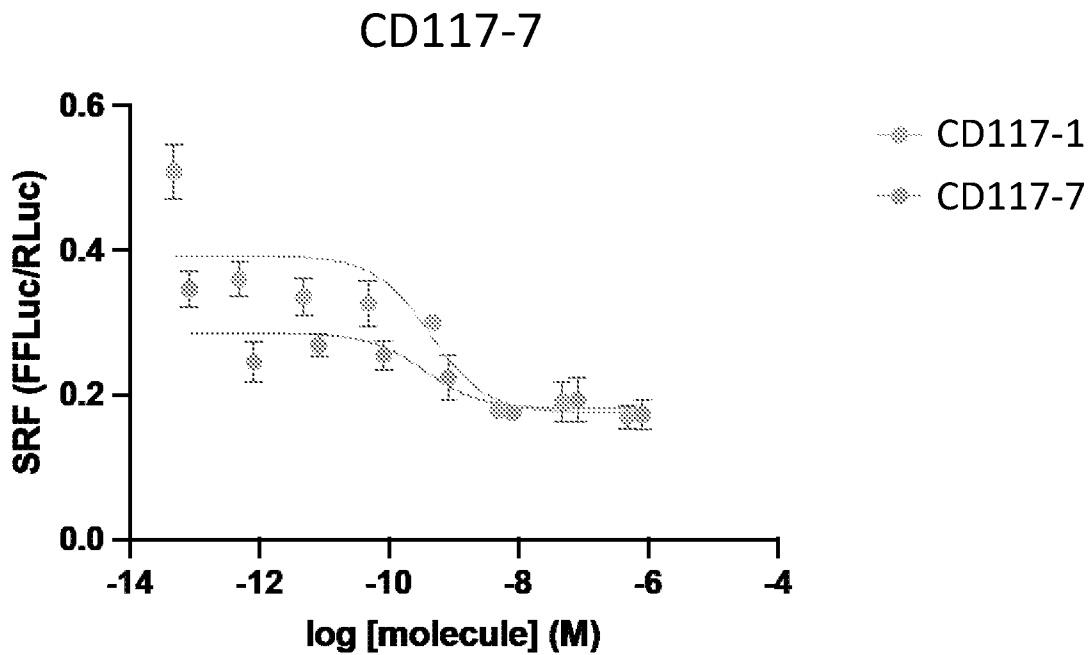


FIG. 27C

Antibody	IC50 (M)	log(IC50)	Span
CD117-1	4.306E-10	-9.366	-0.2174
CD117-2	4.529E-10	-9.344	-0.2266
CD117-6	7.129E-09	-8.147	-0.2026
CD117-7	3.536E-10	-9.451	-0.1049
CD117-14	2.139E-10	-9.67	-0.1208

FIG. 27D

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CD117-131

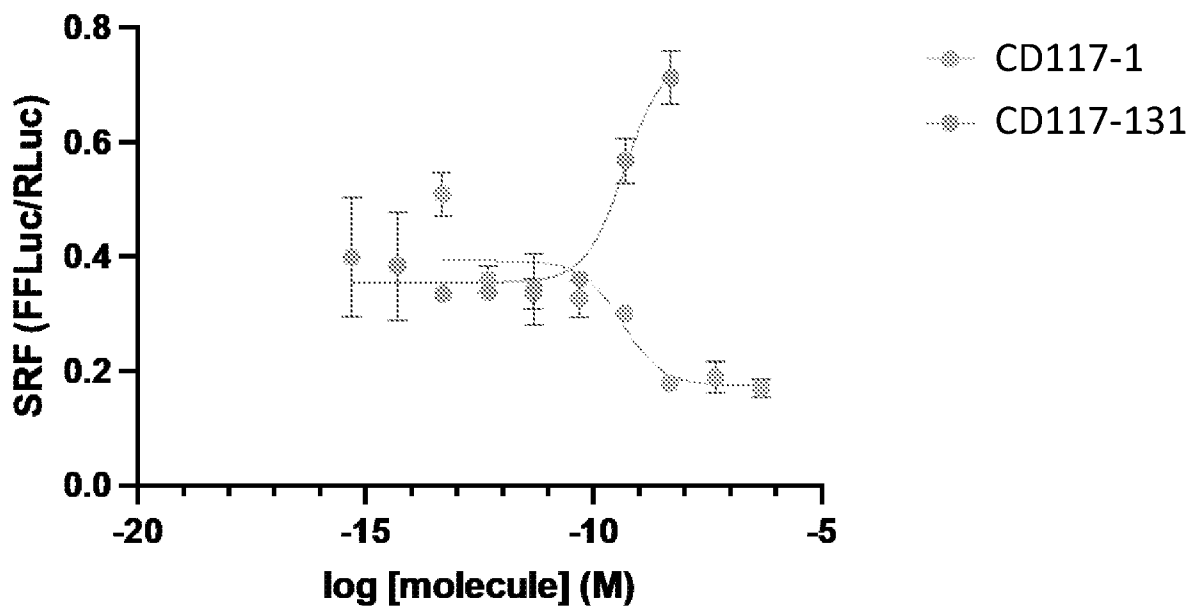


FIG. 28A

CD117-10

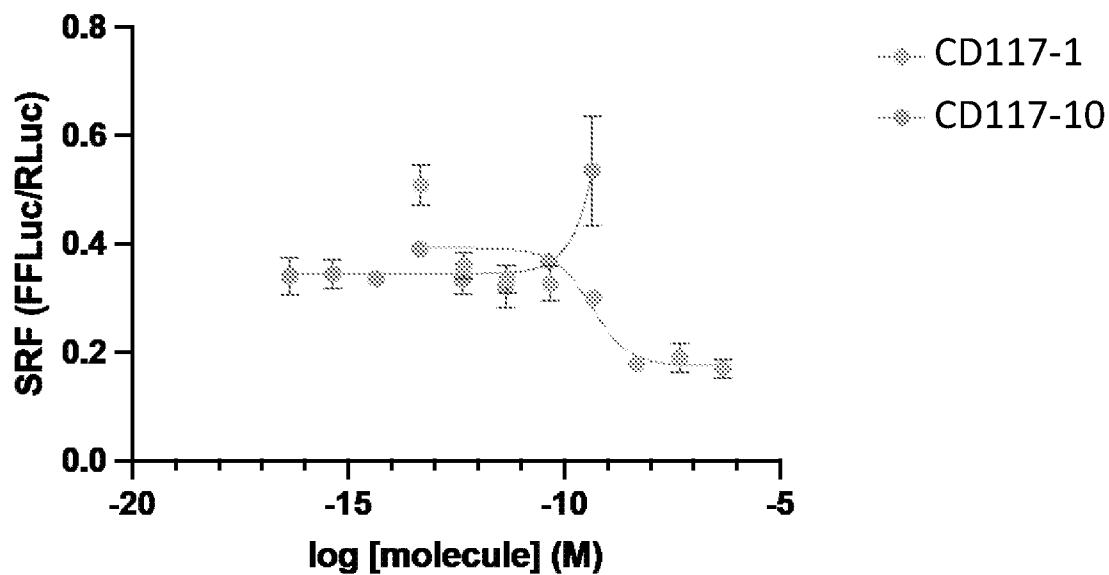


FIG. 28B

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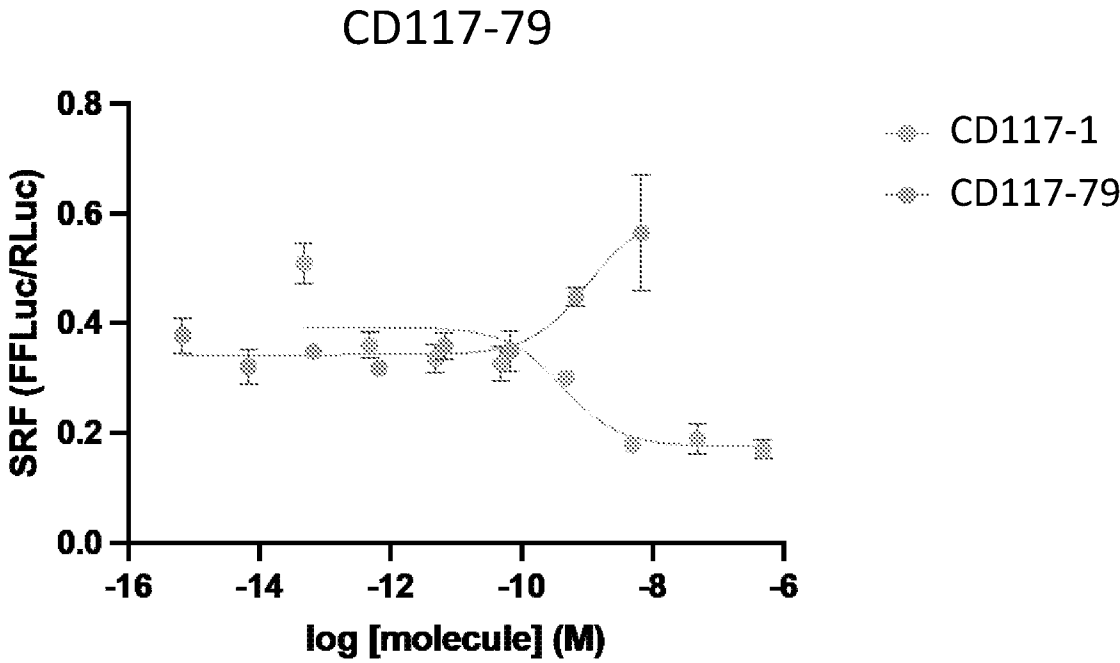


FIG. 28C

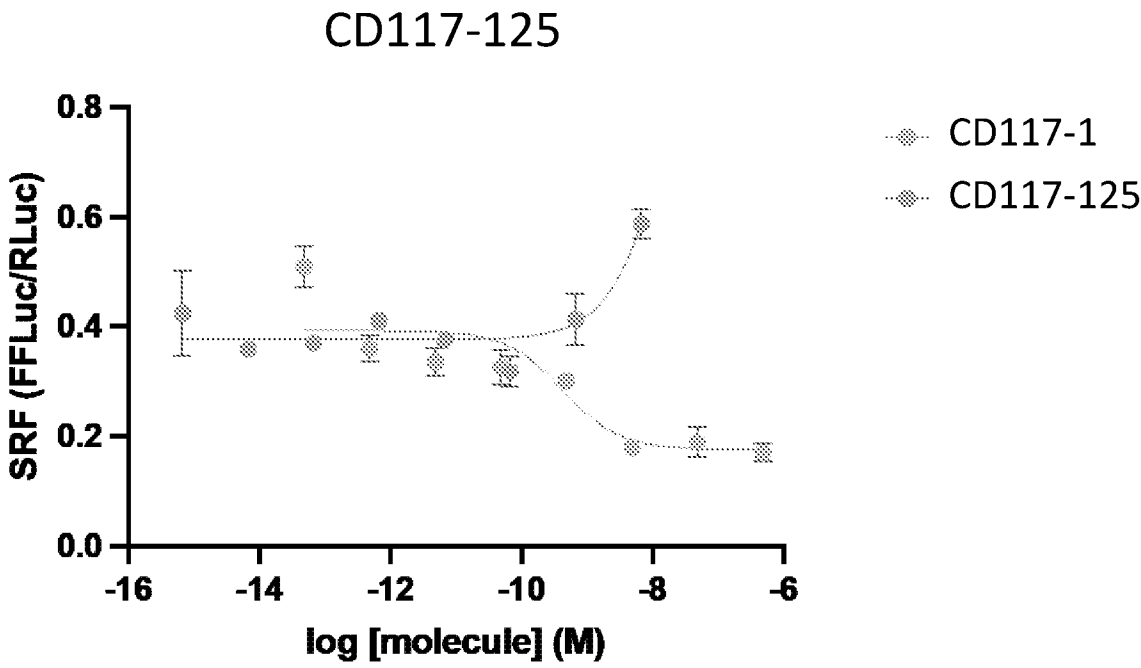


FIG. 28D

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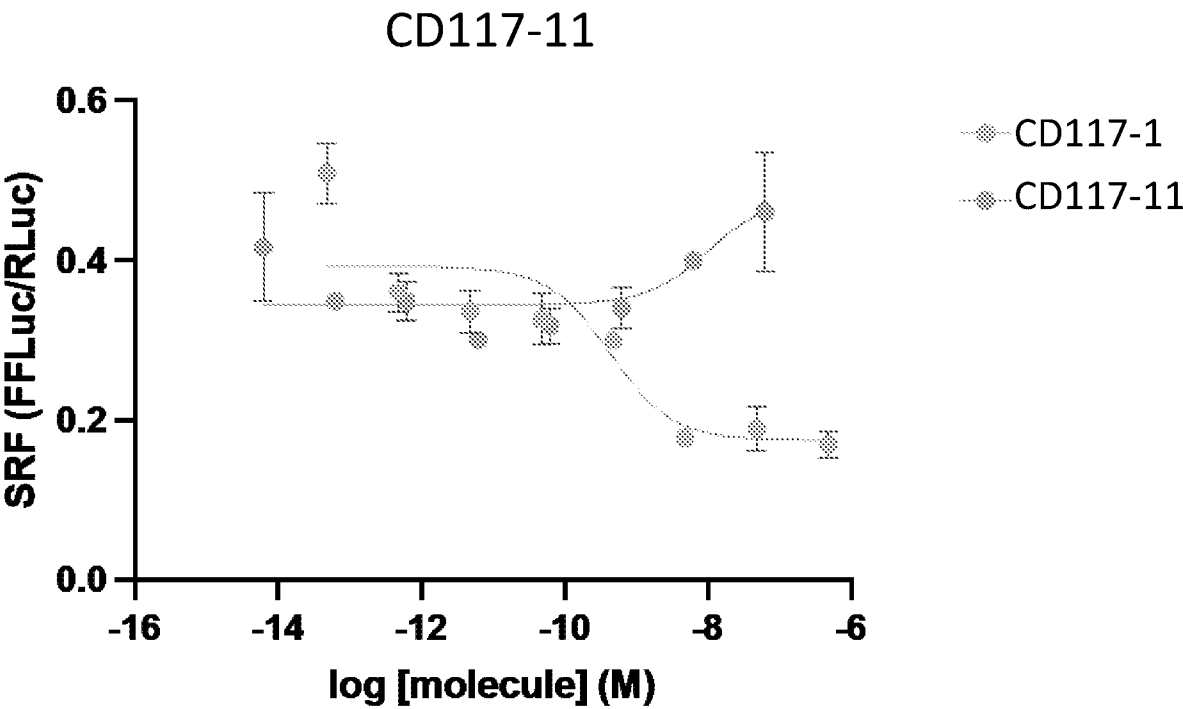


FIG. 28E

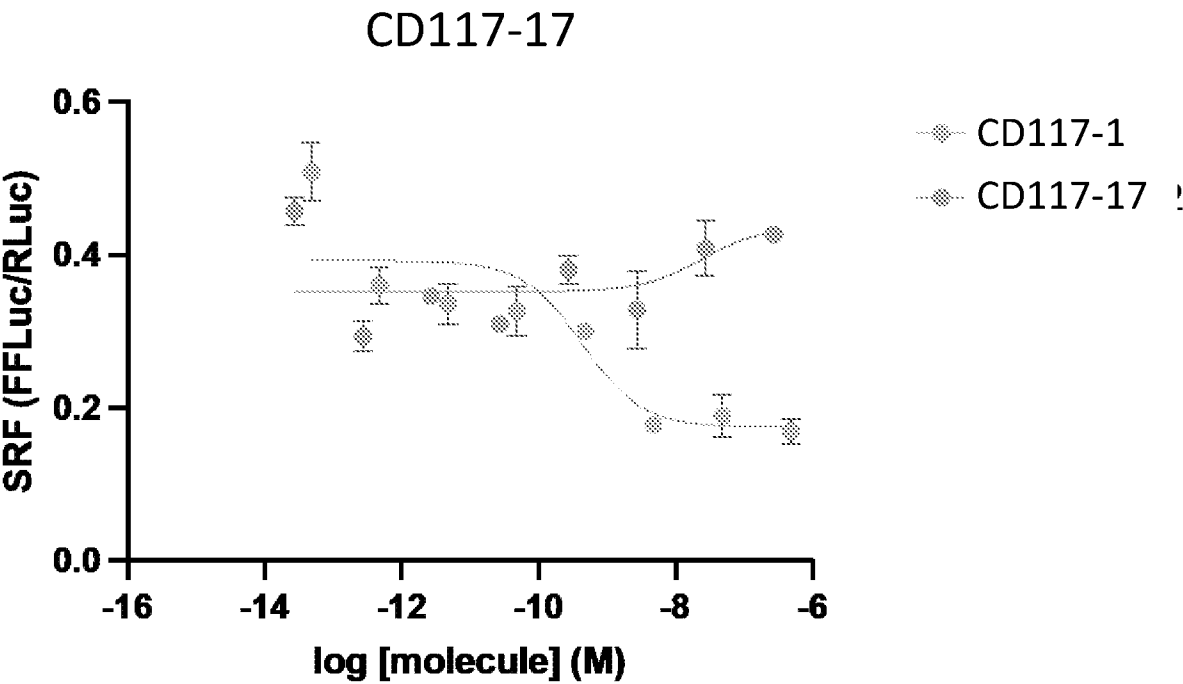


FIG. 28F

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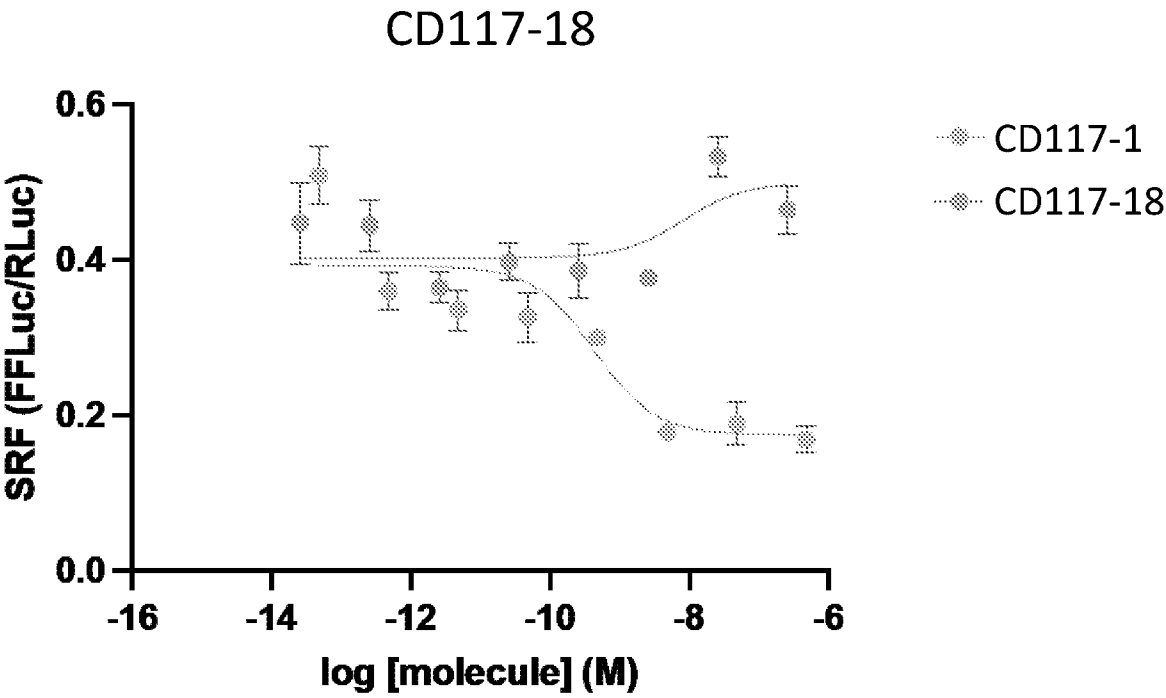


FIG. 28G

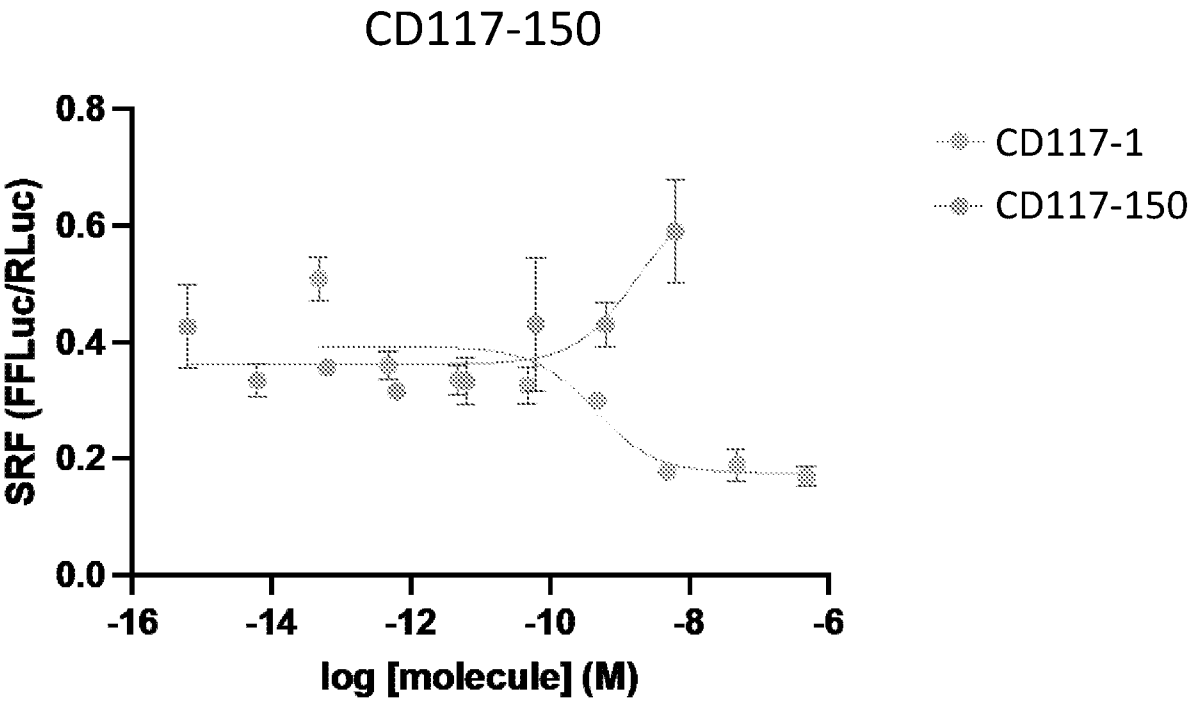
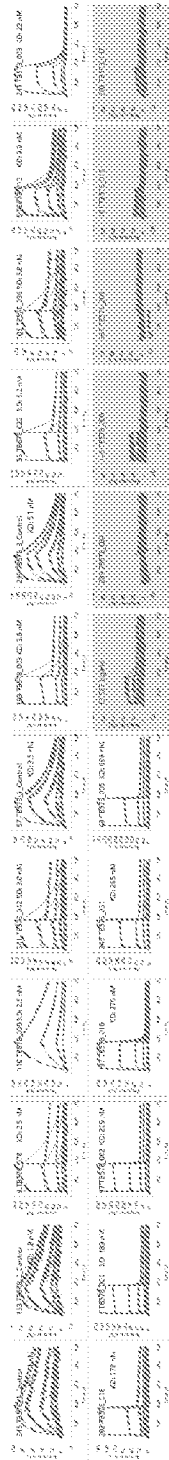


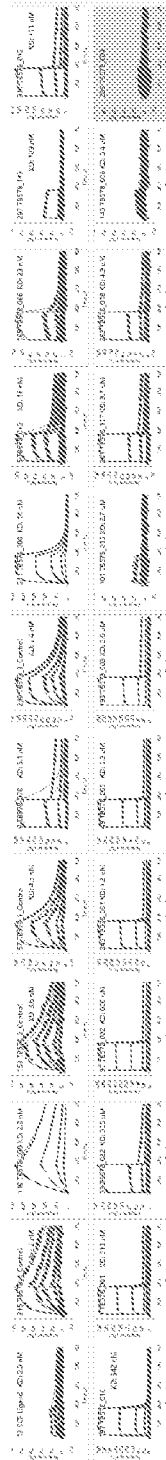
FIG. 28H

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A: Human CD117



B: Cyno CD117



C: Mouse CD117

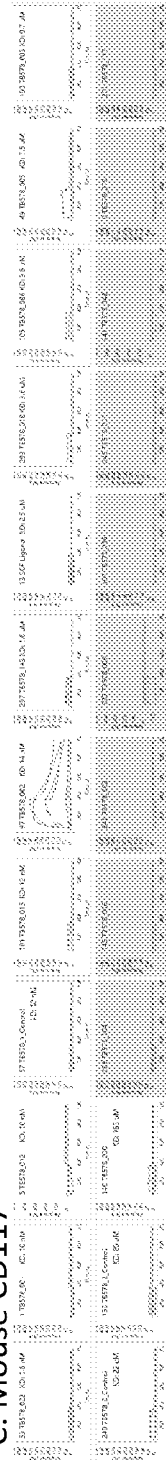
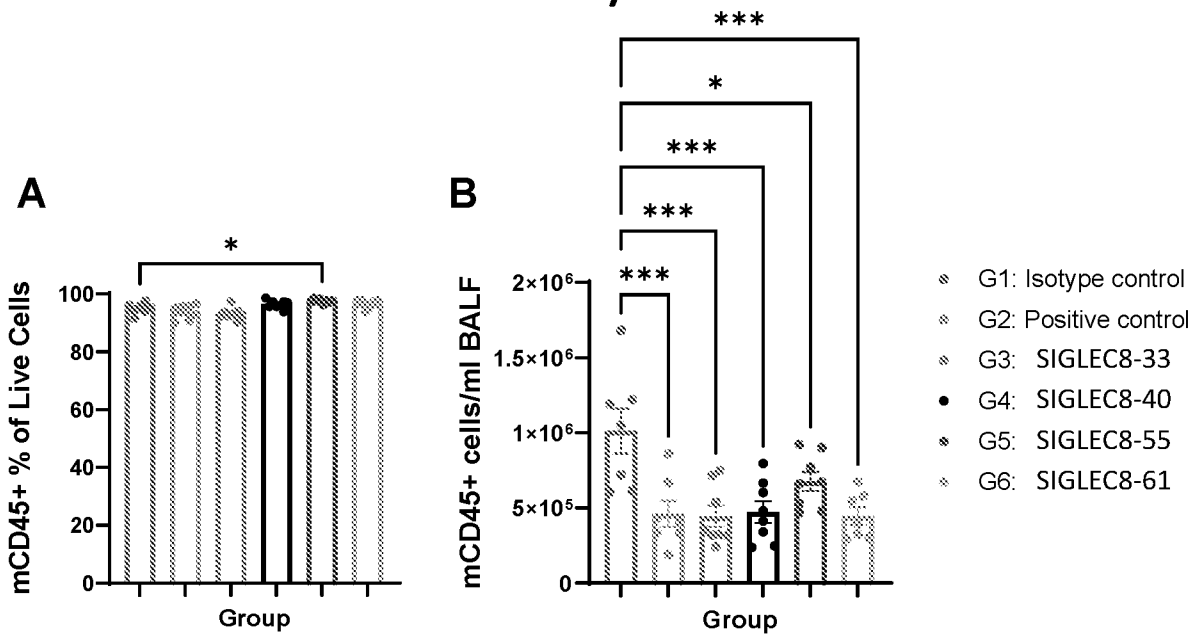


FIG. 29A

Clone	Human CD117			Cyto CD117			mouse CD117		
	k_a (M-1 s-1)	k_d (s-1)	k_D (M)	k_a (M-1 s-1)	k_d (s-1)	k_D (M)	k_a (M-1 s-1)	k_d (s-1)	k_D (M)
CD117-1	5.30E+05	1.00E-01	1.89E-07	3.15E+05	1.60E-01	5.08E-07	N/A	N/A	N/A
CD117-2	6.55E+05	1.36E-01	2.08E-07	3.31E+05	2.01E-01	6.07E-07	1.61E+05	2.22E-03	1.37E-08
CD117-3	1.97E+06	6.98E-03	3.54E-09	1.05E+05	2.89E-01	2.75E-06	N/A	N/A	N/A
CD117-4	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
CD117-5	3.00E+05	2.01E-01	6.70E-07	8.83E+04	2.11E-01	2.39E-06	N/A	N/A	N/A
CD117-6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
CD117-7	8.82E+05	1.94E-02	2.20E-08	1.12E+06	1.59E-02	1.42E-08	N/A	N/A	N/A
CD117-8	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
CD117-9	6.10E+05	5.80E-03	9.51E-09	6.85E+05	1.08E-02	1.57E-08	N/A	N/A	N/A
CD117-10	N/A	N/A	N/A	3.44E+04	9.16E-01	2.66E-05	N/A	N/A	N/A
CD117-11	2.52E+05	6.79E-02	2.70E-07	2.01E+05	6.81E-02	3.38E-07	N/A	N/A	N/A
CD117-12	5.41E+05	1.01E-01	1.87E-07	3.87E+04	2.01E-01	5.19E-06	N/A	N/A	N/A
CD117-13	1.70E+06	8.77E-03	5.17E-09	3.24E+05	1.56E-01	4.80E-07	N/A	N/A	N/A
CD117-14	6.98E+05	1.77E-03	2.53E-09	6.24E+05	1.46E-03	2.34E-09	N/A	N/A	N/A
CD117-15	3.62E+05	9.76E-02	2.70E-07	1.21E+05	1.46E-01	1.21E-06	N/A	N/A	N/A
CD117-16	N.T.	N.T.	N.T.	N.T.	N.T.	N.T.	N.T.	N.T.	N.T.
CD117-17	1.35E+06	4.06E-03	3.00E-09	7.27E+05	6.73E-02	9.26E-08	N/A	N/A	N/A
CD117-18	1.33E+06	3.36E-03	2.53E-09	1.35E+06	6.79E-03	5.02E-09	N/A	N/A	N/A
CD117-19	6.62E+05	3.88E-03	5.87E-09	1.31E+06	2.72E-02	2.08E-08	N/A	N/A	N/A
CD117-20	N/A	N/A	N/A	7.22E+04	2.98E-01	4.12E-06	N/A	N/A	N/A
CD117-21	1.60E+04	1.69E+00	1.05E-04	3.54E+05	3.38E+00	9.56E-06	N/A	N/A	N/A

FIG. 29B

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*P<0.05, ordinary one-way ANOVA,
comparison with Isotype control group
Error bars represent Mean $\pm$ S.E.M.

FIG. 30

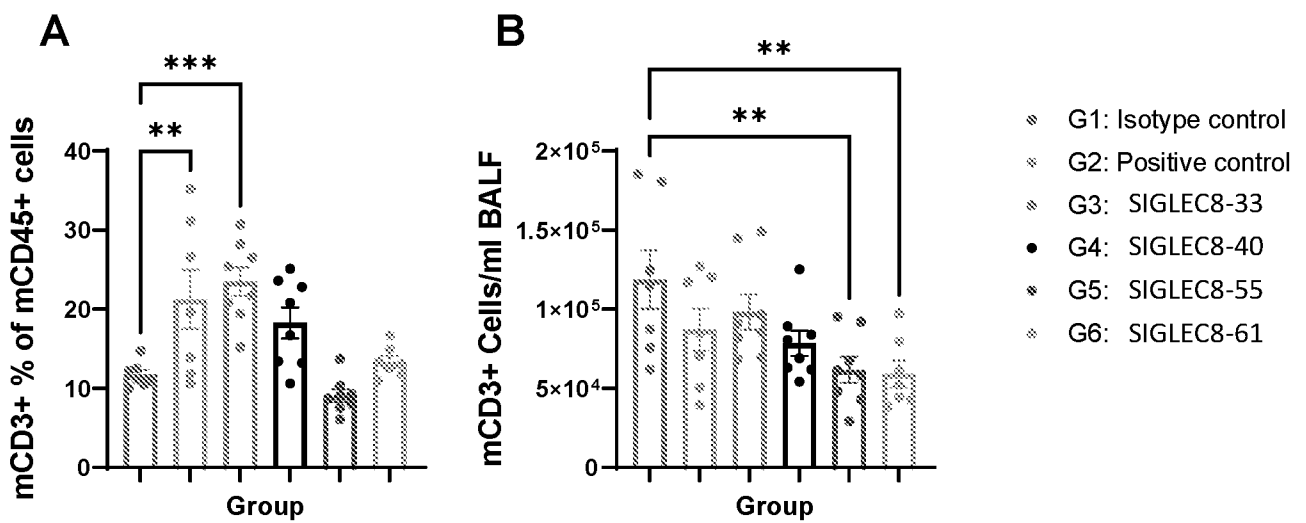


FIG. 31

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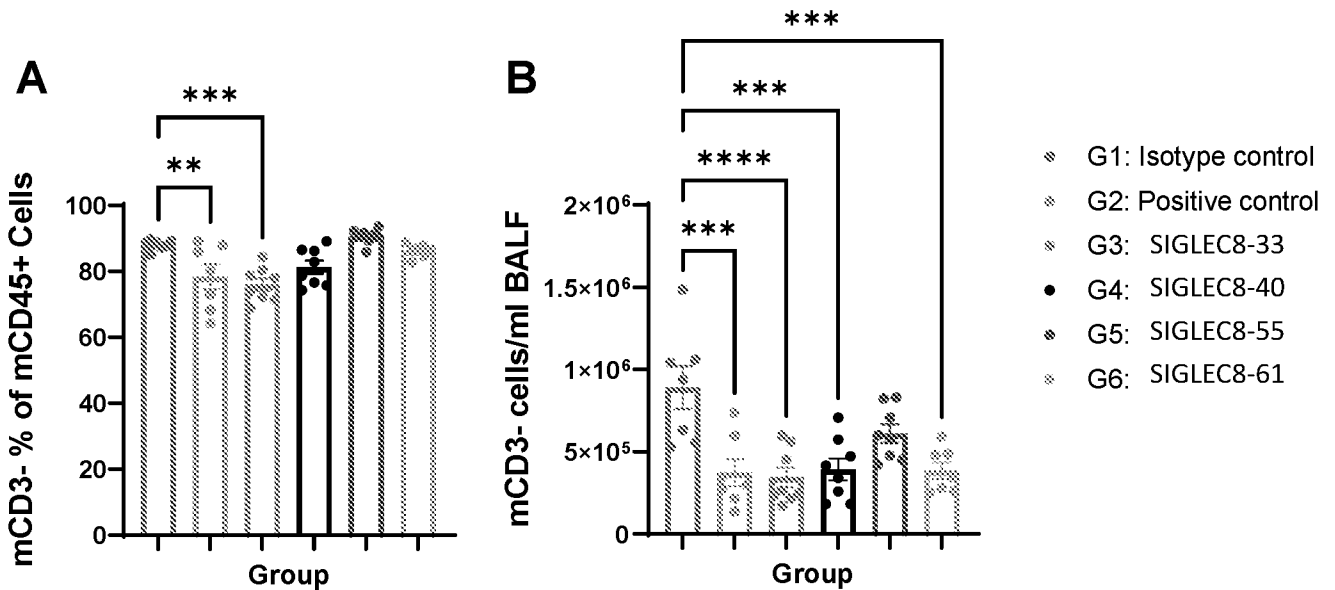
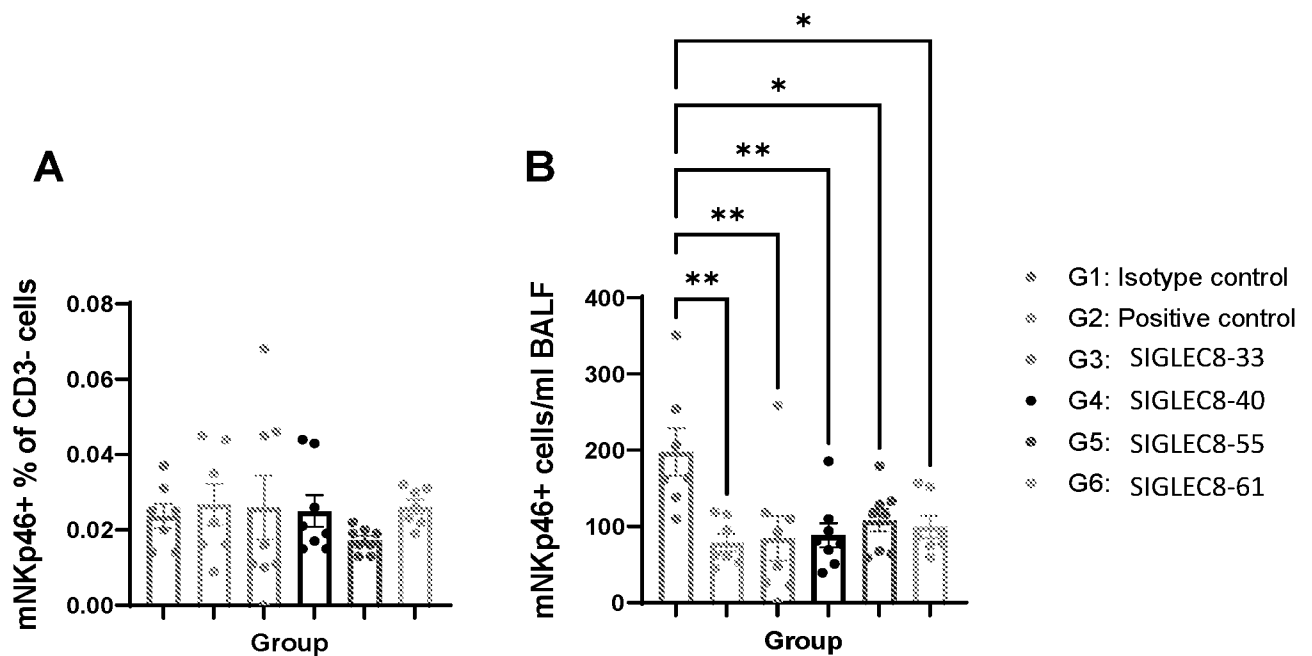


FIG. 32



*P<0.05, ordinary one-way ANOVA,
comparison with Isotype control group
Error bars represent Mean $\pm$ S.E.M.

FIG. 33

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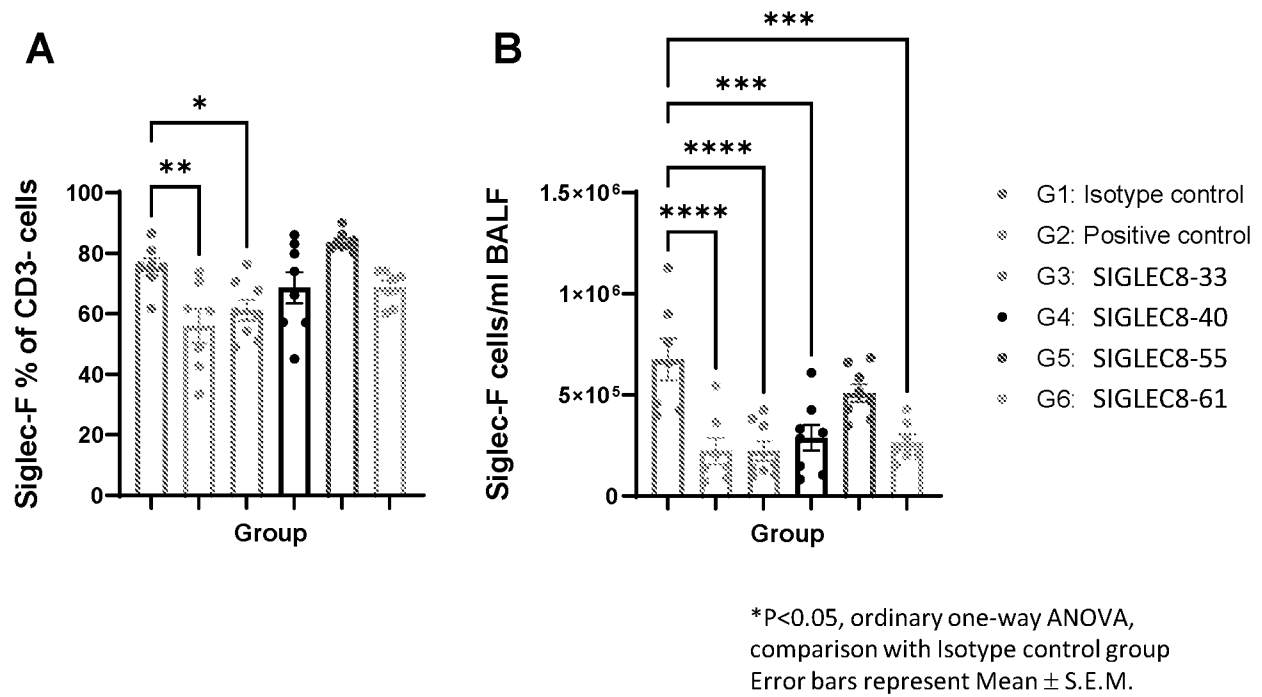


FIG. 34

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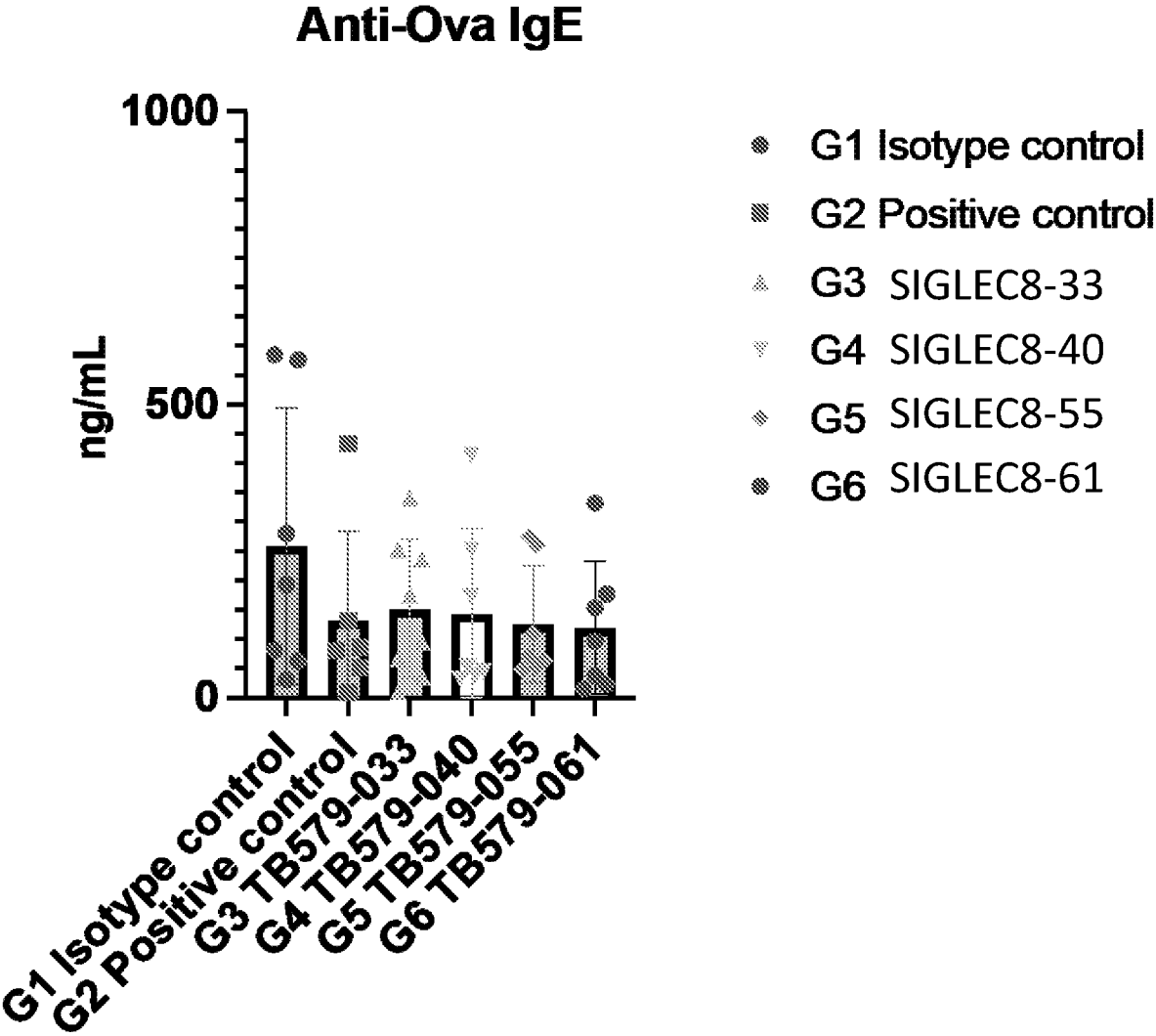


FIG. 35

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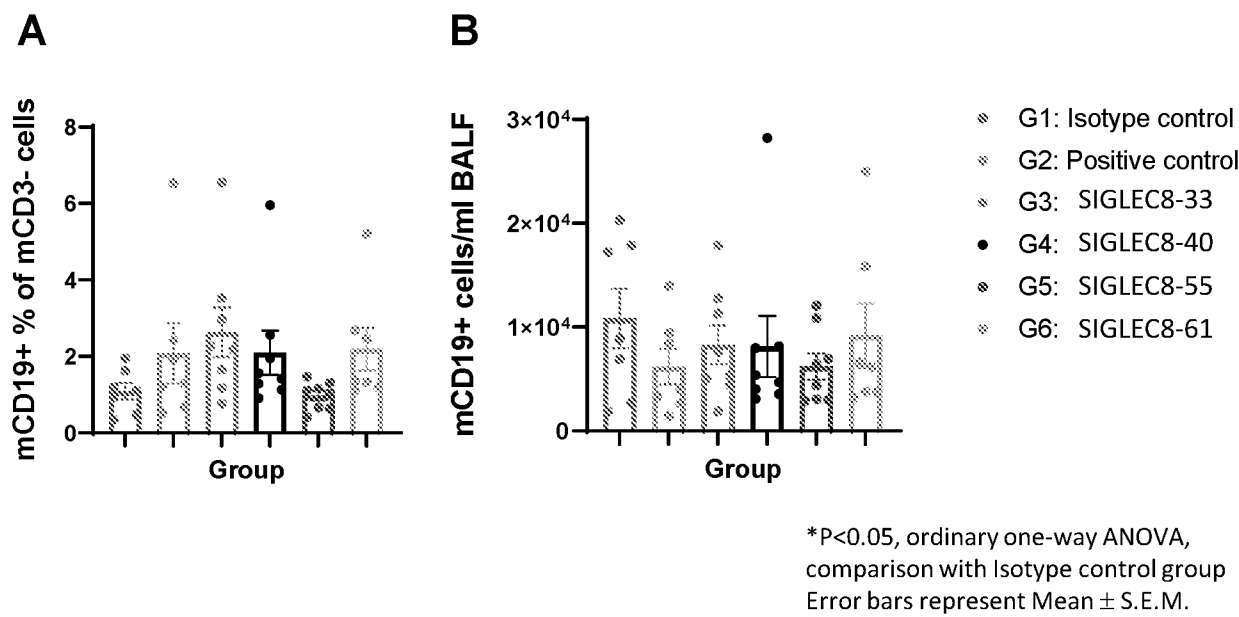


FIG. 36

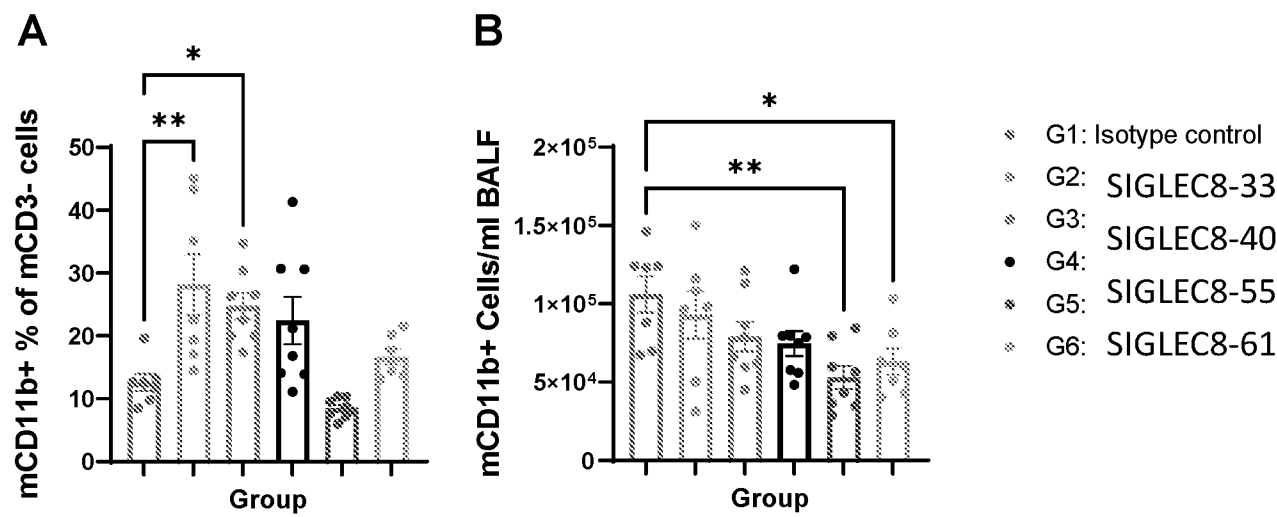


FIG. 37

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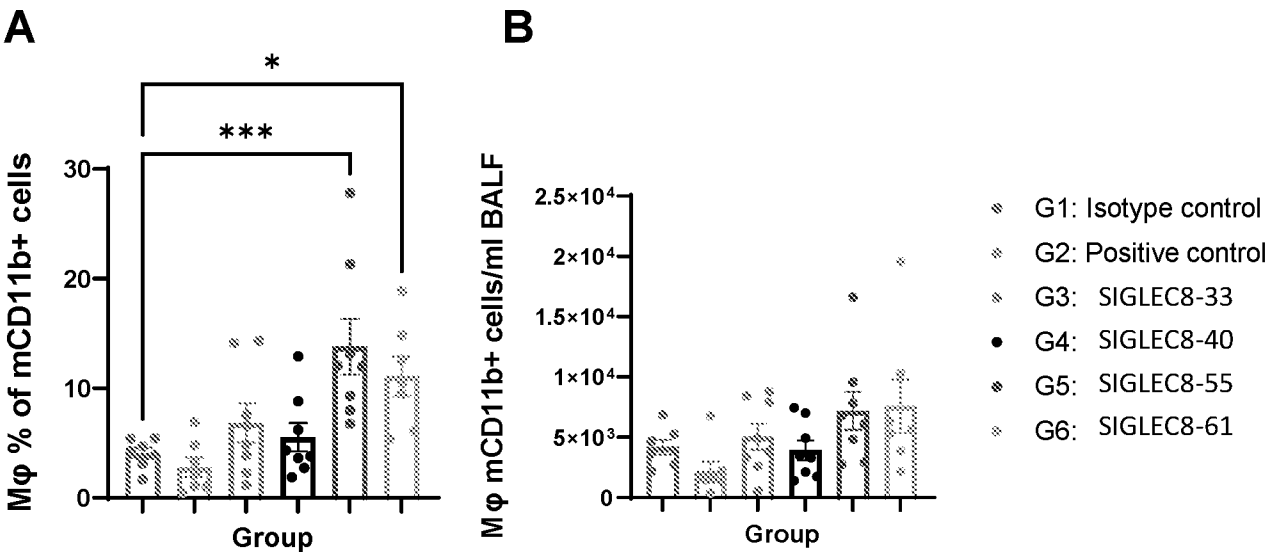


FIG. 38

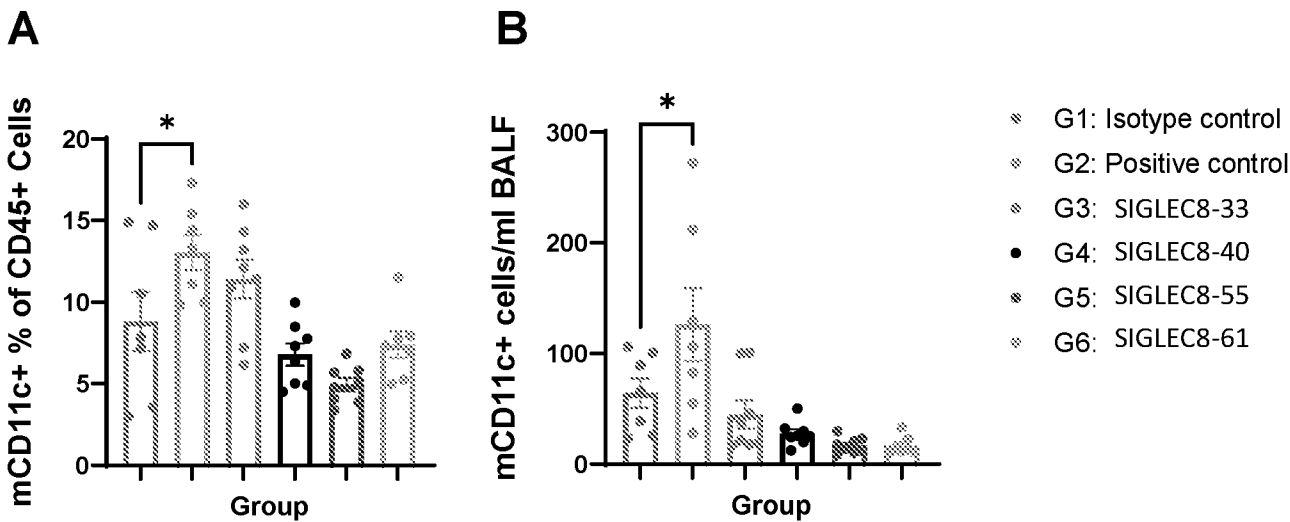


FIG. 39

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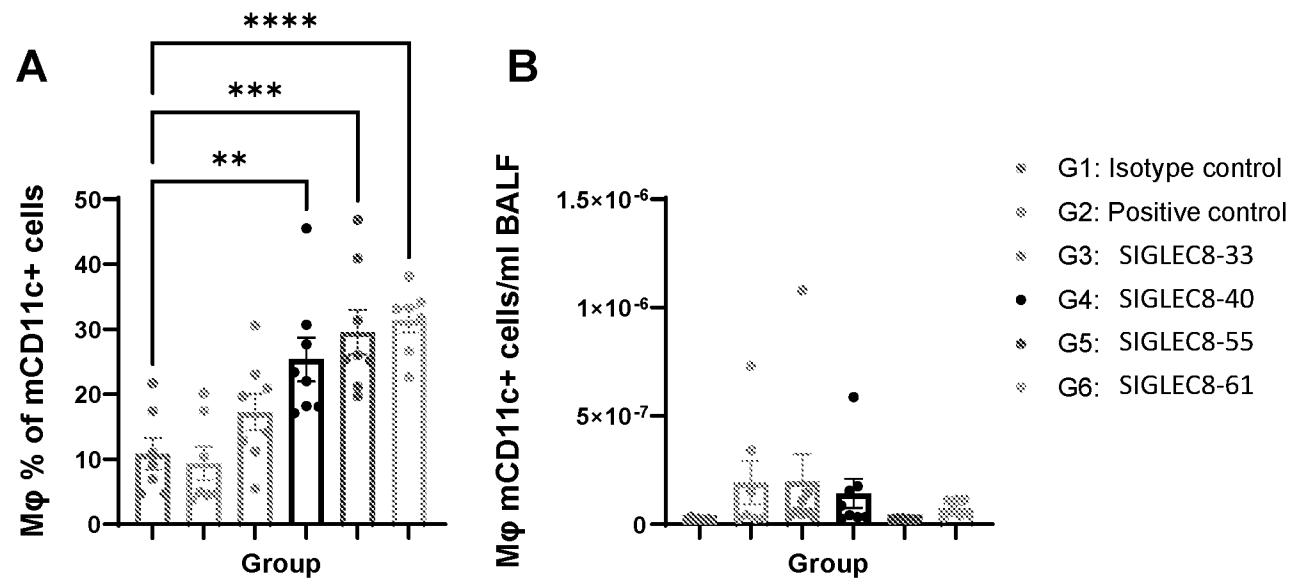


FIG. 40