BISPECIFIC IMMUNE CELL ENGAGERS WITH BINDING SPECIFICITY FOR HLA-G AND ANOTHER ANTIGEN

FIELD

[0001] Provided herein are bispecific immune cell engagers with binding specificity for HLA-G and an additional antigen, including pharmaceutical compositions, diagnostic compositions, and kits.

BACKGROUND

[0002] A bispecific antibody is a protein that can bind to two different antigens. Bispecific antibodies are widely used in cancer immunotherapy, where bispecific antibodies that function as immune cell engagers are engineered to simultaneously bind a cytotoxic cell and a target like a tumor cell to be killed. For example, the link between T cells and tumor cells causes T cells to exert cytotoxic activity on tumor cells by producing proteins like perforin and granzymes. These proteins enter tumor cells and initiate a cell's apoptosis process.

[0003] Bispecific antibodies can direct a host's immune system against cancer cells. For example, a bispecific antibody can be made that binds to CD3 in a T cell and a second antigen on a tumor cell. Bridging T cells and tumor cells and killing tumor cells as a result can induce dramatic regression of malignancies. This can even lead to complete remission in some cases.

[0004] Bispecific T-cell engagers (BiTEs) are a class of bispecific antibodies that are particularly useful as anti-cancer compounds. BiTEs and other bispecific immune cell engagers are usually fusion proteins consisting of two different antibodies or amino acid sequences, such as, for example, two different single-chain variable fragments (scFvs). One of the scFvs binds to an activating receptor on immune cells, for example CD3 on T cells, and the other targets a tumor cell via a specific molecule. Bispecific T-cell engagers can thus be used to eliminate target-expressing tumor cells by activated T cells.

[0005] Human leukocyte antigen-G (HLA-G) is an immune regulatory molecule that belongs to the non-classical HLA-class I family of receptors and is encoded by the *HLA-G* gene. HLA-G is a heterodimer consisting of a heavy chain and a light chain (beta-2

microglobulin). There are membrane bound and soluble forms of HLA-G.

[0006] HLA-G was first identified in placenta samples. HLA-G is normally expressed at the maternal-fetal interface and other immune-privileged sites. HLA-G may play a role in immune tolerance in pregnancy, being expressed in the placenta by extravillous trophoblast cells, while the classical MHC class I genes (HLA-A and HLA-B) are not.

[0007] HLA-G has been shown to be immune-suppressive. By binding receptors expressed on various myeloid and lymphoid cells, HLA-G may directly inhibit the functions of NK cells, cytotoxic T-lymphocytes, B cells, neutrophils, monocytes, macrophages, and dendritic cells. HLA-G also inhibits T and NK cell proliferation and cytolytic activities. HLA-G suppresses phagocytosis and induces the generation or expansion of regulatory T cells.

[0008] HLA-G mediates immune function through at least three ITIM-containing inhibitory receptors, ILT2, ILT4, and KIR2DL4. On lymphoid cells, for example, HLA-G mediates function through ILT2. On myeloid cells, HLA-G mediates function through ILT2 and ILT4. On decidual NK cells, HLA-G mediates immune function through KIR2DL4 and ILT2.

[0009] HLA-G is an immune checkpoint target. HLA-G can directly inhibit immune cell function through receptor binding and/or trogocytosis and impairment of chemotaxis. HLA-G can lend tumor cells a higher invasive and metastatic potential. HLA-G promotes evasion of tumor immune surveillance and enhances metastasis and the progression of malignancies. During tumor progression, HLA-G has other effects, such as inhibition of immune cell cytolysis, induction of immune cell apoptosis, and/or the generation of regulatory cells through receptor binding and/or trogocytosis.

[0010] HLA-G is an ideal antigen for a bispecific antibody. HLA-G expression is upregulated on a broad spectrum of tumors and is associated with poor prognosis and disease progression. Serum HLA-G levels are elevated in, for example, without limitation, breast, lung, colorectal cancer (CRC), gastric, esophageal, neuroblastoma, cervical, and hematological cancers. HLA-G has also been found to be correlated with clinical parameters in advanced disease, such as tumor metastasis, poor prognosis, immune escape, and tumor invasiveness.

[0011] A bispecific antibody that binds an immune cell, such as a T cell, and HLA-G would be useful. For example, a bispecific T-cell engager that can bind both CD3 and HLA-G

would be particularly useful.

SUMMARY

[0012] A first aspect provides a bispecific antigen binding construct comprising a binding domain capable of binding to an HLA-G epitope and an additional binding domain capable of binding to a second epitope. In some embodiments, the second epitope comprises or consists of a CD3ε epitope. In some embodiments, the CD3ε epitope comprises or consists of an amino acid sequence set forth in SEQ ID NO: 629.

[0013] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises or consists of a heavy chain variable region (VH) and a light chain variable region (VL), with VH and/or VL comprising 1, 2, 3, 4, 5, or 6 of the following:

a) a VHCDR1 having the sequence set forth in any one of SEQ ID NOS: 346-349 or 354-357,

b) a VHCDR2 having the sequence set forth in any one of SEQ ID NOS: 362-365 or 371-375,

c) a VHCDR3 having the sequence set forth in any one of SEQ ID NOS: 379-382,

d) a VLCDR1 having the sequence set forth in any one of SEQ ID NOS: 388-392,

e) a VLCDR2 having the sequence set forth in any one of SEQ ID NOS: 396-400, and

f) a VLCDR3 having the sequence set forth in any one of SEQ ID NOS: 404-408.

[0014] In some embodiments, the additional binding domain comprises or consists of an NK cell engager, dendritic cell engager, monocyte, or macrophage engager. In some embodiments, the NK cell engager comprises or consists an antibody for a CD16 epitope. In some embodiments, the NK cell engager comprises or consists of an antibody for NKp46. In some embodiments, the NK cell engager comprises or consists of an antibody for NKp30. In some embodiments, the monocyte or macrophage engager comprises or consists of an antibody for a CD16 epitope.

[0015] In some embodiments, the HLA-G epitope comprises or consists of an amino acid sequence set forth in SEQ ID NO: 342. In some embodiements, the binding domain capable of binding to an HLA-G epitope comprises or consists of a heavy chain variable region (VH) and a light chain variable region (VL), with VH and/or VL comprising 1, 2, 3, 4, 5, or 6 of the following:

a) a VHCDR1 having the sequence set forth in any one of SEQ ID NOS: 1-14 or 18-34,

b) a VHCDR2 having the sequence set forth in any one of SEQ ID NOS: 38-50 or 54-71,

c) a VHCDR3 having the sequence set forth in any one of SEQ ID NOS: 76-101,

d) a VLCDR1 having the sequence set forth in any one of SEQ ID NOS: 105-124,

e) a VLCDR2 having the sequence set forth in any one of SEQ ID NOS: 128-145, and

f) a VLCDR3 having the sequence set forth in any one of SEQ ID NOS: 149-166.

[0016] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a heavy chain variable region (VH) and a light chain variable region (VL), with VH comprising, consisting of, or consisting essentially of a VH having the sequence set forth in SEQ ID NOS: 170-200 and with the VL comprising, consisting of, or consisting essentially of a VL having the sequence set forth in SEQ ID NO: 204-228 and the additional binding domain capable of binding to a CD3ε epitope comprises a heavy chain variable region (VH) and a light chain variable region (VL), with VH comprising, consisting of, or consisting essentially of a VH having the sequence set forth in SEQ ID NOS: 413-418 and with the VL comprising, consisting of, or consisting essentially of a VL having the sequence set forth in SEQ ID NOS: 422-427.

[0017] Some embodiments provide a pharmaceutical composition comprising or consisting of any of the bispecific antigen binding constructs provided herein. In some embodiments, the pharmaceutical composition further comprises an effective amount of one or more of:

a) an anti-PD-L1 antibody or small molecule inhibitor;

b) an anti-PD-1 antibody or small molecule inhibitor;

c) an anti-CD38 antibody or small molecule inhibitor;

d) an anti-CD39 antibody or small molecule inhibitor;

e) an anti-CD73 antibody or small molecule inhibitor;

f) an anti-A2A receptor antibody or small molecule inhibitor;

g) an anti-A2B receptor antibody or small molecule inhibitor;

h) an anti-A2A/A2B dual receptor antibody or small molecule inhibitor;

i) an anti-CD47 antibody or small molecule inhibitor;

j) an anti-CTLA-4 antibody or small molecule inhibitor;

k) an anti-LAG-3 antibody or small molecule inhibitor;

l) an anti-TIM-3 antibody or small molecule inhibitor;

m) an anti-TIGIT antibody or small molecule inhibitor;

n) an anti-VISTA antibody or small molecule inhibitor;

o) an anti-CD94 antibody or small molecule inhibitor;

p) a small molecule inhibitor;

q) an oncolytic virus;

r) a chemotherapy;

s) ADCC capable therapies using effector competent antibodies such as anti-CD19, anti-CD20, anti-EGFR, anti-Her2, anti-SLAMF7, anti-CD52, anti-BCMA, anti-GD2, and/or anti-CCR4.

In some embodiments, the pharmaceutical composition further comprises one or both of:

a) an antibody to an immune inhibitory receptor or ligand and/or

b) an antibody to an immune stimulatory receptor or ligand.

[0018] A second aspect provides one or more nucleic acids encoding any of the bispecific antigen binding constructs provided herein. In some embodiments, the one or more nucleic acids comprises one or more vectors. Some embodiments provide a host transformed with the one or more vectors.

[0019] Some embodiments provide a method for the production of one or more bispecific antigen binding construct comprising the steps of expressing any of the one or more nucleic acids provided herein in a prokaryotic or eukaryotic host cell and recovering the one or more bispecific antigen binding construct from the cell or the cell culture supernatant.

[0020] A third aspect provides a method for treating a subject with cancer comprising administering a therapeutically effective amount of any of the bispecific antigen binding constructs or pharmaceutical compositions provided herein to the subject.

[0021] In some embodiments, the cancer is a solid cancer. In some embodiments, the cancer is a hematological cancer. In some embodiments, the cancer is selected from the group consisting of a hematopeietic cancer, hepatocellular carcinoma, leukemia, colorectal cancer (CRC), breast cancer, gastric cancer, esophageal cancer, endometrial cancer, prostate cancer, bladder cancer, thyroid cancer, liver cancer, pancreatic cancer, triple negative breast cancer, cervical cancer, ovarian cancer, uterine cancer, vaginal cancer, vulvar cancer, lung cancer, head and neck cancer, melanoma, renal cell carcinoma, cutaneous squamous cell carcinoma, Hodgkin's lymphoma, a metastasis of the brain, a metastasis of the lung, a metastasis of the liver, and/or a

metastasis of the bone, or an unresectable or metastatic solid tumor with DNA mismatch repair deficiencies or a microsatellite instability-high state. In some embodiments, the cancer is a cancer that expresses HLA-G.

[0022] In some embodiments, the method further comprises one or more of the following:

a) administering chemotherapy to the subject;

b) administering radiation therapy to the subject; and/or

c) administering one or more additional therapeutic agents to the subject.

In some embodiments, the one or more additional therapeutic agents comprise one or more immunomodulatory agents. For example, these agents could be ones that antagonize or block inhibitory signals and interactions. The agents could provide activation signals or costimulation to immune cells.

[0023] In some embodiments, the one or more immunomodulatory agents comprise an antagonist to an inhibitory receptor of an immune cell. In some embodiments, the inhibitory receptor is at least one of LILRB1, LILRB2, LILRB4, KIR2DL4, CTLA-4, PD-1, PD-L1, PD-L2, LAG-3, Tim3, TIGIT, B7-H3, B7-H4, neuritin, BTLA, CECAM-1, CECAM-5, VISTA, LAIR1, CD160, 2B4, TGF-B receptor, NKG2A, and/or a Killer-cell immunoglobulin-like receptor (KIR). In some embodiments, the one or more immunomodulatory agents comprise an agonist of a co-stimulatory receptor of an immune cell. In some embodiments, the co-stimulatory receptor is at least one of OX40, CD2, CD27, ICAM-1, LFA-1, ICOS (CD278), 4-1BB (CD137), GITR, CD28, CD30, CD40, BAFFR, HVEM, CD7, LIGHT, NKG2C, SLAMF7, NKp30, NKp46, NKp80, CD160, and/or CD83.

[0024] In some embodiments, the one or more immunomodulatory agents is one or more cytokines. In some embodiments, the one or more cytokines is at least one of G-CSF, GM-CSF, IFN-alpha, IFN-beta, IFN-gamma, FLt3 ligand, IL-1, IL-2, IL-5, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and/or IL-27.

[0025] In some embodiments, the one or more immunomodulatory agents is one or more oncolytic viruses. In some embodiments, the one or more oncolytic viruses is a Herpes simplex virus, a Vesicular stomatitis virus, an adenovirus, a Newcastle disease virus, a vaccinia virus,

and/or a maraba virus.

BRIEF DESCRIPTION OF THE DRAWINGS

[0026] **FIG. 1** shows evaluation of an HLA-G x CD3 bispecific antibody binding to cancer cell lines with engineered (**FIG. 1A**) or endogenous (**FIG. 1B**) HLA-G expression. The parental anti-HLA-G monoclonal antibody was included for comparison. Control cell lines lacking HLA-G expression are depicted in grey.

[0027] **FIG. 2** provides the binding profiles for an HLA-G x CD3 bispecific antibody and the parental anti-CD3 monoclonal antibody to $CD4^+$ and $CD8^+$ T cells from isolated human peripheral blood mononuclear cells. Representative binding profiles from two individual donors are shown. Isotype controls are depicted with open symbols.

[0028] **FIG. 3** shows the activity of an HLA-G x CD3 bispecific antibody to induce T cell-dependent cellular cytotoxicity of cancer cell lines with engineered (**FIG. 3A**) or endogenous (**FIG. 3B**) HLA-G expression.

DETAILED DESCRIPTION

[0029] Provided herein are bispecific immune cell engagers with binding specificity for HLA-G and another antigen, including pharmaceutical compositions, diagnostic compositions, and kits. In particular, heteromultimeric antibodies e.g., full length antibodies or antigen binding fragments thereof, that specifically bind to HLA-G and another antigen, such as CD3, are provided. Compositions comprising such heteromultimeric antibodies, methods for producing and purifying such heterodimeric antibodies, and their use in diagnostics and therapeutics are also provided.

I. Definitions

[0030] Unless otherwise defined, all terms of art, notations and other scientific terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a difference over what is generally understood in the art. The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodologies by those skilled in the art,

such as, for example, the widely utilized molecular cloning methodologies described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 2nd ed. (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer defined protocols and/or parameters unless otherwise noted.

[0031] As used herein, the singular forms "a," "an," and "the" include the plural referents unless the context clearly indicates otherwise.

[0032] The term "about" indicates and encompasses an indicated value and a range above and below that value. In certain embodiments, the term "about" indicates the designated value ± 10%, ± 5%, or ± 1%. In certain embodiments, the term "about" indicates the designated value ± one standard deviation of that value.

[0033] The term "combinations thereof" includes every possible combination of elements to which the term refers.

[0034] The terms "HLA-G," "MHC-G," and "major histocompatibility complex, class I, G" as well as any terms known to one skilled in the art are used interchangeably herein. HLA-G belongs to the HLA class I heavy chain paralogues. The class I HLA-G molecule is a heterodimer consisting of a heavy chain and a light chain (beta-2 microglobulin). The heavy chain is anchored in the membrane. HLA-G is expressed on fetal derived placental cells. The heavy chain is approximately 45 kDa and its gene contains 8 exons. Exon one encodes the leader peptide, exons 2 and 3 encode the alpha1 and alpha2 domain, which both bind the peptide, exon 4 encodes the alpha3 domain, exon 5 encodes the transmembrane region, and exon 6 encodes the cytoplasmic tail.

[0035] Unless specified otherwise, the terms include any variants, isoforms, and species homologs of human HLA-G that are naturally expressed by cells, or that are expressed by cells transfected with an HLA-G gene.

[0036] The terms "CD3" or "cluster of differentiation 3" as well as any terms known to one skilled in the art are used interchangeably herein. Unless specified otherwise, the terms include any variants, isoforms, and species homologs of human CD3 that are naturally expressed by cells, or that are expressed by cells transfected with a *CD3* gene. In some embodiments, CD3

proteins include murine CD3. In some embodiments, CD3 proteins include cynomolgus CD3.

[0037] The terms "CD16," "cluster of differentiation 16," and "FcγRIII" as well as any terms known to one skilled in the art are used interchangeably herein. Unless specified otherwise, the terms include any variants, isoforms, and species homologs of human CD16 that are naturally expressed by cells, or that are expressed by cells transfected with a *CD16* gene. In some embodiments, CD16 proteins include murine CD16. In some embodiments, CD16 proteins include cynomolgus CD16.

[0038] The terms "NKp46," "NCR1," "natural cytotoxicity triggering receptor 1," "CD335," "NKP46," "NK-p46," and "LY94" as well as any terms known to one skilled in the art are used interchangeably herein. Unless specified otherwise, the terms include any variants, isoforms, and species homologs of human NKp46 that are naturally expressed by cells, or that are expressed by cells transfected with a *NCR1* gene. In some embodiments, NKp46 proteins include murine NKp46. In some embodiments, NKp46 proteins include cynomolgus NKp46.

[0039] The terms "NKp30," "natural cytotoxicity triggering receptor 3," "CD337," "cluster of differentiation 337," as w ell as any terms known to one skilled in the art are used interchangably herein. Unless specified otherwise, the terms include any variants, isoforms, and species homologs of human NKp30 that are naturally expressed by cells, or that are expressed by cells transfected with a *NCR1* gene. In some embodiments, NKp30 proteins include murine NKp30. In some embodiments, NKp30proteins include cynomolgus NKp30.

[0040] The term "immunoglobulin" refers to a class of structurally related proteins generally comprising two pairs of polypeptide chains: one pair of light (L) chains and one pair of heavy (H) chains. In an "intact immunoglobulin," all four of these chains are interconnected by disulfide bonds. The structure of immunoglobulins has been well characterized. *See, e.g.,* Paul, *Fundamental Immunology* 7th ed., Ch. 5 (2013) Lippincott Williams & Wilkins, Philadelphia, PA. Briefly, each heavy chain typically comprises a heavy chain variable region (V_H) and a heavy chain constant region (C_H). The heavy chain constant region typically comprises three domains, CH1, CH2, and CH3. Each light chain typically comprises a light chain variable region (VL) and a light chain constant region. The light chain constant region typically comprises one domain, abbreviated CL.

[0041] The term "antibody" describes a type of immunoglobulin molecule and is used

herein in its broadest sense. An antibody specifically includes intact antibodies (e.g., intact immunoglobulins) and antibody fragments.

[0042] The V_H and V_L regions may be further subdivided into regions of hypervariability ("hypervariable regions (HVRs);" also called "complementarity determining regions" (CDRs)) interspersed with regions that are more conserved. The more conserved regions are called framework regions (FRs). Each V_H and V_L generally comprises three CDRs and four FRs, arranged in the following order (from N-terminus to C-terminus): FR1 - CDR1 - FR2 - CDR2 - FR3 - CDR3 - FR4. The CDRs are involved in antigen binding, and confer antigen specificity and binding affinity to the antibody. See Kabat et al., *Sequences of Proteins of Immunological Interest* 5th ed. (1991) Public Health Service, National Institutes of Health, Bethesda, MD, incorporated by reference in its entirety.

[0043] The light chain from any vertebrate species can be assigned to one of two types, called kappa and lambda, based on the sequence of the constant domain.

[0044] The heavy chain from any vertebrate species can be assigned to one of five different classes (or isotypes): IgA, IgD, IgE, IgG, and IgM. These classes are also designated α, δ, ε, γ, and μ, respectively. The IgG and IgA classes are further divided into subclasses on the basis of differences in sequence and function. Humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

[0045] The amino acid sequence boundaries of a CDR can be determined by one of skill in the art using any of a number of known numbering schemes, including those described by Kabat et al., *supra* ("Kabat" numbering scheme); Al-Lazikani et al., 1997, *J. Mol. Biol.*, 273:927-948 ("Chothia" numbering scheme); MacCallum et al., 1996, *J. Mol. Biol.* 262:732-745 ("Contact" numbering scheme); Lefranc et al., *Dev. Comp. Immunol.*, 2003, 27:55-77 ("IMGT" numbering scheme); and Honegge and Plückthun, *J. Mol. Biol.*, 2001, 309:657-70 ("AHo" numbering scheme), each of which is incorporated by reference in its entirety.

[0046] Table 1 provides the positions of CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, and CDR-H3 as identified by the Kabat and Chothia schemes. For CDR-H1, residue numbering is provided using both the Kabat and Chothia numbering schemes.

[0047] Unless otherwise specified, the numbering scheme used for identification of a

particular CDR herein is the Kabat numbering scheme. Variant and equivalent antibodies with a Chothia numbering scheme are intended to be within the scope of the invention.

Table 1. Residues in CDRs according to Kabat and Chothia numbering schemes.

CDR	Kabat	Chothia
L1	L24-L34	L24-L34
L2	L50-L56	L50-L56
L3	L89-L97	L89-L97
H1 (Kabat Numbering)	H31-H35B	H26-H32 or H34*
H1 (Chothia Numbering)	H31-H35	H26-H32
H2	H50-H65	H52-H56
H3	H95-H102	H95-H102

* The C-terminus of CDR-H1, when numbered using the Kabat numbering convention, varies between H32 and H34, depending on the length of the CDR.

[0048] The "EU numbering scheme" is generally used when referring to a residue in an antibody heavy chain constant region (e.g., as reported in Kabat et al., *supra*). Unless stated otherwise, the EU numbering scheme is used to refer to residues in antibody heavy chain constant regions described herein.

[0049] An "antibody fragment" comprises a portion of an intact antibody, such as the antigen binding or variable region of an intact antibody. Antibody fragments include, for example, Fv fragments, Fab fragments, $F(ab')_2$ fragments, Fab′ fragments, scFv (sFv) fragments, and scFv-Fc fragments. In some embodiments, an antibody or antigen binding fragment that binds HLA-G and an antibody or antigen binding fragment that binds an additional binding domain, such as CD3, includes antibody fragments of binding domain that binds HLA-G and a binding domain that binds an additional binding domain.

[0050] "Fv" fragments comprise a non-covalently linked dimer of one heavy chain variable domain and one light chain variable domain.

[0051] "Fab" fragments comprise, in addition to the heavy and light chain variable domains, the constant domain of the light chain and the first constant domain (C_{H1}) of the heavy chain. Fab fragments may be generated, for example, by papain digestion of a full-length antibody.

[0052] "$F(ab')_2$" fragments contain two Fab′ fragments joined, near the hinge region, by disulfide bonds. $F(ab')_2$ fragments may be generated, for example, by pepsin digestion of an intact

antibody. The F(ab′) fragments can be dissociated, for example, by treatment with ß-mercaptoethanol.

[0053] "Single-chain Fv" or "sFv" or "scFv" antibody fragments comprise a V_H domain and a V_L domain in a single polypeptide chain. The V_H and V_L are generally linked by a peptide linker. *See* Plückthun A. (1994). Antibodies from *Escherichia coli*. In Rosenberg M. & Moore G.P. (Eds.), *The Pharmacology of Monoclonal Antibodies* vol. 113 (pp. 269-315). Springer-Verlag, New York, incorporated by reference in its entirety. "scFv-Fc" fragments comprise an scFv attached to an Fc domain. For example, an Fc domain may be attached to the C-terminal of the scFv. The Fc domain may follow the V_H or V_L depending on the orientation of the variable domains in the scFv (i.e., V_H-V_L or V_L-V_H). Any suitable Fc domain known in the art or described herein may be used.

[0054] A "minibody" comprises an antibody which features a smaller molecular weight than that of a traditional larger antibody.

[0055] The term "monoclonal antibody" refers to an antibody from a population of substantially homogeneous antibodies. A population of substantially homogeneous antibodies comprises antibodies that are substantially similar and that bind the same epitope(s), except for variants that may normally arise during production of the monoclonal antibody. Such variants are generally present in only minor amounts. A monoclonal antibody is typically obtained by a process that includes the selection of a single antibody from a plurality of antibodies. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, yeast clones, bacterial clones, or other recombinant DNA clones. The selected antibody can be further altered, for example, to improve affinity for the target ("affinity maturation"), to humanize the antibody, to improve its production in cell culture, and/or to reduce its immunogenicity in a subject.

[0056] The term "chimeric antibody" refers to an antibody in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species.

[0057] The term "bispecific antigen binding construct" or "bispecific antibody" or any related term known or used by one skilled in the art describes a type of immunoglobulin that can bind at least two different antigens. For example, without limitation, a bispecific antigen binding

construct may bind HLA-G and CD3.

[0058] "Humanized" forms of non-human antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. A humanized antibody is generally a human immunoglobulin (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, llama, 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. Such modifications may be made to further refine antibody function. For further details, *see* Jones et al., *Nature*, 1986, 321:522-525; Riechmann et al., *Nature*, 1988, 332:323-329; and Presta, *Curr. Op. Struct. Biol.*, 1992, 2:593-596, each of which is incorporated by reference in its entirety.

[0059] A "human antibody" is one which possesses an amino acid sequence corresponding to that of an antibody produced by a human or a human cell, or derived from a non-human source that utilizes a human antibody repertoire or human antibody-encoding sequences (e.g., obtained from human sources or designed *de novo*). Human antibodies specifically exclude humanized antibodies.

[0060] An "isolated antibody" is one that has been separated and/or recovered from a component of its natural environment. Components of the natural environment may include enzymes, hormones, and other proteinaceous or nonproteinaceous materials. In some embodiments, an isolated antibody is purified to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence, for example by use of a spinning cup sequenator. In some embodiments, an isolated antibody is purified to homogeneity by gel electrophoresis (e.g., SDS-PAGE) under reducing or nonreducing conditions, with detection by Coomassie blue or silver stain. An isolated antibody includes an antibody *in situ* within recombinant cells, since at least one component of the antibody's natural environment is not present. In some embodiments, an isolated antibody is prepared by at least one purification step.

[0061] "Affinity" refers to the strength of the sum total of non-covalent interactions

between a single binding site of a molecule (e.g., an antibody) and its binding partner (e.g., an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity, which reflects a 1:1 interaction between members of a binding pair (e.g., antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured by common methods known in the art, including those described herein. Affinity can be determined, for example, using surface plasmon resonance (SPR) technology, such as a Biacore® instrument.

[0062] With regard to the binding of an antibody to a target molecule, the terms "binding" or "binds to" a particular antigen (e.g., a polypeptide target) or an epitope on a particular antigen mean binding that is measurably different from a non-selective interaction. Binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule. Binding can also be determined by competition with a control molecule that is similar to the target, such as an excess of non-labeled target. In that case, binding is indicated if the binding of the labeled target to a probe is competitively inhibited by the excess non-labeled target.

[0063] The term "k_d" (sec^{-1}), as used herein, refers to the dissociation rate constant of a particular antibody-antigen interaction. This value is also referred to as the k_{off} value.

[0064] The term "k_a" ($M^{-1} \times sec^{-1}$), as used herein, refers to the association rate constant of a particular antibody-antigen interaction. This value is also referred to as the k_{on} value.

[0065] The term "K_D" (M), as used herein, refers to the dissociation equilibrium constant of a particular antibody-antigen interaction. $K_D = k_d/k_a$.

[0066] The term "K_A" (M^{-1}), as used herein, refers to the association equilibrium constant of a particular antibody-antigen interaction. $K_A = k_a/k_d$.

[0067] Percent "identity" between a polypeptide sequence and a reference sequence is defined as the percentage of amino acid residues in the polypeptide sequence that are identical to the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, MEGALIGN (DNASTAR), CLUSTALW, or CLUSTAL OMEGA software.

Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

[0068] A "conservative substitution" or a "conservative amino acid substitution," refers to the substitution of one or more amino acids with one or more chemically or functionally similar amino acids. Conservative substitution tables providing similar amino acids are well known in the art. Polypeptide sequences having such substitutions are known as "conservatively modified variants." Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles. By way of example, the following groups of amino acids are considered conservative substitutions for one another.

Acidic Residues	D and E
Basic Residues	K, R, and H
Hydrophilic Uncharged Residues	S, T, N, and Q
Aliphatic Uncharged Residues	G, A, V, L, and I
Non-polar Uncharged Residues	C, M, and P
Aromatic Residues	F, Y, and W

Alcohol Group-Containing Residues	S and T
Aliphatic Residues	I, L, V, and M
Cycloalkenyl-associated Residues	F, H, W, and Y
Hydrophobic Residues	A, C, F, G, H, I, L, M, T, V, W, and Y
Negatively Charged Residues	D and E
Polar Residues	C, D, E, H, K, N, Q, R, S, and T
Positively Charged Residues	H, K, and R
Small Residues	A, C, D, G, N, P, S, T, and V
Very Small Residues	A, G, and S
Residues Involved in Turn Formation	A, C, D, E, G, H, K, N, Q, R, S, P, and T
Flexible Residues	Q, T, K, S, G, P, D, E, and R

Group 1	A, S, and T
Group 2	D and E
Group 3	N and Q
Group 4	R and K
Group 5	I, L, and M
Group 6	F, Y, and W

Group A	A and G

Group B	D and E
Group C	N and Q
Group D	R, K, and H
Group E	I, L, M, V
Group F	F, Y, and W
Group G	S and T
Group H	C and M

Additional conservative substitutions may be found, for example, in Creighton, *Proteins: Structures and Molecular Properties* 2nd ed. (1993) W. H. Freeman & Co., New York, NY. An antibody generated by making one or more conservative substitutions of amino acid residues in a parent antibody is referred to as a "conservatively modified variant."

[0069] The term "amino acid" refers to the twenty common naturally occurring amino acids**.** Naturally occurring amino acids include alanine (Ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C); glutamic acid (Glu; E), glutamine (Gln; Q), Glycine (Gly; G); histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

[0070] "Treating" or "treatment" of any cancer refers, in certain embodiments, to ameliorating a cancer that exists in a subject. In another embodiment, "treating" or "treatment" includes ameliorating at least one physical parameter, which may be indiscernible by the subject. In yet another embodiment, "treating" or "treatment" includes modulating the cancer, either physically (e.g., stabilization of a discernible symptom) or physiologically (e.g., stabilization of a physical parameter) or both.

[0071] As used herein, the term "therapeutically effective amount" or "effective amount" refers to an amount of an antibody or composition that when administered to a subject is effective to treat a cancer. In some embodiments, a therapeutically effective comprises or consists of exemplary doses of each antibody. In some embodiments, a therapeutically effective amount comprises or consists of determining an amount used to achieve a response according to a clinical endpoint. In some embodiments, the clinical endpoint comprises Objective Response Rate (ORR), Progression Free Survival (PFS), and/or Response Evaluation Criteria in Solid Tumors ("RECIST").

[0072] As used herein, the term "subject" means a mammal or a human. In some embodiments subjects include, but are not limited to, monkeys, dogs, cats, mice, rats, cows, horses, camels, avians, goats, and sheep.

[0073] A first aspect provides a bispecific antigen binding construct comprising a binding domain capable of binding to an HLA-G epitope and an additional binding domain capable of binding to a second epitope.

[0074] In some embodiments, the binding domain comprises a light chain. In some aspects, the light chain is a kappa light chain. In some embodiments, the light chain is a lambda light chain.

[0075] In some embodiments, the binding domain comprises a heavy chain. In some embodiments, the heavy chain is an IgA. In some embodiments, the heavy chain is an IgD. In some embodiments, the heavy chain is an IgE. In some embodiments, the heavy chain is an IgG. In some embodiments, the heavy chain is an IgM. In some embodiments, the heavy chain is an IgG1. In some embodiments, the heavy chain is an IgG2. In some embodiments, the heavy chain is an IgG3. In some embodiments, the heavy chain is an IgG4. In some embodiments, the heavy chain is an IgA1. In some embodiments, the heavy chain is an IgA2.

[0076] In some embodiments, the binding domain is an antibody fragment. In some embodiments, the antibody fragment is an Fv fragment. In some embodiments, the antibody fragment is a Fab fragment. In some embodiments, the antibody fragment is a $F(ab')_2$ fragment. In some embodiments, the antibody fragment is a Fab′ fragment. In some embodiments, the antibody fragment is an scFv (sFv) fragment. In some embodiments, the antibody fragment is an scFv-Fc fragment. In some embodiments, the antibody fragment is a minibody. In some embodiments, the antibody fragment is a single domain antibody.

[0077] In some embodiments, the binding domain is a chimeric antibody. In some embodiments, the binding domain is a humanized antibody. In some embodiments, the binding domain is a human antibody.

[0078] In some embodiments, the binding domain is an affinity matured antibody. In some embodiments, the binding domain is an affinity matured antibody derived from an illustrative sequence provided in this disclosure.

Binding Domains Capable of Binding to HLA-G

[0079] In some embodiments, the HLA-G epitope comprises or consists of an amino acid sequence set forth in SEQ ID NO: 342.

V_H Sequences Comprising Illustrative CDRs

[0080] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising one or more CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-H sequences provided in this disclosure, and variants thereof.

V_H Sequences Comprising Illustrative Kabat CDRs

[0081] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising one or more Kabat CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Kabat CDR-H sequences provided in this disclosure, and variants thereof.

Kabat CDR-H3

[0082] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 77. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 78. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting

essentially of SEQ ID NO: 79. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 80. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 81. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 82. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 83. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 84. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 85. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 86. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 87. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 88. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 89. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 90. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 91. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 92. In some embodiments, the binding

domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 94. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 95. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 96. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 97. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 98. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 99. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 100. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 101.

[0083] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Kabat CDR-H2

[0084] In some embodiments, the binding domain capable of binding to an HLA-G

epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 54-71. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 54. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 55. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 56. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 57. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 58. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 59. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 60. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 61. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 62. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 63. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 64. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 65. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H

sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 66. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 67. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 68. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 69. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 70. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 71.

Kabat CDR-H1

[0085] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 18-34. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 18. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 19. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 20. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 21. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 22. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat

CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 23. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 24. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 25. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 26. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 27. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 28. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 29. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 30. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 31. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 32. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 33. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 34.

Kabat CDR-H3 + Kabat CDR-H2

[0086] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting

of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101, and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 54-71. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

Kabat CDR-H3 + Kabat CDR-H1

[0087] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101, and a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 18-34. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

Kabat CDR-H1 + Kabat CDR-H2

[0088] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 18-34 and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 54-71. In some embodiments, the Kabat CDR-H1 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

Kabat CDR-H1 + Kabat CDR-H2 + Kabat CDR-H3

[0089] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting

of, or consisting essentially of a sequence selected from SEQ ID NOS: 18-34, a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 54-71, and a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101. In some embodiments, the Kabat CDR-H1 sequence, Kabat CDR-H2 sequence, and Kabat CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1, Kabat CDR-H2, and Kabat CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

[0090] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 18, a Kabat CDR-H2 sequence comprising SEQ ID NO: 54, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 19, a Kabat CDR-H2 sequence comprising SEQ ID NO: 55, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 77. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 20, a Kabat CDR-H2 sequence comprising SEQ ID NO: 56, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 78. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 79. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 22, a Kabat CDR-H2 sequence comprising SEQ ID NO: 58, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 80. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an

HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 60, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 81. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 82. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 81. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 83. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 84. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 24, a Kabat CDR-H2 sequence comprising SEQ ID NO: 61, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 85. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 24, a Kabat CDR-H2 sequence comprising SEQ ID NO: 61, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 86. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 62, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 87. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 63, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 88. In some

embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 63, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 89. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 63, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 90. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 27, a Kabat CDR-H2 sequence comprising SEQ ID NO: 64, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 90. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 28, a Kabat CDR-H2 sequence comprising SEQ ID NO: 62, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 91. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 29, a Kabat CDR-H2 sequence comprising SEQ ID NO: 64, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 92. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 65, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 93. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 30, a Kabat CDR-H2 sequence comprising SEQ ID NO: 66, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 94. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 31, a Kabat CDR-H2 sequence comprising SEQ ID NO: 67, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 95. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 32, a Kabat CDR-H2 sequence comprising SEQ ID NO: 68, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 96. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 33, a Kabat CDR-H2 sequence comprising SEQ ID NO: 69, and a

Kabat CDR-H3 sequence comprising SEQ ID NO: 97. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 34, a Kabat CDR-H2 sequence comprising SEQ ID NO: 70, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 98. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 18, a Kabat CDR-H2 sequence comprising SEQ ID NO: 54, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 99. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 31, a Kabat CDR-H2 sequence comprising SEQ ID NO: 71, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 100. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 24, a Kabat CDR-H2 sequence comprising SEQ ID NO: 61, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 101.

Variants of V_H Sequences Comprising Illustrative Kabat CDRs

[0091] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Kabat CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[0092] In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H3 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H3 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[0093] In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H2 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or

consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H2 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[0094] In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H1 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H1 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative Chothia CDRs

[0095] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising one or more Chothia CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Chothia CDR-H sequences provided in this disclosure, and variants thereof.

Chothia CDR-H3

[0096] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence

comprising, consisting of, or consisting essentially of SEQ ID NO: 77. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 78. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 79. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 80. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 81. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 82. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 83. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 84. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 85. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 86. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 87. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 88. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 89. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia

CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 90. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 91. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 92. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 93. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 94. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 95. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 96. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 97. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 98. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 99. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 100. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 101.

Chothia CDR-H2

[0097] In some embodiments, the binding domain capable of binding to an HLA-G

epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 38-50. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 38. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 39. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 40. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 41. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 42. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 43. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 44. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 45. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 46. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 47. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 48. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 49. In some embodiments,

the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 50.

Chothia CDR-H1

[0098] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 1-14. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 1. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 2. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 3. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 4. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 5. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 6. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 7. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 8. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 9. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting

essentially of SEQ ID NO: 10. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 11. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 12. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 13. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 14.

Chothia CDR-H3 + Chothia CDR-H2

[0099] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101, and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 38-50. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

Chothia CDR-H3 + Chothia CDR-H1

[00100] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101, and a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 1-14. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

Chothia CDR-H1 + Chothia CDR-H2

[00101] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 1-14 and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 38-50. In some embodiments, the Chothia CDR-H1 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

Chothia CDR-H1 + Chothia CDR-H2 + Chothia CDR-H3

[00102] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 1-14, a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 38-50, and a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 76-101. In some embodiments, the Chothia CDR-H1 sequence, Chothia CDR-H2 sequence, and Chothia CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1, Chothia CDR-H2, and Chothia CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 170-200.

[00103] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 1, a Chothia CDR-H2 sequence comprising SEQ ID NO: 38, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 39, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 77. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia

CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 40, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 78. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 79. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 4, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 80. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 43, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 81. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 82. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 5, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 81. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 83. In some embodiments, the binding

domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 84. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 85. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 86. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 7, a Chothia CDR-H2 sequence comprising SEQ ID NO: 45, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 87. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 8, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 88. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 8, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 89. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 7, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 90. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 9, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 90. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 45, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 91. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 8, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a

Chothia CDR-H3 sequence comprising SEQ ID NO: 92. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 7, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 93. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 10, a Chothia CDR-H2 sequence comprising SEQ ID NO: 46, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 94. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 11, a Chothia CDR-H2 sequence comprising SEQ ID NO: 47, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 95. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 12, a Chothia CDR-H2 sequence comprising SEQ ID NO: 48, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 96. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 13, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 97. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 14, a Chothia CDR-H2 sequence comprising SEQ ID NO: 49, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 98. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 1, a Chothia CDR-H2 sequence comprising SEQ ID NO: 38, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 99. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 11, a Chothia CDR-H2 sequence comprising SEQ ID NO: 50, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 100. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 101.

Variants of V_H Sequences Comprising Illustrative Chothia CDRs

[00104] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Chothia CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00105] In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H3 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H3 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00106] In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H2 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H2 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00107] In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H1 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H1 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences

[00108] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 170-200. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 170. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 171. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 172. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 173. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 174. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 175. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 176. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 177. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 178. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 179. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 180. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 181. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 182. In some embodiments, the binding domain capable

of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 183. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 184. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 185. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 186. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 187. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 188. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 189. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 190. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 191. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 192. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 193. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 194. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 195. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 196. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 197. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or

consisting essentially of SEQ ID NO: 198. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 199. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 200.

[00109] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VH having the sequence set forth in one of SEQ ID NOS: 170-200.

Variants of V_H Sequences

[00110] In some embodiments, the V_H sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_H sequence provided in this disclosure.

[00111] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.5% identity with any of the illustrative V_H sequences provided in this disclosure.

[00112] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

CDR-L3 Sequences

[00113] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 149-166. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 149. In some embodiments, the binding domain

capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 150. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 152. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 153. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 154. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 156. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 158. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 159. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 160. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 161. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 162. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 163. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 164. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting

of, or consisting essentially of SEQ ID NO: 165. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 166.

[00114] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences Comprising Illustrative CDRs

[00115] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising one or more CDR-L sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-L sequences provided in this disclosure, and variants thereof.

CDR-L3

[00116] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 149-166. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 150. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence

comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 152. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 153. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 154. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 156. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 158. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 159. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 160. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 161. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 162. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 163. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 164. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or

consisting essentially of SEQ ID NO: 165. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 166.

CDR-L2

[00117] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 128-145. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 128. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 129. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 130. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 131. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 132. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 133. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 134. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 135. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 136. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID

NO: 137. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 138. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 139. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 140. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 141. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 142. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 143. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 144. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 145.

CDR-L1

[00118] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 105-124. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 105. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 106. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 107. In some embodiments,

the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 108. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 109. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 110. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 111. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 112. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 113. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 114. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 115. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 116. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 117. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 118. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 119. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 120. In some embodiments, the binding domain capable of binding to an HLA-G epitope

comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 121. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 122. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 123. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 124.

CDR-L3 + CDR-L2

[00119] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 149-166 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 128-145. In some embodiments, the CDR-L3 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 204-228.

CDR-L3 + CDR-L1

[00120] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 149-166 and a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 105-124. In some embodiments, the CDR-L3 sequence and the CDR-L1 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L1 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 204-228.

CDR-L1 + CDR-L2

[00121] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 105-124 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 128-145. In some embodiments, the CDR-L1 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 204-228.

CDR-L1 + CDR-L2 + CDR-L3

[00122] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 105-124, a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 128-145, and a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L1 sequence, CDR-L2 sequence, and CDR-L3 sequence are all from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1, CDR-L2, and CDR-L3 are all from a single illustrative V_L sequence selected from SEQ ID NOS: 204-228.

[00123] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 106, a CDR-L2 sequence comprising SEQ ID NO: 129, and a CDR-L3 sequence SEQ ID NO: 150. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 107, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-

L1 sequence comprising SEQ ID NO: 108, a CDR-L2 sequence comprising SEQ ID NO: 130, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 109, a CDR-L2 sequence comprising SEQ ID NO: 131, and a CDR-L3 sequence SEQ ID NO: 152. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 107, a CDR-L2 sequence comprising SEQ ID NO: 132, and a CDR-L3 sequence SEQ ID NO: 153. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 132, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 111, a CDR-L2 sequence comprising SEQ ID NO: 133, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 154. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 112, a CDR-L2 sequence comprising SEQ ID NO: 134, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 113, a CDR-L2 sequence comprising SEQ ID NO: 135, and a CDR-L3 sequence SEQ ID NO: 156. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 114, a CDR-L2 sequence comprising SEQ ID NO: 136, and a CDR-L3 sequence SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 115, a CDR-L2 sequence comprising SEQ ID NO: 135, and a CDR-L3 sequence SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 116, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence

comprising a CDR-L1 sequence comprising SEQ ID NO: 117, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 118, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 158. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 118, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 119, a CDR-L2 sequence comprising SEQ ID NO: 139, and a CDR-L3 sequence SEQ ID NO: 159. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 120, a CDR-L2 sequence comprising SEQ ID NO: 140, and a CDR-L3 sequence SEQ ID NO: 160. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 141, and a CDR-L3 sequence SEQ ID NO: 161. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 122, a CDR-L2 sequence comprising SEQ ID NO: 142, and a CDR-L3 sequence SEQ ID NO: 162. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 143, and a CDR-L3 sequence SEQ ID NO: 163. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 143, and a CDR-L3 sequence SEQ ID NO: 164. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 123, a CDR-L2 sequence comprising SEQ ID NO: 144, and a CDR-L3 sequence SEQ ID NO: 165. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 124, a CDR-L2 sequence comprising SEQ ID NO: 145, and a CDR-L3 sequence SEQ ID NO: 166.

Variants of V_L Sequences Comprising Illustrative CDR-Ls

[00124] In some embodiments, the V_L sequences provided herein comprise a variant of an illustrative CDR-L3, CDR-L2, and/or CDR-L1 sequence provided in this disclosure.

[00125] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00126] In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L2 sequence provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L2 sequences provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00127] In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L1 sequence provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L1 sequences provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences

[00128] In some embodiments, the binding domain capable of binding to an HLA-G

epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 204-228. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 204. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 205. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 206. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 207. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 208. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 209. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 210. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 211. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 212. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 213. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 214. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 215. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 216. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 217. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or

consisting essentially of SEQ ID NO: 218. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 219. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 220. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 221. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 222. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 223. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 224. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 225. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 226. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 227. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 228.

[00129] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VL having the sequence set forth in one of SEQ ID NO: 204-228.

Variants of V_L Sequences

[00130] In some embodiments, the V_L sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_L sequence provided in this disclosure.

[00131] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some

embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00132] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Pairs

CDR-H3 – CDR-L3 Pairs

[00133] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a CDR-H3 sequence and a CDR-L3 sequence. In some embodiments, the CDR-H3 sequence is part of a V_H and the CDR-L3 sequence is part of a V_L.

[00134] In some embodiments, the CDR-H3 sequence is a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 76-101, and the CDR-L3 sequence is a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 149-166.

[00135] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 76 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00136] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 77 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00137] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 78 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00138] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 79 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00139] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 80 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00140] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 81 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00141] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 82 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00142] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 83 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00143] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 84 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00144] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 85 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00145] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 86 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00146] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 87 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00147] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 88 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00148] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 89 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00149] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 90 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00150] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 91 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00151] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 92 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00152] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 93 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00153] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 94 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00154] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 95 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00155] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 96 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00156] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 97 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00157] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 98 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ

ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00158] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 99 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00159] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 100 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3

sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

[00160] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 101 and the CDR-L3 sequence is selected from SEQ ID NOS: 149-166. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 149. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 150. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 151. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 152. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 153. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 154. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 155. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 156. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 157. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 158. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 159. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 160. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 161. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 162. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 163. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 164. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 165. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 166.

1.1.1.1.Variants of CDR-H3 – CDR-L3 Pairs

[00161] In some embodiments, the CDR-H3 – CDR-L3 pairs provided herein comprise a variant of an illustrative CDR-H3 and/or CDR-L1 sequence provided in this disclosure.

[00162] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00163] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H – V_L Pairs

[00164] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence and/or a V_L sequence.

[00165] In some embodiments, the V_H sequence is a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 170-200 and the V_L sequence is a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 204-228.

[00166] In some embodiments, the V_H sequence is SEQ ID NO: 170 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L

sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00167] In some embodiments, the V_H sequence is SEQ ID NO: 171 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00168] In some embodiments, the V_H sequence is SEQ ID NO: 172 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L

sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00169] In some embodiments, the V_H sequence is SEQ ID NO: 173 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00170] In some embodiments, the V_H sequence is SEQ ID NO: 174 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L

sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00171] In some embodiments, the V_H sequence is SEQ ID NO: 175 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In

some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00172] In some embodiments, the V_H sequence is SEQ ID NO: 176 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00173] In some embodiments, the V_H sequence is SEQ ID NO: 177 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In

some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00174] In some embodiments, the V_H sequence is SEQ ID NO: 178 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00175] In some embodiments, the V_H sequence is SEQ ID NO: 179 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In

some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00176] In some embodiments, the V_H sequence is SEQ ID NO: 180 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L

sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00177] In some embodiments, the V_H sequence is SEQ ID NO: 181 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00178] In some embodiments, the V_H sequence is SEQ ID NO: 182 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L

sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00179] In some embodiments, the V_H sequence is SEQ ID NO: 183 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00180] In some embodiments, the V_H sequence is SEQ ID NO: 184 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L

sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00181] In some embodiments, the V_H sequence is SEQ ID NO: 185 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00182] In some embodiments, the V_H sequence is SEQ ID NO: 186 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00183] In some embodiments, the V_H sequence is SEQ ID NO: 187 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L

sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00184] In some embodiments, the V_H sequence is SEQ ID NO: 188 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00185] In some embodiments, the V_H sequence is SEQ ID NO: 189 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L

sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00186] In some embodiments, the V_H sequence is SEQ ID NO: 190 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00187] In some embodiments, the V_H sequence is SEQ ID NO: 191 and the V_L sequence

is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00188] In some embodiments, the V_H sequence is SEQ ID NO: 192 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In

some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00189] In some embodiments, the V_H sequence is SEQ ID NO: 193 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00190] In some embodiments, the V_H sequence is SEQ ID NO: 194 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In

some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00191] In some embodiments, the V_H sequence is SEQ ID NO: 195 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00192] In some embodiments, the V_H sequence is SEQ ID NO: 196 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO:

204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00193] In some embodiments, the V_H sequence is SEQ ID NO: 197 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L

sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00194] In some embodiments, the V_H sequence is SEQ ID NO: 198 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00195] In some embodiments, the V_H sequence is SEQ ID NO: 199 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L

sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00196] In some embodiments, the V_H sequence is SEQ ID NO: 200 and the V_L sequence is selected from SEQ ID NOS: 204-228. In some embodiments, the V_L sequence is SEQ ID NO: 204. In some embodiments, the V_L sequence is SEQ ID NO: 205. In some embodiments, the V_L sequence is SEQ ID NO: 206. In some embodiments, the V_L sequence is SEQ ID NO: 207. In some embodiments, the V_L sequence is SEQ ID NO: 208. In some embodiments, the V_L sequence is SEQ ID NO: 209. In some embodiments, the V_L sequence is SEQ ID NO: 210. In some embodiments, the V_L sequence is SEQ ID NO: 211. In some embodiments, the V_L sequence is SEQ ID NO: 212. In some embodiments, the V_L sequence is SEQ ID NO: 213. In some embodiments, the V_L sequence is SEQ ID NO: 214. In some embodiments, the V_L sequence is SEQ ID NO: 215. In some embodiments, the V_L sequence is SEQ ID NO: 216. In some embodiments, the V_L sequence is SEQ ID NO: 217. In some embodiments, the V_L sequence is SEQ ID NO: 218. In some embodiments, the V_L sequence is SEQ ID NO: 219. In some embodiments, the V_L sequence is SEQ ID NO: 220. In some embodiments, the V_L sequence is SEQ ID NO: 221. In some embodiments, the V_L sequence is SEQ ID NO: 222. In some embodiments, the V_L sequence is SEQ ID NO: 223. In some embodiments, the V_L sequence is SEQ ID NO: 224. In some embodiments, the V_L sequence is SEQ ID NO: 225. In some embodiments, the V_L sequence is SEQ ID NO: 226. In some embodiments, the V_L sequence is SEQ ID NO: 227. In some embodiments, the V_L sequence is SEQ ID NO: 228.

[00197] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth above. In

some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth in Table S.

CDR-H1 + CDR-H2 + CDR-H3 + CDR-L1 + CDR-L2 + CDR-L3

[00198] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 18, a Kabat CDR-H2 sequence comprising SEQ ID NO: 54, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 19, a Kabat CDR-H2 sequence comprising SEQ ID NO: 55, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 77 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 20, a Kabat CDR-H2 sequence comprising SEQ ID NO: 56, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 78 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 79 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 22, a Kabat CDR-H2 sequence comprising SEQ ID NO: 58, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 80 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence

SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 106, a CDR-L2 sequence comprising SEQ ID NO: 129, and a CDR-L3 sequence SEQ ID NO: 150. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 107, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 60, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 81 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 108, a CDR-L2 sequence comprising SEQ ID NO: 130, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 82 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 109, a CDR-L2 sequence comprising SEQ ID NO: 131, and a CDR-L3 sequence SEQ ID NO: 152. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 107, a CDR-L2 sequence comprising SEQ ID NO: 132, and a CDR-L3 sequence SEQ ID NO:153. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 23, a Kabat CDR-H2 sequence comprising SEQ ID NO: 59, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 81 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 132, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G

epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 83 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 111, a CDR-L2 sequence comprising SEQ ID NO: 133, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 21, a Kabat CDR-H2 sequence comprising SEQ ID NO: 57, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 84 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 24, a Kabat CDR-H2 sequence comprising SEQ ID NO: 61, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 85 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 154. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 24, a Kabat CDR-H2 sequence comprising SEQ ID NO: 61, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 86 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 154. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 62, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 87 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 112, a CDR-L2 sequence comprising SEQ ID NO: 134, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 63, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 88 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 113, a CDR-L2 sequence comprising SEQ ID NO: 135, and a CDR-L3 sequence SEQ ID NO: 156. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID

NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 63, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 89 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 114, a CDR-L2 sequence comprising SEQ ID NO: 136, and a CDR-L3 sequence SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 63, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 90 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 115, a CDR-L2 sequence comprising SEQ ID NO: 135, and a CDR-L3 sequence SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 27, a Kabat CDR-H2 sequence comprising SEQ ID NO: 64, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 90 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 116, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 28, a Kabat CDR-H2 sequence comprising SEQ ID NO: 62, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 91 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 117, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 29, a Kabat CDR-H2 sequence comprising SEQ ID NO: 64, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 92 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 118, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 158. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 65, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 93 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 118, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 30, a Kabat CDR-H2 sequence comprising SEQ ID NO: 66, and a Kabat CDR-H3 sequence

comprising SEQ ID NO: 94 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 119, a CDR-L2 sequence comprising SEQ ID NO: 139, and a CDR-L3 sequence SEQ ID NO: 159. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 31, a Kabat CDR-H2 sequence comprising SEQ ID NO: 67, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 95 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 120, a CDR-L2 sequence comprising SEQ ID NO: 140, and a CDR-L3 sequence SEQ ID NO: 160. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 32, a Kabat CDR-H2 sequence comprising SEQ ID NO: 68, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 96 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 141, and a CDR-L3 sequence SEQ ID NO: 161. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 33, a Kabat CDR-H2 sequence comprising SEQ ID NO: 69, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 97 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 122, a CDR-L2 sequence comprising SEQ ID NO: 142, and a CDR-L3 sequence SEQ ID NO: 162. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 34, a Kabat CDR-H2 sequence comprising SEQ ID NO: 70, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 98 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 143, and a CDR-L3 sequence SEQ ID NO: 163. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 18, a Kabat CDR-H2 sequence comprising SEQ ID NO: 54, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 99 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 143, and a CDR-L3 sequence SEQ ID NO: 164. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 31, a Kabat CDR-H2 sequence comprising SEQ ID NO: 71, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 100 and a VL sequence comprising a CDR-L1 sequence comprising

SEQ ID NO: 123, a CDR-L2 sequence comprising SEQ ID NO: 144, and a CDR-L3 sequence SEQ ID NO: 165. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 24, a Kabat CDR-H2 sequence comprising SEQ ID NO: 61, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 101 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 124, a CDR-L2 sequence comprising SEQ ID NO: 145, and a CDR-L3 sequence SEQ ID NO: 166.

[00199] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 1, a Chothia CDR-H2 sequence comprising SEQ ID NO: 38, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 39, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 77 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 40, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 78 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 79 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 4, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 80 and a VL sequence comprising a CDR-L1 sequence

comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 106, a CDR-L2 sequence comprising SEQ ID NO: 129, and a CDR-L3 sequence SEQ ID NO: 150. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 107, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 43, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 81 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 108, a CDR-L2 sequence comprising SEQ ID NO: 130, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 82 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 109, a CDR-L2 sequence comprising SEQ ID NO: 131, and a CDR-L3 sequence SEQ ID NO: 152. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 5, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 76 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 107, a CDR-L2 sequence comprising SEQ ID NO: 132, and a CDR-L3 sequence SEQ ID NO: 153. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 42, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 81 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 132, and a CDR-L3

sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 83 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 111, a CDR-L2 sequence comprising SEQ ID NO: 133, and a CDR-L3 sequence SEQ ID NO: 151. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 41, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 84 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 149. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 85 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 154. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 86 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 154. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 7, a Chothia CDR-H2 sequence comprising SEQ ID NO: 45, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 87 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 112, a CDR-L2 sequence comprising SEQ ID NO: 134, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 8, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 88 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 113, a CDR-L2 sequence comprising SEQ ID NO: 135, and a CDR-L3 sequence SEQ ID NO: 156. In some embodiments, the binding domain capable of binding to an

HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 8, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 89 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 114, a CDR-L2 sequence comprising SEQ ID NO: 136, and a CDR-L3 sequence SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 7, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 90 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 115, a CDR-L2 sequence comprising SEQ ID NO: 135, and a CDR-L3 sequence SEQ ID NO: 157. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 9, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 90 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 116, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 45, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 91 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 117, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 8, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 92 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 118, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 158. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 7, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 93 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 118, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 155. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising

SEQ ID NO: 10, a Chothia CDR-H2 sequence comprising SEQ ID NO: 46, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 94 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 119, a CDR-L2 sequence comprising SEQ ID NO: 139, and a CDR-L3 sequence SEQ ID NO: 159. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 11, a Chothia CDR-H2 sequence comprising SEQ ID NO: 47, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 95 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 120, a CDR-L2 sequence comprising SEQ ID NO: 140, and a CDR-L3 sequence SEQ ID NO: 160. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 12, a Chothia CDR-H2 sequence comprising SEQ ID NO: 48, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 96 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 141, and a CDR-L3 sequence SEQ ID NO: 161. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 13, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 97 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 122, a CDR-L2 sequence comprising SEQ ID NO: 142, and a CDR-L3 sequence SEQ ID NO: 162. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 14, a Chothia CDR-H2 sequence comprising SEQ ID NO: 49, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 98 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 143, and a CDR-L3 sequence SEQ ID NO: 163. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 1, a Chothia CDR-H2 sequence comprising SEQ ID NO: 38, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 99 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 105, a CDR-L2 sequence comprising SEQ ID NO: 143, and a CDR-L3 sequence SEQ ID NO: 164. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 11, a Chothia CDR-H2 sequence comprising SEQ ID NO: 50, and a Chothia CDR-

H3 sequence comprising SEQ ID NO: 100 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 123, a CDR-L2 sequence comprising SEQ ID NO: 144, and a CDR-L3 sequence SEQ ID NO: 165. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 6, a Chothia CDR-H2 sequence comprising SEQ ID NO: 44, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 101 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 124, a CDR-L2 sequence comprising SEQ ID NO: 145, and a CDR-L3 sequence SEQ ID NO: 166.

[00200] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair, with the VH having the sequence set forth in one of SEQ ID NOS: 170-200 and with the VL having the sequence set forth in one of SEQ ID NOS: 204-228.

Variants of V_H – V_L Pairs

[00201] In some embodiments, the V_H – V_L pairs provided herein comprise a variant of an illustrative V_H and/or V_L sequence provided in this disclosure.

[00202] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.1% identity with any of the illustrative V_H sequences provided in this disclosure.

[00203] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00204] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some

embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00205] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

HC + LC

[00206] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises or consists of one or more heavy chains consisting of an HC sequence and one or more light chains consisting of an LC sequence. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises or consists of two identical heavy chains consisting of an HC sequence and two identical light chains consisting of an LC sequence.

[00207] In some embodiments, the HC sequence is an HC sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 232-262 and the LC sequence is an LC sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 300-330. In some embodiments, the HC sequence is an HC sequence consisting of a sequence selected from SEQ ID NOS: 232-262 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the HC sequence is an HC sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 266-296 and the LC sequence is an LC sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 300-330. In some embodiments, the HC sequence is an HC sequence consisting of a sequence selected from SEQ ID NOS: 266-296 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330.

[00208] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 232 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00209] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 233 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00210] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 234 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00211] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 235 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00212] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 236 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00213] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 237 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00214] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 238 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00215] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 239 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00216] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 240 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00217] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 241 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00218] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 242 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00219] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 243 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00220] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 244 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00221] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 245 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00222] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 246 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00223] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 247 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00224] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 248 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00225] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 249 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00226] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 250 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00227] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 251 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00228] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 252 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00229] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 253 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00230] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 254 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00231] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 255 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00232] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 256 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00233] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 257 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00234] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 258 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00235] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 259 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00236] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 260 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00237] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 261 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00238] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 262 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00239] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 266 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00240] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 267 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00241] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 268 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00242] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 269 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00243] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 270 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00244] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 271 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00245] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 272 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00246] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 273 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00247] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 274 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00248] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 275 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00249] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 276 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00250] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 277 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00251] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 278 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00252] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 279 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00253] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 280 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00254] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 281 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00255] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 282 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00256] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 283 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00257] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 284 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00258] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 285 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00259] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 286 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00260] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 287 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00261] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 288 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00262] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 289 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00263] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 290 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00264] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 291 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00265] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 292 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00266] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 293 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some

embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00267] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 294 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00268] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID

NO: 295 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00269] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 296 and the LC sequence is an LC sequence consisting of a sequence selected from SEQ ID NOS: 300-330. In some embodiments, the LC sequence is SEQ ID NO: 300. In some embodiments, the LC sequence is SEQ ID NO: 301. In some embodiments, the LC sequence is SEQ ID NO: 302. In some embodiments, the LC sequence is SEQ ID NO: 303. In some embodiments, the LC sequence is SEQ ID NO: 304. In some embodiments, the LC sequence is SEQ ID NO: 305. In some embodiments, the LC sequence is SEQ ID NO: 306. In some embodiments, the LC sequence is SEQ ID NO: 307. In some embodiments, the LC sequence is SEQ ID NO: 308. In some embodiments, the LC sequence is SEQ ID NO: 309. In some

embodiments, the LC sequence is SEQ ID NO: 310. In some embodiments, the LC sequence is SEQ ID NO: 311. In some embodiments, the LC sequence is SEQ ID NO: 312. In some embodiments, the LC sequence is SEQ ID NO: 313. In some embodiments, the LC sequence is SEQ ID NO: 314. In some embodiments, the LC sequence is SEQ ID NO: 315. In some embodiments, the LC sequence is SEQ ID NO: 316. In some embodiments, the LC sequence is SEQ ID NO: 317. In some embodiments, the LC sequence is SEQ ID NO: 318. In some embodiments, the LC sequence is SEQ ID NO: 319. In some embodiments, the LC sequence is SEQ ID NO: 320. In some embodiments, the LC sequence is SEQ ID NO: 321. In some embodiments, the LC sequence is SEQ ID NO: 322. In some embodiments, the LC sequence is SEQ ID NO: 323. In some embodiments, the LC sequence is SEQ ID NO: 324. In some embodiments, the LC sequence is SEQ ID NO: 325. In some embodiments, the LC sequence is SEQ ID NO: 326. In some embodiments, the LC sequence is SEQ ID NO: 327. In some embodiments, the LC sequence is SEQ ID NO: 328. In some embodiments, the LC sequence is SEQ ID NO: 329. In some embodiments, the LC sequence is SEQ ID NO: 330.

[00270] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 232 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 300. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 233 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 301. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 234 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 302. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 235 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 303. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 236 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 304. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 237 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 305. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 238 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 306. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 239 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 307. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 240 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 308. In some

embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 241 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 309. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 242 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 310. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 243 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 311. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 244 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 312. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 245 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 313. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 246 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 314. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 247 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 315. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 248 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 316. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 249 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 317. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 250 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 318. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 251 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 319. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 252 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 320. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 253 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 321. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 254 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 322. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 255 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 323. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 256 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 324. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 257 and the LC sequence is an LC sequence

consisting of sequence SEQ ID NO: 325. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 258 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 326. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 259 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 327. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 260 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 328. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 261 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 329. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 262 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 330.

[00271] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 266 and the LC sequence is an LC sequence consisting of a sequence SEQ ID NO: 300. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 267 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 301. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 268 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 302. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 269 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 303. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 270 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 304. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 271 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 305. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 272 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 306. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 273 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 307. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 274 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 308. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 275 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 309. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 276 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 310. In some embodiments, the HC sequence is

an HC sequence consisting of SEQ ID NO: 277 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 311. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 278 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 312. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 279 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 313. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 280 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 314. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 281 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 315. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 282 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 316. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 283 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 317. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 284 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 318. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 285 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 319. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 286 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 320. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 287 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 321. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 288 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 322. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 289 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 323. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 290 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 324. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 291 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 325. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 292 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 326. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 293 and the LC sequence is an LC sequence consisting of sequence

SEQ ID NO: 327. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 294 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 328. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 295 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 329. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 296 and the LC sequence is an LC sequence consisting of sequence SEQ ID NO: 330.

[00272] In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a HC-LC pair set forth above. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a HC-LC pair set forth in Table S.

Binding Domains Capable of Binding to CD3

[00273] In some embodiments, the second epitope comprises a CD3ε epitope. In some embodiments, the CD3ε epitope comprises or consists of an amino acid sequence set forth in SEQ ID NO: 629.

[00274] CD3 is a protein complex and T cell co-receptor that is involved in activating the cytotoxic T cell ($CD8^+$ T cells), T helper cells ($CD4^+$ T cells) and natural killer T cells (NKT cells)." CD3 is composed of four distinct chains. In mammals, the complex contains a CD3γ chain, a CD3δ chain, and two CD3ε chains. These chains associate with the T-cell receptor (TCR) and the ζ-chain (zeta-chain) to generate an activation signal in T lymphocytes. The TCR, ζ-chain, and CD3 molecules together constitute the TCR complex.

[00275] The CD3γ, CD3δ, and CD3ε chains are highly related cell-surface proteins of the immunoglobulin superfamily containing a single extracellular immunoglobulin domain. The intracellular tails of the CD3γ, CD3ε, and CD3δ molecules each contain a single conserved motif known as an *immunoreceptor tyrosine-based activation motif* or ITAM for short, which is essential for the signaling capacity of the TCR. The intracellular tail of CD3ζ contains 3 ITAM motifs. Phosphorylation of the ITAM on CD3 renders the CD3 chain capable of binding an enzyme called ZAP70 (zeta associated protein), a kinase that is important in the signaling cascade of the T cell.

In some embodiments, CD3 proteins include murine CD3. In some embodiments, CD3 proteins include cynomolgus CD3.

CDR-H3 Sequences

[00276] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 379.

[00277] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative CDRs

[00278] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising one or more CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-H sequences provided in this disclosure, and variants thereof.

V_H Sequences Comprising Illustrative Kabat CDRs

[00279] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising one or more Kabat CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Kabat CDR-H sequences provided in this disclosure, and variants thereof.

Kabat CDR-H3

[00280] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 379.

Kabat CDR-H2

[00281] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 371-375. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 371.

Kabat CDR-H1

[00282] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 354-357. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 354.

Kabat CDR-H3 + Kabat CDR-H2

[00283] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382, and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 371-375. In some embodiments, the Kabat CDR-H3 sequence and

the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

Kabat CDR-H3 + Kabat CDR-H1

[00284] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382, and a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 354-357. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

Kabat CDR-H1 + Kabat CDR-H2

[00285] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 354-357 and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 371-375. In some embodiments, the Kabat CDR-H1 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

Kabat CDR-H1 + Kabat CDR-H2 + Kabat CDR-H3

[00286] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 354-357, a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 371-375, and a Kabat CDR-H3 sequence comprising, consisting of,

or consisting essentially of a sequence selected from SEQ ID NOS: 379-382. In some embodiments, the Kabat CDR-H1 sequence, Kabat CDR-H2 sequence, and Kabat CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1, Kabat CDR-H2, and Kabat CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

[00287] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 354, a Kabat CDR-H2 sequence comprising SEQ ID NO: 371, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 379.

Variants of V_H Sequences Comprising Illustrative Kabat CDRs

[00288] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Kabat CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00289] In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H3 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H3 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00290] In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H2 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H2 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino

acid substitutions.

[00291] In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H1 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H1 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative Chothia CDRs

[00292] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising one or more Chothia CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Chothia CDR-H sequences provided in this disclosure, and variants thereof.

Chothia CDR-H3

[00293] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 413-418. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 379.

Chothia CDR-H2

[00294] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising,

consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 362-365. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 413-418. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 362.

Chothia CDR-H1

[00295] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 346-349. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 413-418. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 346.

Chothia CDR-H3 + Chothia CDR-H2

[00296] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382, and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 362-365. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

Chothia CDR-H3 + Chothia CDR-H1

[00297] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising,

consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382, and a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 346-349. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

Chothia CDR-H1 + Chothia CDR-H2

[00298] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 346-349 and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 362-365. In some embodiments, the Chothia CDR-H1 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

Chothia CDR-H1 + Chothia CDR-H2 + Chothia CDR-H3

[00299] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 346-349, a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 362-365, and a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 379-382. In some embodiments, the Chothia CDR-H1 sequence, Chothia CDR-H2 sequence, and Chothia CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1, Chothia CDR-H2, and Chothia CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 413-418.

[00300] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising

SEQ ID NO: 346, a Chothia CDR-H2 sequence comprising SEQ ID NO: 362, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 379.

Variants of V_H Sequences Comprising Illustrative Chothia CDRs

[00301] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Chothia CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00302] In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H3 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H3 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00303] In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H2 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H2 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00304] In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H1 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H1 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of

any of the illustrative Chothia CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences

[00305] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 413-418. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 413. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 414. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 415. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 416. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 417. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 418.

[00306] In some embodiments, the binding domain capable of binding to a CD3ε epitope comprises three heavy chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VH having the sequence set forth in one of SEQ ID NOS: 413-418.

Variants of V_H Sequences

[00307] In some embodiments, the V_H sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_H sequence provided in this disclosure.

[00308] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence

having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.5% identity with any of the illustrative V_H sequences provided in this disclosure.

[00309] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

CDR-L3 Sequences

[00310] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 404-408. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 404.

[00311] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences Comprising Illustrative CDRs

[00312] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising one or more CDR-L sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-L sequences provided in this disclosure, and variants thereof.

CDR-L3

[00313] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 404-408. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 404.

CDR-L2

[00314] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 396-400. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 396.

CDR-L1

[00315] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 388-392. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 388.

CDR-L3 + CDR-L2

[00316] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 404-408 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID

NOS: 396-400. In some embodiments, the CDR-L3 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 422-427.

CDR-L3 + CDR-L1

[00317] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 404-408 and a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 388-392. In some embodiments, the CDR-L3 sequence and the CDR-L1 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L1 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 422-427.

CDR-L1 + CDR-L2

[00318] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 388-392 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 396-400. In some embodiments, the CDR-L1 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 422-427.

CDR-L1 + CDR-L2 + CDR-L3

[00319] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 388-392, a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID

NOS: 396-400, and a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 404-408. In some embodiments, the CDR-L1 sequence, CDR-L2 sequence, and CDR-L3 sequence are all from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1, CDR-L2, and CDR-L3 are all from a single illustrative V_L sequence selected from SEQ ID NOS: 422-427.

[00320] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 388, a CDR-L2 sequence comprising SEQ ID NO: 396, and a CDR-L3 sequence SEQ ID NO: 404.

Variants of V_L Sequences Comprising Illustrative CDR-Ls

[00321] In some embodiments, the V_L sequences provided herein comprise a variant of an illustrative CDR-L3, CDR-L2, and/or CDR-L1 sequence provided in this disclosure.

[00322] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00323] In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L2 sequence provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L2 sequences provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00324] In some embodiments, the CDR-L1 sequence comprises, consists of, or consists

essentially of a variant of an illustrative CDR-L1 sequence provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L1 sequences provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences

[00325] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 422-427. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 422. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 423. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 424. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 425. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 426. In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 427.

[00326] In some embodiments, the binding domain capable of binding to a CD3ε epitope comprises three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VL having the sequence set forth in one of SEQ ID NO: 422-427.

Variants of V_L Sequences

[00327] In some embodiments, the V_L sequences provided herein comprise, consist of, or

consist essentially of a variant of an illustrative V_L sequence provided in this disclosure.

[00328] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00329] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Pairs

CDR-H3 – CDR-L3 Pairs

[00330] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a CDR-H3 sequence and a CDR-L3 sequence. In some embodiments, the CDR-H3 sequence is part of a V_H and the CDR-L3 sequence is part of a V_L.

[00331] In some embodiments, the CDR-H3 sequence is a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 379-382, and the CDR-L3 sequence is a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 404-408.

[00332] In some embodiments, the CDR-H3 sequence is SEQ ID NO: 379 and the CDR-L3 sequence is selected from SEQ ID NOS: 404-408. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 404. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 405. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 406. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 407. In some embodiments, the CDR-L3 sequence is SEQ ID NO: 408.

Variants of CDR-H3 – CDR-L3 Pairs

[00333] In some embodiments, the CDR-H3 – CDR-L3 pairs provided herein comprise a variant of an illustrative CDR-H3 and/or CDR-L1 sequence provided in this disclosure.

[00334] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00335] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H – V_L Pairs

[00336] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence and a V_L sequence.

[00337] In some embodiments, the V_H sequence is a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 413-418 and the V_L sequence is a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 422-427.

[00338] In some embodiments, the V_H sequence is SEQ ID NO: 413 and the V_L sequence is selected from SEQ ID NOS: 422-427. In some embodiments, the V_L sequence is SEQ ID NO: 422. In some embodiments, the V_L sequence is SEQ ID NO: 423. In some embodiments, the V_L sequence is SEQ ID NO: 424. In some embodiments, the V_L sequence is SEQ ID NO: 425. In

some embodiments, the V_L sequence is SEQ ID NO: 426. In some embodiments, the V_L sequence is SEQ ID NO: 427.

[00339] In some embodiments, the V_H sequence is SEQ ID NO: 414 and the V_L sequence is selected from SEQ ID NOS: 422-427. In some embodiments, the V_L sequence is SEQ ID NO: 422. In some embodiments, the V_L sequence is SEQ ID NO: 423. In some embodiments, the V_L sequence is SEQ ID NO: 424. In some embodiments, the V_L sequence is SEQ ID NO: 425. In some embodiments, the V_L sequence is SEQ ID NO: 426. In some embodiments, the V_L sequence is SEQ ID NO: 427.

[00340] In some embodiments, the V_H sequence is SEQ ID NO: 415 and the V_L sequence is selected from SEQ ID NOS: 422-427. In some embodiments, the V_L sequence is SEQ ID NO: 422. In some embodiments, the V_L sequence is SEQ ID NO: 423. In some embodiments, the V_L sequence is SEQ ID NO: 424. In some embodiments, the V_L sequence is SEQ ID NO: 425. In some embodiments, the V_L sequence is SEQ ID NO: 426. In some embodiments, the V_L sequence is SEQ ID NO: 427.

[00341] In some embodiments, the V_H sequence is SEQ ID NO: 416 and the V_L sequence is selected from SEQ ID NOS: 422-427. In some embodiments, the V_L sequence is SEQ ID NO: 422. In some embodiments, the V_L sequence is SEQ ID NO: 423. In some embodiments, the V_L sequence is SEQ ID NO: 424. In some embodiments, the V_L sequence is SEQ ID NO: 425. In some embodiments, the V_L sequence is SEQ ID NO: 426. In some embodiments, the V_L sequence is SEQ ID NO: 427.

[00342] In some embodiments, the V_H sequence is SEQ ID NO: 417 and the V_L sequence is selected from SEQ ID NOS: 422-427. In some embodiments, the V_L sequence is SEQ ID NO: 422. In some embodiments, the V_L sequence is SEQ ID NO: 423. In some embodiments, the V_L sequence is SEQ ID NO: 424. In some embodiments, the V_L sequence is SEQ ID NO: 425. In some embodiments, the V_L sequence is SEQ ID NO: 426. In some embodiments, the V_L sequence is SEQ ID NO: 427.

[00343] In some embodiments, the V_H sequence is SEQ ID NO: 418 and the V_L sequence is selected from SEQ ID NOS: 422-427. In some embodiments, the V_L sequence is SEQ ID NO: 422. In some embodiments, the V_L sequence is SEQ ID NO: 423. In some embodiments, the V_L sequence is SEQ ID NO: 424. In some embodiments, the V_L sequence is SEQ ID NO: 425. In

some embodiments, the V_L sequence is SEQ ID NO: 426. In some embodiments, the V_L sequence is SEQ ID NO: 427.

[00344] In some embodiments, the binding domain capable of binding to a CD3ε epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth above. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth in Table S.

CDR-H1 + CDR-H2 + CDR-H3 + CDR-L1 + CDR-L2 + CDR-L3

[00345] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 354, a Kabat CDR-H2 sequence comprising SEQ ID NO: 371, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 379 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 388, a CDR-L2 sequence comprising SEQ ID NO: 396, and a CDR-L3 sequence SEQ ID NO: 404.

[00346] In some embodiments, the additional binding domain capable of binding to a CD3ε epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 346, a Chothia CDR-H2 sequence comprising SEQ ID NO: 362, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 379 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 388, a CDR-L2 sequence comprising SEQ ID NO: 396, and a CDR-L3 sequence SEQ ID NO: 404.

Variants of V_H – V_L Pairs

[00347] In some embodiments, the V_H – V_L pairs provided herein comprise a variant of an illustrative V_H and/or V_L sequence provided in this disclosure.

[00348] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence

having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.1% identity with any of the illustrative V_H sequences provided in this disclosure.

[00349] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00350] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00351] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Additional Binding Domains Capable of Binding CD16, NKp46, and/or NKp30

CD16

[00352] In some embodiments, the additional binding domain comprises an NK cell engager, dendritic cell engager, monocyte, or macrophage engager. In some embodiments, the NK cell engager comprises an antibody for a CD16 epitope. In some embodiments, the monocyte or macrophage engager comprises an antibody for a CD16 epitope. In some embodiments, the epitope comprises one or more amino acids on SEQ ID NOS: 630-631.

[00353] In some embodiments, the epitope comprises one or more amino acids on a polymorphism of SEQ ID NO: 630. In some embodiments, the polymorphism comprises a polypeptide sequence comprising or consisting of SEQ ID NO: 630, wherein the amino acid at

position 176 is a V. In some embodiments, the polymorphism comprises a polypeptide sequence comprising or consisting of SEQ ID NO: 630, wherein the amino acid at position 176 is an F. In some embodiments, the polymorphism comprises or consists of a polypeptide sequence having an F or having a V at the bold and underlined position or SEQ ID NO: 630 set forth in Table S, herein.

[00354] CD16 is a cluster of differentiation molecule found on the surface of natural killer cells, neutrophils, monocytes, dendritic cells, and macrophages. CD16 has been identified as Fc receptors FcγRIIIa (CD16a) and FcγRIIIb (CD16b), which participate in signal transduction. The most well-researched membrane receptor implicated in triggering lysis by NK cells, CD16 is a molecule of the immunoglobulin superfamily (IgSF) involved in antibody-dependent cellular cytotoxicity (ADCC). CD16 can be used to isolate populations of specific immune cells through fluorescent-activated cell sorting (FACS) or magnetic-activated cell sorting, using antibodies directed towards CD16.

[00355] In humans, CD16 exists in two different forms: FcγRIIIa (CD16a) and FcγRIIIb (CD16b), which have 96% sequence similarity in the extracellular immunoglobulin binding regions. While FcγRIIIa is expressed on mast cells, macrophages, and natural killer cells as a transmembrane receptor, FcγRIIIb is only expressed on neutrophils. In addition, FcγRIIIb is the only Fc receptor anchored to the cell membrane by a glycosyl-phosphatidylinositol (GPI) linker, and also plays a significant role in triggering calcium mobilization and neutrophil degranulation. FcγRIIIa and FcγRIIIb together are able to activate degranulation, phagocytosis, and oxidative burst, which allows neutrophils to clear opsonized pathogens.

[00356] CD16 is required for ADCC processes carried out by human monocytes. In humans, monocytes expressing CD16 have a variety of ADCC capabilities in the presence of specific antibodies and can kill primary leukemic cells, cancer cell lines, and cells infected with hepatitis B virus. In addition, CD16 is able to mediate the direct killing of some virally infected and cancer cells without antibodies.

[00357] After binding to ligands such as the conserved section of IgG antibodies, CD16 on human NK cells induce gene transcription of surface activation molecules such as IL-2R (CD25) and inflammatory cytokines such as IFN-gamma and TNF. CD16-induced expression of cytokine mRNA in NK cells is mediated by the nuclear factor of activated T cells (NFATp), a cyclosporin A (CsA)-sensitive factor that regulates the transcription of various cytokines. The upregulated

expression of specific cytokine genes occurs via a CsA-sensitive and calcium-dependent mechanism.

[00358] The crystal structures of FcεRIα, FcγRIIa, FcγRIIb, and FcγRIII have been experimentally determined. These structures revealed a conserved immunoglobulin-like (Ig-like) structure. In addition, the structures demonstrated a common feature in all known Ig superfamily Fc receptors: the acute hinge angle between the N- and C-terminal Ig domains. Specifically, the structure of CD16 (FcγRIIIb) consists of two immunoglobulin-like domains, with an interdomain hinge angle of around 50°. The receptor's Fc binding region also carries a net positive charge, which complements the negatively charged receptor binding regions on Fc.

CDR-H3 Sequences

[00359] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472.

[00360] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative CDRs

[00361] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising one or more CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-H sequences provided in this disclosure, and variants thereof.

V_H Sequences Comprising Illustrative Kabat CDRs

[00362] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising one or more Kabat CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Kabat CDR-H sequences provided in this disclosure, and variants thereof.

Kabat CDR-H3

[00363] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472.

Kabat CDR-H2

[00364] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 458-461.

Kabat CDR-H1

[00365] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 441-444.

Kabat CDR-H3 + Kabat CDR-H2

[00366] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472, and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 458-461. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H2 are

both from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Kabat CDR-H3 + Kabat CDR-H1

[00367] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472, and a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 441-444. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Kabat CDR-H1 + Kabat CDR-H2

[00368] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 441-444 and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 458-461. In some embodiments, the Kabat CDR-H1 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Kabat CDR-H1 + Kabat CDR-H2 + Kabat CDR-H3

[00369] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 441-444, a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 458-461, and a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472. In some embodiments, the Kabat CDR-H1 sequence, Kabat CDR-H2 sequence, and Kabat CDR-H3

sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1, Kabat CDR-H2, and Kabat CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Variants of V_H Sequences Comprising Illustrative Kabat CDRs

[00370] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Kabat CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00371] In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H3 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H3 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00372] In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H2 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H2 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00373] In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H1 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H1 sequences provided in this disclosure. In some

embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative Chothia CDRs

[00374] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising one or more Chothia CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Chothia CDR-H sequences provided in this disclosure, and variants thereof.

Chothia CDR-H3

[00375] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472.

Chothia CDR-H2

[00376] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 448-454.

Chothia CDR-H1

[00377] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 431-437.

Chothia CDR-H3 + Chothia CDR-H2

[00378] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472, and a

Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 448-454. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Chothia CDR-H3 + Chothia CDR-H1

[00379] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472, and a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 431-437. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Chothia CDR-H1 + Chothia CDR-H2

[00380] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 431-437 and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 448-454. In some embodiments, the Chothia CDR-H1 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Chothia CDR-H1 + Chothia CDR-H2 + Chothia CDR-H3

[00381] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 431-437, a

Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 448-454, and a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 465-472. In some embodiments, the Chothia CDR-H1 sequence, Chothia CDR-H2 sequence, and Chothia CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1, Chothia CDR-H2, and Chothia CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 501-513.

Variants of V_H Sequences Comprising Illustrative Chothia CDRs

[00382] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Chothia CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00383] In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H3 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H3 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00384] In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H2 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H2 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00385] In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or

consists essentially of a variant of an illustrative Chothia CDR-H1 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H1 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences

[00386] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 501-513. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 501. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 502. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 503. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 504. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 505. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 506. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 507. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 508. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting

of, or consisting essentially SEQ ID NO: 509. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 510. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 511. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 512. In some embodiments, the additional binding doimain capable of binding to a CD16 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially SEQ ID NO: 513.

[00387] In some embodiments, the binding domain capable of binding to a CD16 epitope comprises three heavy chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VH having the sequence set forth in one of SEQ ID NOS: 501-513.

Variants of V_H Sequences

[00388] In some embodiments, the V_H sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_H sequence provided in this disclosure.

[00389] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.5% identity with any of the illustrative V_H sequences provided in this disclosure.

[00390] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

CDR-L3 Sequences

[00391] In some embodiments, the additional binding domain capable of binding to a

CD16 epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 492-497.

[00392] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences Comprising Illustrative CDRs

[00393] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising one or more CDR-L sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-L sequences provided in this disclosure, and variants thereof.

CDR-L3

[00394] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 492-497.

CDR-L2

[00395] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 484-488.

CDR-L1

[00396] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting

of, or consisting essentially of a sequence selected from SEQ ID NOS: 476-480.

CDR-L3 + CDR-L2

[00397] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 492-497 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 484-488. In some embodiments, the CDR-L3 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 517-524.

CDR-L3 + CDR-L1

[00398] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 492-497 and a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 476-480. In some embodiments, the CDR-L3 sequence and the CDR-L1 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L1 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 517-524.

CDR-L1 + CDR-L2

[00399] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 476-480 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 484-488. In some embodiments, the CDR-L1 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1 and CDR-L2 are both from a single illustrative V_L sequence selected

from SEQ ID NOS: 517-524.

CDR-L1 + CDR-L2 + CDR-L3

[00400] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 476-480, a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 484-488, and a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 492-497. In some embodiments, the CDR-L1 sequence, CDR-L2 sequence, and CDR-L3 sequence are all from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1, CDR-L2, and CDR-L3 are all from a single illustrative V_L sequence selected from SEQ ID NOS: 517-524.

Variants of V_L Sequences Comprising Illustrative CDR-Ls

[00401] In some embodiments, the V_L sequences provided herein comprise a variant of an illustrative CDR-L3, CDR-L2, and/or CDR-L1 sequence provided in this disclosure.

[00402] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00403] In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L2 sequence provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L2 sequences provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L2 sequences provided in this

disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00404] In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L1 sequence provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L1 sequences provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences

[00405] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 517-524. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 517. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 518. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 519. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 520. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 521. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 522. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 523. In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_L sequence comprising, consisting

of, or consisting essentially of SEQ ID NO: 524.

[00406] In some embodiments, the binding domain capable of binding to a CD16 epitope comprises three light chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VL having the sequence set forth in one of SEQ ID NOS: 517-524.

Variants of V_L Sequences

[00407] In some embodiments, the V_L sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_L sequence provided in this disclosure.

[00408] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00409] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Pairs

CDR-H3 – CDR-L3 Pairs

[00410] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a CDR-H3 sequence and a CDR-L3 sequence. In some embodiments, the CDR-H3 sequence is part of a V_H and the CDR-L3 sequence is part of a V_L.

[00411] In some embodiments, the CDR-H3 sequence is a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 465-472, and the CDR-L3 sequence is a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 492-497.

Variants of CDR-H3 – CDR-L3 Pairs

[00412] In some embodiments, the CDR-H3 – CDR-L3 pairs provided herein comprise a variant of an illustrative CDR-H3 and/or CDR-L1 sequence provided in this disclosure.

[00413] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00414] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H – V_L Pairs

[00415] In some embodiments, the additional binding domain capable of binding to a CD16 epitope comprises a V_H sequence and a V_L sequence.

[00416] In some embodiments, the V_H sequence is a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 501-513 and the V_L sequence is a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 517-524.

Variants of V_H – V_L Pairs

[00417] In some embodiments, the V_H – V_L pairs provided herein comprise a variant of an

illustrative V_H and/or V_L sequence provided in this disclosure.

[00418] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.1% identity with any of the illustrative V_H sequences provided in this disclosure.

[00419] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00420] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00421] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

NKp46

[00422] In some embodiments, the NK cell engager comprises an antibody for an NKp46 epitope. In some embodiments, the NKp46 epitopes comprises at least one of SEQ ID NOS: 632-637. In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a sequence comprising, consisting of, or consisting essentially of SEQ ID NO:

544.

[00423] NKp46 is a protein that in humans is encoded by the *NCR1* gene. NKp46 is a major NK cell-activating receptor that is involved in the elimination of target cells. NK cells form different types of synapses that result in distinct functional outcomes: cytotoxic, inhibitory, and regulatory. NKp46 is a member of the natural cytotoxicity receptor (NCR) family.

[00424] Engagement of the NKp46 receptor on NK cells results in increased cellular activation, manifesting as increased cytokine production and release of cytolytic granules. The receptor can confer tumor cell recognition by NK cells and can specifically bind viral hemagglutinins. Normal NK cells in humans and in rodents uniformly express NKp46, which is upregulated during NK cell maturation following commitment to the NK cell lineage.

[00425] NKp46 is often considered a highly selective if not specific marker of NK cells in basic immunology. NKp46 is a highly specific marker of NK cells and is of potential utility in the diagnosis of NK cell and some T-cell–derived neoplasms.

V_H Sequences Comprising Illustrative CDRs

[00426] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising one or more CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-H sequences provided in this disclosure, and variants thereof.

[00427] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative Kabat CDRs

[00428] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising one or more Kabat CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Kabat CDR-H sequences provided in this disclosure, and variants thereof.

Kabat CDR-H3

[00429] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 544.

Kabat CDR-H2

[00430] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 540.

Kabat CDR-H1

[00431] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 532.

Kabat CDR-H3 + Kabat CDR-H2

[00432] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 544, and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 540. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H2 are both from a single illustrative V_H sequence having SEQ ID NO: 560.

Kabat CDR-H3 + Kabat CDR-H1

[00433] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 544, and a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 532. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H1 are both from a single illustrative V_H sequence having SEQ ID NO: 560.

Kabat CDR-H1 + Kabat CDR-H2

[00434] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of SEQ ID NO: 532 and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 540. In some embodiments, the Kabat CDR-H1 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1 and Kabat CDR-H2 are both from a single illustrative V_H sequence having SEQ ID NO: 560.

Kabat CDR-H1 + Kabat CDR-H2 + Kabat CDR-H3

[00435] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 532, a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 540, and a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 544. In some embodiments, the Kabat CDR-H1 sequence, Kabat CDR-H2 sequence, and Kabat CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1, Kabat CDR-H2, and Kabat CDR-H3 are all from a single illustrative V_H sequence having SEQ ID NO: 560.

Variants of V_H Sequences Comprising Illustrative Kabat CDRs

[00436] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Kabat CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00437] In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H3 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H3 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00438] In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H2 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H2 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00439] In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H1 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H1 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative Chothia CDRs

[00440] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising one or more Chothia CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Chothia CDR-H sequences provided in this disclosure, and variants thereof.

Chothia CDR-H3

[00441] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 544.

Chothia CDR-H2

[00442] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 536.

Chothia CDR-H1

[00443] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 528.

Chothia CDR-H3 + Chothia CDR-H2

[00444] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 544, and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence SEQ ID NO: 536. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H2 are both from a single illustrative V_H

sequence having SEQ ID NO: 560.

Chothia CDR-H3 + Chothia CDR-H1

[00445] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 544, and a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 528. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H1 are both from a single illustrative V_H having SEQ ID NO: 560.

Chothia CDR-H1 + Chothia CDR-H2

[00446] In some embodiments, the additional binding domain capable of binding to an NKp46 comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 528 and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 536. In some embodiments, the Chothia CDR-H1 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1 and Chothia CDR-H2 are both from a single illustrative V_H sequence SEQ ID NO: 560.

Chothia CDR-H1 + Chothia CDR-H2 + Chothia CDR-H3

[00447] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 528, a Chothia CDR-H2 sequence comprising SEQ ID NO: 536, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 544. For example, in some embodiments, the Chothia CDR-H1, Chothia CDR-H2, and Chothia-H3 are all from a single illustrative V_H sequence having SEQ ID NO: 560.

Variants of V_H Sequences Comprising Illustrative Chothia CDRs

[00448] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Chothia CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00449] In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H3 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H3 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00450] In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H2 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H2 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00451] In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H1 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H1 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences

[00452] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 560.

[00453] In some embodiments, the binding domain capable of binding to an NKp46 epitope comprises three heavy chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VH having the sequence set forth in one of SEQ ID NO: 560.

Variants of V_H Sequences

[00454] In some embodiments, the V_H sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_H sequence provided in this disclosure.

[00455] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.5% identity with any of the illustrative V_H sequences provided in this disclosure.

[00456] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

CDR-L3 Sequences

[00457] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 556.

[00458] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists

essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences Comprising Illustrative CDRs

[00459] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising one or more CDR-L sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-L sequences provided in this disclosure, and variants thereof.

CDR-L3

[00460] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 556.

CDR-L2

[00461] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 552.

CDR-L1

[00462] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 548.

CDR-L3 + CDR-L2

[00463] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 556 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 552. In some embodiments, the CDR-L3 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L2 are both from a single illustrative V_L sequence having SEQ ID NOS: 564.

CDR-L3 + CDR-L1

[00464] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 556 and a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 548. In some embodiments, the CDR-L3 sequence and the CDR-L1 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L1 are both from a single illustrative V_L sequence having SEQ ID NO: 564.

CDR-L1 + CDR-L2

[00465] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 548 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 552. In some embodiments, the CDR-L1 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1 and CDR-L2 are both from a single illustrative V_L sequence having SEQ ID NO: 564.

CDR-L1 + CDR-L2 + CDR-L3

[00466] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID

NO: 548, a CDR-L2 sequence comprising SEQ ID NO: 552, and a CDR-L3 sequence SEQ ID NO: 556. In some embodiments, the CDR-L1 sequence, CDR-L2 sequence, and CDR-L3 sequence are all from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1, CDR-L2, and CDR-L3 are all from a single illustrative V_L sequence having SEQ ID NOS: 564.

Variants of V_L Sequences Comprising Illustrative CDR-Ls

[00467] In some embodiments, the V_L sequences provided herein comprise a variant of an illustrative CDR-L3, CDR-L2, and/or CDR-L1 sequence provided in this disclosure.

[00468] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00469] In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L2 sequence provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L2 sequences provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00470] In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L1 sequence provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L1 sequences provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises,

consists of, or consists essentially of any of the illustrative CDR-L1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences

[00471] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 564.

[00472] In some embodiments, the binding domain capable of binding to an NKp46 epitope comprises three light chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VL having the sequence set forth in one of SEQ ID NO: 564.

Variants of V_L Sequences

[00473] In some embodiments, the V_L sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_L sequence provided in this disclosure.

[00474] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00475] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Pairs

CDR-H3 – CDR-L3 Pairs

[00476] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a CDR-H3 sequence and a CDR-L3 sequence. In some embodiments, the CDR-H3 sequence is part of a V_H and the CDR-L3 sequence is part of a V_L. In some embodiments, the CDR-H3 sequence is SEQ ID NO: 544 and the CDR-L3 sequence is SEQ ID NO: 556.

Variants of CDR-H3 – CDR-L3 Pairs

[00477] In some embodiments, the CDR-H3 – CDR-L3 pairs provided herein comprise a variant of an illustrative CDR-H3 and/or CDR-L1 sequence provided in this disclosure.

[00478] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00479] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H – V_L Pairs

[00480] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence and a V_L sequence. In some embodiments, the V_H sequence is SEQ ID NO: 560 and the V_L sequence is SEQ ID NO: 564.

[00481] In some embodiments, the binding domain capable of binding to an NKp46 epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth above. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth in Table S.

CDR-H1 + CDR-H2 + CDR-H3 + CDR-L1 + CDR-L2 + CDR-L3

[00482] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 532, a Kabat CDR-H2 sequence comprising SEQ ID NO: 540, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 544 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 548, a CDR-L2 sequence comprising SEQ ID NO: 552, and a CDR-L3 sequence SEQ ID NO: 556.

[00483] In some embodiments, the additional binding domain capable of binding to an NKp46 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 528, a Chothia CDR-H2 sequence comprising SEQ ID NO: 536, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 544 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 548, a CDR-L2 sequence comprising SEQ ID NO: 552, and a CDR-L3 sequence SEQ ID NO: 556.

Variants of V_H – V_L Pairs

[00484] In some embodiments, the V_H – V_L pairs provided herein comprise a variant of an illustrative V_H and/or V_L sequence provided in this disclosure.

[00485] In some embodiments, the V_H sequence comprises, consists of, or consists

essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.1% identity with any of the illustrative V_H sequences provided in this disclosure.

[00486] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00487] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00488] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

NKp30

[00489] In some embodiments, the NK cell engager comprises an antibody for an NKp30 epitope. In some embodiments, the NKp30 epitope comprises one or more amino acids in SEQ ID NOS: 638-643. In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 568-570.

[00490] NKp30 is a protein that is encoded by the *NCR3* gene. NKp30, also known as natural cytotoxicity receptor 3 (NCR3), was identified as a 30 kDa protein that, similarly to

NKp46, is expressed on all mature resting and activated NK cells. Molecular cloning of the NKp30 cDNA revealed an open reading frame predicted to encode one extracellular IgV domain and a hydrophobic TM domain with a charged arginine residue capable of associating with the ITAM adaptors, CD3ζ and/or FcRγ. The crystal structure of NKp30 reveals some structural similarity to CTLA-4 and PD-1 and NKp30 is thus considered a member of the CD28 family of receptors (83, 89). Both NKp30 and NKp46 have reduced surface expression on adaptive memory NK cells most likely due to the downregulated expression of the FcRγ signaling chain required for the surface expression of these receptors.

[00491] Six alternatively spliced transcripts are transcribed from the NKp30 gene, termed NKp30a-f. Whilst NKp30a and NKp30b evoke NK cell activation, the NKp30c isoform was shown to elicit secretion of the immunosuppressive cytokine, IL-10, from NK cells (93). NKp30 has also been shown to be expressed by γδ T cells (30), $CD8^+$ T cells (94), and UCB T cells cultured in IL-15.

V_H Sequences Comprising Illustrative CDRs

[00492] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising one or more CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-H sequences provided in this disclosure, and variants thereof.

V_H Sequences Comprising Illustrative Kabat CDRs

[00493] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising one or more Kabat CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Kabat CDR-H sequences provided in this disclosure, and variants thereof.

Kabat CDR-H3

[00494] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594.

Kabat CDR-H2

[00495] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 586-588.

Kabat CDR-H1

[00496] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 574-576.

Kabat CDR-H3 + Kabat CDR-H2

[00497] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594, and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 586-588. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Kabat CDR-H3 + Kabat CDR-H1

[00498] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594, and a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 574-576. In some embodiments, the Kabat CDR-H3 sequence and the Kabat CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H3 and Kabat CDR-H1 are both

from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Kabat CDR-H1 + Kabat CDR-H2

[00499] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 574-576 and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 586-588. In some embodiments, the Kabat CDR-H1 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Kabat CDR-H1 + Kabat CDR-H2 + Kabat CDR-H3

[00500] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 574-576, a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 586-588, and a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594. In some embodiments, the Kabat CDR-H1 sequence, Kabat CDR-H2 sequence, and Kabat CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Kabat CDR-H1, Kabat CDR-H2, and Kabat CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Variants of V_H Sequences Comprising Illustrative Kabat CDRs

[00501] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Kabat CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00502] In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H3 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity

with any of the illustrative Kabat CDR-H3 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00503] In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H2 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H2 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00504] In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H1 sequence provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H1 sequences provided in this disclosure. In some embodiments, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences Comprising Illustrative Chothia CDRs

[00505] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising one or more Chothia CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Chothia CDR-H sequences provided in this disclosure, and variants thereof.

Chothia CDR-H3

[00506] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594.

Chothia CDR-H2

[00507] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 580-582.

Chothia CDR-H1

[00508] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 568-570.

Chothia CDR-H3 + Chothia CDR-H2

[00509] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594, and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 580-582. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Chothia CDR-H3 + Chothia CDR-H1

[00510] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594, and a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence

selected from SEQ ID NOS: 568-570. In some embodiments, the Chothia CDR-H3 sequence and the Chothia CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H3 and Chothia CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Chothia CDR-H1 + Chothia CDR-H2

[00511] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 568-570 and a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 580-582. In some embodiments, the Chothia CDR-H1 sequence and the Chothia CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1 and Chothia CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Chothia CDR-H1 + Chothia CDR-H2 + Chothia CDR-H3

[00512] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 568-570, a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 580-582, and a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 592-594. In some embodiments, the Chothia CDR-H1 sequence, Chothia CDR-H2 sequence, and Chothia CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some embodiments, the Chothia CDR-H1, Chothia CDR-H2, and Chothia CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOS: 613-616.

Variants of V_H Sequences Comprising Illustrative Chothia CDRs

[00513] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Chothia CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[00514] In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H3 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H3 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00515] In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H2 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H2 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00516] In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H1 sequence provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H1 sequences provided in this disclosure. In some embodiments, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H Sequences

[00517] In some embodiments, the additional binding domain capable of binding to an

NKp30 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 613-616. In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 613. In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 614. In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 615. In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 616.

[00518] In some embodiments, the binding domain capable of binding to an NKp30 epitope comprises three heavy chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VH having the sequence set forth in one of SEQ ID NOS: 613-616.

Variants of V_H Sequences

[00519] In some embodiments, the V_H sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_H sequence provided in this disclosure.

[00520] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.5% identity with any of the illustrative V_H sequences provided in this disclosure.

[00521] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

CDR-L3 Sequences

[00522] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 608-609.

[00523] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences Comprising Illustrative CDRs

[00524] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising one or more CDR-L sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-L sequences provided in this disclosure, and variants thereof.

CDR-L3

[00525] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 608-609.

CDR-L2

[00526] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 603-604.

CDR-L1

[00527] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 598-599.

CDR-L3 + CDR-L2

[00528] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 608-609 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 603-604. In some embodiments, the CDR-L3 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 624-625.

CDR-L3 + CDR-L1

[00529] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 608-609 and a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 598-599. In some embodiments, the CDR-L3 sequence and the CDR-L1 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L3 and CDR-L1 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 624-625.

CDR-L1 + CDR-L2

[00530] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 598-599 and a CDR-L2

sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 603-604. In some embodiments, the CDR-L1 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOS: 624-625.

CDR-L1 + CDR-L2 + CDR-L3

[00531] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 598-599, a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 603-604, and a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 608-609. In some embodiments, the CDR-L1 sequence, CDR-L2 sequence, and CDR-L3 sequence are all from a single illustrative V_L sequence provided in this disclosure. For example, in some embodiments, the CDR-L1, CDR-L2, and CDR-L3 are all from a single illustrative V_L sequence selected from SEQ ID NOS: 624-625.

Variants of V_L Sequences Comprising Illustrative CDR-Ls

[00532] In some embodiments, the V_L sequences provided herein comprise a variant of an illustrative CDR-L3, CDR-L2, and/or CDR-L1 sequence provided in this disclosure.

[00533] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00534] In some embodiments, the CDR-L2 sequence comprises, consists of, or consists

essentially of a variant of an illustrative CDR-L2 sequence provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L2 sequences provided in this disclosure. In some embodiments, the CDR-L2 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00535] In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L1 sequence provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L1 sequences provided in this disclosure. In some embodiments, the CDR-L1 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_L Sequences

[00536] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 624-625. In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 624. In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 625.

[00537] In some embodiments, the binding domain capable of binding to an NKp30 epitope comprises three light chain CDRs each comprising, consisting of, or consisting essentially of a CDR sequence of a VL having the sequence set forth in one of SEQ ID NOS: 624-625.

Variants of V_L Sequences

[00538] In some embodiments, the V_L sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_L sequence provided in this disclosure.

[00539] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00540] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Pairs

CDR-H3 – CDR-L3 Pairs

[00541] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a CDR-H3 sequence and a CDR-L3 sequence. In some embodiments, the CDR-H3 sequence is part of a V_H and the CDR-L3 sequence is part of a V_L.

[00542] In some embodiments, the CDR-H3 sequence is a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 592-594, and the CDR-L3 sequence is a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 608-609.

Variants of CDR-H3 – CDR-L3 Pairs

[00543] In some embodiments, the CDR-H3 – CDR-L3 pairs provided herein comprise a variant of an illustrative CDR-H3 and/or CDR-L1 sequence provided in this disclosure.

[00544] In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some

embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some embodiments, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00545] In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some embodiments, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

V_H – V_L Pairs

[00546] In some embodiments, the additional binding domain capable of binding to an NKp30 epitope comprises a V_H sequence and a V_L sequence.

[00547] In some embodiments, the V_H sequence is a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 613-616 and the V_L sequence is a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NOS: 624-625.

[00548] In some embodiments, the binding domain capable of binding to an NKp30 epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth above. In some embodiments, the binding domain capable of binding to an HLA-G epitope comprises three heavy chain CDRs and three light chain CDRs, each comprising, consisting of, or consisting essentially of a CDR sequence of a VH-VL pair set forth in Table S.

Variants of V_H – V_L Pairs

[00549] In some embodiments, the V_H – V_L pairs provided herein comprise a variant of an illustrative V_H and/or V_L sequence provided in this disclosure.

[00550] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some embodiments, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.1% identity with any of the illustrative V_H sequences provided in this disclosure.

[00551] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

[00552] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some embodiments, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[00553] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions.

Pharmaceutical Compositions

[00554] Some embodiments provide a pharmaceutical composition comprising or consisting of any of the bispecific antigen binding constructs provided herein. Suitable routes of

administration include, but are not limited to, the inhalation, intra-arterial, intradermal, intramuscular, intraperitoneal, intravenous, nasal, parenteral, pulmonary, and subcutaneous routes.

[00555] The pharmaceutical composition may comprise one or more pharmaceutical excipients. Any suitable pharmaceutical excipient may be used, and one of ordinary skill in the art is capable of selecting suitable pharmaceutical excipients. Accordingly, the pharmaceutical excipients provided below are intended to be illustrative, and not limiting. Additional pharmaceutical excipients include, for example, those described in the *Handbook of Pharmaceutical Excipients*, Rowe et al. (Eds.) 6th Ed. (2009), incorporated by reference in its entirety.

[00556] Further encompassed herein are anhydrous pharmaceutical compositions and dosage forms comprising an antibody, since water can facilitate the degradation of some antibodies. Anhydrous pharmaceutical compositions and dosage forms provided herein can be prepared using anhydrous or low moisture containing ingredients and low moisture or low humidity conditions. Pharmaceutical compositions and dosage forms that comprise lactose and at least one active ingredient that comprises a primary or secondary amine can be anhydrous if substantial contact with moisture and/or humidity during manufacturing, packaging, and/or storage is expected.

[00557] An anhydrous pharmaceutical composition should be prepared and stored such that its anhydrous nature is maintained. Accordingly, anhydrous compositions can be packaged using materials known to prevent exposure to water such that they can be included in suitable formulary kits. Examples of suitable packaging include, but are not limited to, hermetically sealed foils, plastics, unit dose containers (*e.g.*, vials), blister packs, and strip packs.

[00558] In some embodiments, the pharmaceutical composition further comprises one or both of an antibody to an immune inhibitory receptor or ligand and/or an antibody to an immune stimulatory receptor and/or ligand. In some embodiments, the pharmaceutical composition further comprises an effective amount of at least one of the following: an anti-ILT2 antibody or a small molecule inhibitor; an anti-ILT4 antibody or small molecule inhibitor; an anti-KIR2DL4 antibody or small molecule inhibitor; an anti-PD-L1 antibody or small molecule inhibitor; an anti-PD-1 antibody or small molecule inhibitor; an anti-CTLA4 antibody or small molecule

inhibitor; an anti-CD38 antibody or small molecule inhibitor; an anti-CD73 antibody or small molecule inhibitor; an anti-A2A receptor antibody or small molecule inhibitor; an anti-A2B receptor antibody or small molecule inhibitor; an anti-A2A/A2B dual receptor antibody or small molecule inhibitor or a combination thereof; an anti-CD39 antibody or small molecule inhibitor; an anti-CD73 antibody or small molecule inhibitor; an anti-CD47 antibody or small molecule inhibitor; and/or a small molecule inhibitor. In some embodiments, the pharmaceutical composition further comprises an anti-ILT2 antibody or small molecule inhibitor, an anti-ILT4 antibody or small molecule inhibitor, an anti-PD-L1 antibody or small molecule inhibitor, and/or an anti-CD47 antibody or small molecule inhibitor.

[00559] In some embodiments, the pharmaceutical composition further comprises an effective amount of one or more of:

a) an anti-PD-L1 antibody or small molecule inhibitor;

b) an anti-PD-1 antibody or small molecule inhibitor;

c) an anti-CD38 antibody or small molecule inhibitor;

d) an anti-CD39 antibody or small molecule inhibitor;

e) an anti-CD73 antibody or small molecule inhibitor;

f) an anti-A2A receptor antibody or small molecule inhibitor;

g) an anti-A2B receptor antibody or small molecule inhibitor;

h) an anti-A2A/A2B dual receptor antibody or small molecule inhibitor;

i) an anti-CD47 antibody or small molecule inhibitor;

j) an anti-CTLA-4 antibody or small molecule inhibitor;

k) an anti-LAG-3 antibody or small molecule inhibitor;

l) an anti-TIM-3 antibody or small molecule inhibitor;

m) an anti-TIGIT antibody or small molecule inhibitor;

n) an anti-VISTA antibody or small molecule inhibitor;

o) an anti-CD94 antibody or small molecule inhibitor;

p) a small molecule inhibitor;

q) an oncolytic virus;

r) a chemotherapy;

s) ADCC capable therapies using effector competent antibodies such as anti-CD19, anti-CD20, anti-EGFR, anti-Her2, anti-SLAMF7, anti-CD52, anti-BCMA, anti-GD2, and/or anti-CCR4.

[00560] In some embodiments, chemotherapy comprises one or more receptor tyrosine kinase inhibitors. Examples of receptor tyrosine inhibitors include acalabrutinibafatinib, alecensa, alectinib, avapritinib, axitinib, bosulif, bosutinib, brukinsa cabozantinib, calquence, caprelsa, cometriq, crizotinib, dacomitinib, dasatinib, entrectinib, erlotinib, gilotrif, gilteritinib, gleevec, ibrutinib, iclusig, imatinib, imbruvica, inlyta, lapatinib, midostaurin, neratinib, nerlynx, nexavar, nilotinib, pacritinib, pazopanib, pexidartinib, ponatinib, quizartinib, regorafenib, Rozlytrek, rydapt, sorafenib, sprycel, stivarga, sunitinib, sutent, tarceva, tasigna, turalio, tykerb, vandetanib, vizimpro, votrient, xalkori, xospata, zaltrap, zanubrutinib, ziv-aflibercept.

[00561] In some embodiments, chemotherapy comprises one or more antimetabolites. Antimetabolities include, without limitation, zacitidine, 5-fluorouracil (5-FU), 6-mercaptopurine (6-MP), capecitabine (Xeloda), cladribine, clofarabine, cytarabine (Ara-C), decitabine, floxuridine, fludarabine, gemcitabine (Gemzar), hydroxyurea, methotrexate, nelarabine, pemetrexed (Alimta), pentostatin, pralatrexate, thioguanine, and/or trifluridine/tipiracil.

[00562] In some embodiments, chemotherapy comprises one or more alkylating agents. Alkylating agents include, with out limitation, altretamine, bendamustine, busulfan, carboplatin, carmustine, chlorambucil, cisplatin, cyclophosphamide, dacarbazin, iosfamide, lomustine, mechlorethamine, melphalan, oxaliplatin, temozolomide, thiotepa, and/or trabectedin.

[00563] In some embodiments, chemotherapy comprises one or more anthracyclines. Anthracyclines include, without limitation, daunorubicin, doxorubicin (Adriamycin), doxorubicin liposomal, epirubicin, idarubicin, and/or valrubicin.

[00564] In some embodiments, chemotherapy comprises one or more topoisomerase inhibitors such as, for example, without limitation, irinotecan, irinotecan liposomal, and/or topotecan.

[00565] In some embodiments, chemotherapy comprises one or more taxanes such as, for example, without limitation, cabazitaxel, docetaxel, nab-paclitaxel, and/or paclitaxel.

[00566] In some embodiments, chemotherapy comprises one or more, vinca alkaloids such, for example, without limitation, vinblastine, vincristine, vincristine liposomal, and/or vinorelbine.

[00567] In some embodiments, chemotherapy comprises one or more of all-trans-retinoic acid, arsenic trioxide, asparaginase, eribulin, hydroxyurea, ixabepilone, mitotane, omacetaxine, pegaspargase, procarbazine, romidepsin, and/or vorinostat.

[00568] In some embodiments, the pharmaceutical composition further comprises one or both of:

c) an antibody to an immune inhibitory receptor or ligand and/or

d) an antibody to an immune stimulatory receptor or ligand.

[00569] In some embodiments, the one or more immunomodulatory agents comprise an antagonist to an inhibitory receptor of an immune cell. In some embodiments, the inhibitory receptor is at least one of LILRB1, LILRB2, LILRB4, KIR2DL4, CTLA-4, PD-1, PD-L1, PD-L2, LAG-3, Tim3, TIGIT, B7-H3, B7-H4, neuritin, BTLA, CECAM-1, CECAM-5, VISTA, LAIR1, CD160, 2B4, TGF-B receptor, NKG2A, and/or a Killer-cell immunoglobulin-like receptor (KIR). In some embodiments, the one or more immunomodulatory agents comprise an agonist of a co-stimulatory receptor of an immune cell. In some embodiments, the co-stimulatory receptor is at

least one of OX40, CD2, CD27, ICAM-1, LFA-1, ICOS (CD278), 4-1BB (CD137), GITR, CD28, CD30, CD40, BAFFR, HVEM, CD7, LIGHT, NKG2C, SLAMF7, NKp30, NKp46, NKp80, CD160, and/or CD83.

[00570] In some embodiments, the one or more immunomodulatory agents is one or more cytokines. In some embodiments, the one or more cytokines is at least one of G-CSF, GM-CSF, IFN-alpha, IFN-beta, IFN-gamma, FLt3 ligand, IL-1, IL-2, IL-5, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and/or IL-27.

[00571] In some embodiments, the one or more immunomodulatory agents is one or more oncolytic viruses. In some embodiments, the one or more oncolytic viruses is a Herpes simplex virus, a Vesicular stomatitis virus, an adenovirus, a Newcastle disease virus, a vaccinia virus, and/or a maraba virus.

Nucleic Acids, Vectors, Hosts, and Cell Lines

[00572] A second aspect provides a one or more nucleic acids encoding any of the bispecific antigen binding constructs provided herein. In some embodiments, the one or more nucleic acids comprises one or more vectors. Some embodiments provide a host transformed with the one or more vectors. Some embodiments provide a method for the production of one or more bispecific antigen binding construct comprising the steps of expressing any of the one or more nucleic acids provided herein in a prokaryotic or eukaryotic host cell and recovering the one or more bispecific antigen binding construct from the cell or the cell culture supernatant.

[00573] For recombinant production of the antibody or bispecific antigen binding construct, the one or more nucleic acids encoding it may be isolated and inserted into one or more replicable vectors for further cloning (i.e., amplification of the DNA) or expression. In some aspects, the one or more nucleic acids may be produced by homologous recombination, for example as described in U.S. Patent No. 5,204,244, which is incorporated by reference in its entirety herein.

[00574] Many different vectors are known in the art. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription

termination sequence, for example as described in U.S. Patent No. 5,534,615, which is incorporated in its entirety herein.

[00575] Suitable host cells include any prokaryotic (e.g., bacterial), lower eukaryotic (e.g., yeast), or higher eukaryotic (e.g., mammalian) cells. Suitable prokaryotes include eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *Escherichia (E. coli), Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella (S. typhimurium), Serratia (S. marcescans), Shigella, Bacilli (B. subtilis* and *B. licheniformis), Pseudomonas (P. aeruginosa),* and *Streptomyces.* One useful *E. coli* cloning host is *E. coli* 294, although other strains such as *E. coli* B, *E. coli* X1776, and *E. coli* W3110 are suitable.

[00576] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are also suitable cloning or expression hosts for antibody-encoding vectors. *Saccharomyces cerevisiae,* or common baker's yeast, is a commonly used lower eukaryotic host microorganism. However, a number of other genera, species, and strains are available and useful, such as *Schizosaccharomyces pombe, Kluyveromyces (K. lactis, K fragilis, K bulgaricus K wickeramii, K waltii, K drosophilarum, K thermotolerans,* and *K. marxianus), Yarrowia, Pichia pastoris, Candida (C. albicans), Trichoderma reesia, Neurospora crassa, Schwanniomyces (S. occidentalis),* and filamentous fungi such as, for example *Penicillittm, Tolypocladium,* and *Aspergillus (A. nidulans* and *A. niger).*

[00577] Useful mammalian host cells include COS-7 cells, HEK293 cells; baby hamster kidney (BHK) cells; Chinese hamster ovary (CHO); mouse sertoli cells; African green monkey kidney cells (VERO-76), and the like.

[00578] The host cells used to produce the bispecific antigen binding construct or antibody of this invention may be cultured in a variety of media. Commercially available media such as, for example, Ham's F10, Minimal Essential Medium (MEM), RPMI-1640, and Dulbecco's Modified Eagle's Medium (DMEM) are suitable for culturing the host cells. In addition, any of the media described in Ham et al., *Meth. Enz.,* 1979, 58:44; Barnes et al., *Anal. Biochem.,* 1980, 102:255; and U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, and 5,122,469, or WO 90/03430 and WO 87/00195 may be used; each of the above-noted references are incorporated by reference herein in their entirety.

[00579] Any of these media may be supplemented as necessary with hormones and/or

other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics, trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art.

[00580] The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

[00581] When using recombinant techniques, the bispecific antigen binding construct or antibody can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody or bispecific antigen binding construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, is removed, for example, by centrifugation or ultrafiltration. For example, Carter et al. *(BioTechnology,* 1992, 10:163-167, which is incorporated by reference in its entirety herein) describes a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli.* Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 minutes. Cell debris can be removed by centrifugation.

[00582] In some embodiments, the bispecific antigen binding construct or antibody is produced in a cell-free system. In some embodiments, the cell-free system is an *in vitro* transcription and translation system as described in Yin et al., *mAbs,* 2012, 4:217-225, incorporated by reference in its entirety. In some embodiments, the cell-free system utilizes a cell-free extract from a eukaryotic cell or from a prokaryotic cell. In some embodiments, the prokaryotic cell is *E. coli.* Cell-free expression of the antibody or bispecific antigen binding construct may be useful, for example, where the antibody or bispecific antigen binding construct accumulates in a cell as an insoluble aggregate, or where yields from periplasmic expression are low.

[00583] Where the bispecific antigen binding construct or antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon® or Millipore® Pelicon® ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of

adventitious contaminants.

[00584] The bispecific antigen binding construct or antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being a particularly useful purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human 71, y2, or y4 heavy chains (Lindmark et al., *J. Immunol. Meth.,* 1983, 62:1-13). Protein G is useful for all mouse isotypes and for human y3 (Guss et al., *EMBO J.,* 1986, 5:1567-1575).

[00585] The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the bispecific antigen binding construct or antibody comprises a CH3 domain, the BakerBond ABX® resin is useful for purification.

[00586] Other techniques for protein purification, such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin Sepharose®, chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available, and can be applied by one of skill in the art.

[00587] Following any preliminary purification step(s), the mixture comprising the antibody or bispecific antigen binding construct of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5 to about 4.5, generally performed at low salt concentrations (e.g., from about 0 to about 0.25 M salt).

Preparation of Anti-HLA-G Bispecific Antigen Binding Constructs

[00588] Methods for making bispecific antigen binding constructs or bispecific antibodies are known in the art (*See*, e.g., Suresh et al., Methods in Enzymology 121:210, 1986, which is incorporated by refernce herein in its entirety). Traditionally, recombinant production of bispecific antigen binding constructs or bispecific antibodies was based on the coexpression of two IgG heavy chain-light chain pairs, with the two heavy chains having different specificities (*See*, Millstein and Cuello, Nature 305: 537-539, 1983, which is incorporated by reference in its entirety

herein).

[00589] For example, in one approach, bispecific antigen binding constructs or bispecific antibodies may be composed of a hybrid IgG heavy chain with a first binding specificity in one arm and a hybrid IgG heavy chain-light chain pair (providing a second binding specificity) in the other arm. This asymmetric structure, with an IgG light chain in only one half of the bispecific molecule, facilitates the separation of the desired bispecific compound from unwanted IgG chain combinations. The approach is described in PCT Publication No. WO 94/04690, which is incorporated by reference in its entirety herein.

[00590] In another approach, for example, bispecific antigen binding constructs or bispecific antibodies are composed of amino acid modification by replacement of a small amino acid with a larger one in the CH3 domain in one arm to introduce a protuberance at the IgG Fc interface ('knob') and replacement of a large residue with a smaller one in the CH3 domain in another arm to introduce a cavity of the corresponding IgG Fc interface ('hole'). The 'knob' can be positioned in the 'hole' so as to promote heteromultimer formation and hinder homomultimer formation. This 'knobs-into-holes' approach is described in Ridgway et al Protein Engineering 9: 617-621, 1996, and US Patent No. US 8679785 B2, which is incorportaed by reference herein in its entirety.

[00591] In another approach, bispecific antigen binding constructs or bispecific antibodies are composed of amino acid modification in the first hinge region in one arm and the substituted/replaced amino acid in the first hinge region has an opposite charge to the corresponding amino acid in a second hinge region in another arm. The formation of the bispecific antigen binding constructs or bispecific antibody is enhanced by altering or engineering an interface between a first and a second IgG Fc region (e.g., a hinge region and/or a CH3 region). In this approach, the bispecific antigen binding constructs or bispecific antibodies may be composed of a CH3 region, wherein the CH3 region comprises a first CH3 polypeptide and a second CH3 polypeptide which interact together to form a CH3 interface, wherein one or more amino acids within the CH3 interface destabilize homodimer formation and are not electrostatically unfavorable to homodimer formation. This approach is described in International Patent Application No. PCT/US2011/036419 (WO2011/143545) and Strop et al. JMB 420: 204-219, 2012, which is incorporated by reference in its entirety herein.

[00592] In some embodiments, the bispecific antigen binding construct comprises or consist

of one or more diabodies. Diabodies are bivalent, bispecific antigen binding constructs or bispecific antibodies in which heavy chain variable (VH) and light chain variable (VL) domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen binding sites (*See,* e.g., Holliger, P., et al., Proc. Natl. Acad Sci. USA 90:6444-6448, 1993; Poljak, R. J., et al., Structure 2:1121-1123, 1994, which is incorporated by reference in its entirety herein). The short linking peptide bridges between the carboxy terminus of one variable region (e.g. of HLA-G) and the amino terminus of the other variable region (e.g. of CD3), producing a VL-VH sequence. The VL-VH sequence may be further linked to an IgG Fc region. In some embodiments, the IgG Fc can be either human or mouse or human/mouse IgG1, IgG2, IgG3, or IgG4 isotype.

[00593] In some embodiments, a bispecific diabody-Fc antibody comprises or consists of a diabody fused to an IgG Fc domain, wherein a first antibody variable domain of the diabody is capable of specifically binding to a target antigen (e.g. HLA-G), and wherein a second antibody variable domain of the diabody is capable of recruiting the activity of a human immune effector cell by specifically binding to an effector antigen located on a human immune effector cell. In some embodiments, the effector antigen is CD3. In some embodiments, the human immune effector cell is a $CD8^+$ T cell.

[00594] In some embodiments, bispecific antigen binding fragments comprise or consist of one or more of an scFv, minibodies, or VHH single domain antibodies. For scFv, single chain variable region fragments are made by linking light and/or heavy chain variable regions by using a short linking peptide (*See*, Bird et al., Science 242:423-426, 1988, which is incorporated by reference in its entirety). An example of a linking peptide is $(GGGGS)_4$, which bridges between the carboxy terminus of one variable region and the amino terminus of the other variable region. Linkers of other sequences have been designed and used (*See*, Bird et al., Science 242:423-426, 1988). For example, two scFvs targeting two different antigens can be linked by another linker to form a bispecific scFv.

[00595] In some embodiments, the bispecific antigen binding construct comprises or consists of a minibody. A minibody is an antibody which features a smaller molecular weight that a traditional large antibody while still maintaining binding. Because of the smaller size, a minibody features faster clearance from a subject's system and could also feature enhanced

penetration when targeting a tumor tissue.

[00596] A minibody may be composed of a pair of scFv fragments which are linked via CH3 domains, and Fvs with distinct specificity, which are paired to scFv fragments through heterodimerization process. To promote the heterodimerization efficiency, single-residue mutations can be introduced into each CH3 domain to achieve the knob and hole approach. Far more than that, additional cysteine residues can also be introduced into CH3 domains to stabilize the bispecific minibody structure.

[00597] Minibodies can also include the VL and VH domains of a native antibody fused to the hinge region and CH3 domain of the immunoglobulin molecule. *See*, e.g., US Patent No. 5,837,821, which is incorporated by reference in its entirety herein.

[00598] In some embodiments, the bispecific antigen binding construct comprises or consists of one or more VHH single domain antibodies. A VHH single domain antibody is engineered from VH domain found in camelids (*See*, Muyldermans and Lauwereys, Journal of Molecular Recognition, 1999, which is incorporated by reference herein), and can be fused to IgG Fc domain to form a bispecific antigen binding construct VHH antibody. Exemplary heterologous sequences include, but are not limited to, a "tag" such as a Avi tag or a 8His tag. Tags are well known in the art.

Methods of Treatment

[00599] A third aspect provides a method for treating a subject with cancer comprising administering any of the bispecific antigen binding constructs or pharmaceutical compositions provided herein to the subject in a therapeutically effective amount.

[00600] In some embodiments, the cancer is a solid cancer. In some embodiments, the cancer is a hematological cancer. In some embodiments, the cancer is selected from the group consisting of a hematopeietic cancer, hepatocellular carcinoma, leukemia, colorectal cancer (CRC), breast cancer, gastric cancer, esophageal cancer, endometrial cancer, prostate cancer, bladder cancer, thyroid cancer, liver cancer, pancreatic cancer, triple negative breast cancer, cervical cancer, ovarian cancer, uterine cancer, vaginal cancer, vulvar cancer, lung cancer, head and neck cancer, melanoma, renal cell carcinoma, cutaneous squamous cell carcinoma, Hodgkin's lymphoma, a metastasis of the brain, a metastasis of the lung, a metastasis of the liver, and/or a metastasis of the bone, or an unresectable or metastatic solid tumor with DNA mismatch repair

deficiencies or a microsatellite instability-high state. In some embodiments, the cancer is a cancer that expresses HLA-G.

[00601] In some embodiments, the method further comprises one or more of the following:

a) administering chemotherapy to the subject;

b) administering radiation therapy to the subject; and/or

c) administering one or more additional therapeutic agents to the subject.

In some embodiments, the one or more additional therapeutic agents comprise one or more immunomodulatory agents.

Dosage

[00602] Parenteral dosage forms of the bispecific antigen binding constructs are provided in some embodiments. Parenteral dosage forms can be administered to subjects by various routes including, but not limited to, subcutaneous, intravenous (including bolus injection), intramuscular, and intra-arterial. Because their administration typically bypasses subjects' natural defenses against contaminants, parenteral dosage forms are typically sterile or capable of being sterilized prior to administration to a subject. Examples of parenteral dosage forms include, but are not limited to, solutions ready for injection, dry products ready to be dissolved or suspended in a pharmaceutically acceptable vehicle for injection, suspensions ready for injection, and emulsions.

[00603] Suitable vehicles that can be used to provide parenteral dosage forms are well known to those skilled in the art. Examples include, but are not limited to, water for injection; aqueous vehicles such as for example including, but not limited to, sodium chloride injection, ringer's injection, dextrose injection, dextrose and sodium chloride injection, lactated ringer's injection; water miscible vehicles such as for example including, but not limited to, ethyl alcohol, polyethylene glycol, and polypropylene glycol; and non-aqueous vehicles such as for example including, but not limited to, corn oil, cottonseed oil, peanut oil, sesame oil, ethyl oleate, isopropyl myristate, and benzyl benzoate.

[00604] Excipients that increase the solubility of one or more of the bispecific antigen

binding constructs disclosed herein can also be incorporated into the parenteral dosage forms.

[00605] In human therapeutics, the doctor will determine the dosology which she considers most appropriate according to a preventive or curative treatment and according to the age, weight, condition, and other factors specific to the subject to be treated.

[00606] The amount of the bispecific antigen binding construct or composition which will be effective in the prevention or treatment of a disorder or one or more symptoms thereof will vary with the nature and severity of the disease or condition, and the route by which the antibody is administered. The frequency and dosage will also vary according to factors specific for each subject depending on the specific therapy (*e.g.*, therapeutic or prophylactic agents) administered, the severity of the disorder, disease, or condition, the route of administration, as well as age, body, weight, response, and the past medical history of the subject. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

[00607] Bispecific antigen binding constructs or pharmaceutical compositions according to the invention may be administered according to any suitable schedule. Bispecific antigen binding constructs or pharmaceutical compositions may be administered multiple times and at the same of different dosages. Bispecific antigen binding constructs or pharmaceutical compositions may be administered in any order and at any dose with respect to any of the other agents. Some embodiments comprise or consist of administering to the subject a bispecific antigen binding constructs or pharmaceutical compositions simultaneously or sequentially with any other agents provided herein. In some embodiments, bispecific antigen binding constructs or pharmaceutical compositions are administered before other agents. In some embodiments, bispecific antigen binding constructs or pharmaceutical compositions are administered after other agents. In some embodiments, bispecific antigen binding constructs or pharmaceutical compositions are administered multiple times and at the same of different dosages, or a combination thereof, as other agents.

[00608] In certain embodiments, exemplary doses of a bispecific antigen binding construct or composition include milligram or microgram amounts of the antibody per kilogram of subject or sample weight (*e.g.*, about 10 micrograms per kilogram to about 50 milligrams per kilogram, about 100 micrograms per kilogram to about 25 milligrams per kilogram, or about 100 microgram per kilogram to about 10 milligrams per kilogram). In certain embodiment, the dosage of the bispecific antigen binding construct provided herein, based on weight, administered to prevent,

treat, manage, or ameliorate a disorder, or one or more symptoms thereof in a subject is 0.1 mg/kg, 1 mg/kg, 2 mg/kg, 3 mg/kg, 4 mg/kg, 5 mg/kg, 6 mg/kg, 10 mg/kg, or 15 mg/kg or more of a subject's body weight. In another embodiment, the dosage of the bispecific antigen binding construct or a composition provided herein administered to prevent, treat, manage, or ameliorate a disorder, or one or more symptoms thereof in a subject is 0.1 mg to 200 mg, 0.1 mg to 100 mg, 0.1 mg to 50 mg, 0.1 mg to 25 mg, 0.1 mg to 20 mg, 0.1 mg to 15 mg, 0.1 mg to 10 mg, 0.1 mg to 7.5 mg, 0.1 mg to 5 mg, 0.1 to 2.5 mg, 0.25 mg to 20 mg, 0.25 to 15 mg, 0.25 to 12 mg, 0.25 to 10 mg, 0.25 mg to 7.5 mg, 0.25 mg to 5 mg, 0.25 mg to 2.5 mg, 0.5 mg to 20 mg, 0.5 to 15 mg, 0.5 to 12 mg, 0.5 to 10 mg, 0.5 mg to 7.5 mg, 0.5 mg to 5 mg, 0.5 mg to 2.5 mg, 1 mg to 20 mg, 1 mg to 15 mg, 1 mg to 12 mg, 1 mg to 10 mg, 1 mg to 7.5 mg, 1 mg to 5 mg, or 1 mg to 2.5 mg.

[00609] The dose can be administered according to a suitable schedule, for example, once, two times, three times, or four times weekly. It may be necessary to use dosages of the bispecific antigen binding construct outside the ranges disclosed herein in some cases, as will be apparent to those of ordinary skill in the art. Furthermore, it is noted that the clinician or treating physician will know how and when to interrupt, adjust, or terminate therapy in conjunction with subject response.

[00610] In certain embodiments, treatment or prevention can be initiated with one or more loading doses of a bispecific antigen binding construct or composition provided herein followed by one or more maintenance doses.

[00611] In certain embodiments, a dose of a bispecific antigen binding construct or composition provided herein can be administered to achieve a steady-state concentration of the bispecific antigen binding construct in blood or serum of the subject. The steady-state concentration can be determined by measurement according to techniques available to those of skill or can be based on the physical characteristics of the subject such as height, weight and age.

[00612] In certain embodiments, administration of the same bispecific antigen binding construct or composition may be repeated and the administrations may be separated by at least 1 day, 2 days, 3 days, 5 days, 10 days, 15 days, 30 days, 45 days, 2 months, 75 days, 3 months, or 6 months. In other embodiments, administration of the same prophylactic or therapeutic agent may be repeated and the administration may be separated by at least 1 day, 2 days, 3 days, 5 days, 10 days, 15 days, 30 days, 45 days, 2 months, 75 days, 3 months, or 6 months.

[00613] In some embodiments, a therapeutically effective amount comprises or consists of

determining an amount used to achieve a response according to a clinical endpoint. In some embodiments, the clinical endpoint comprises Objective Response Rate (ORR), Progression Free Survival (PFS), and/or Response Evaluation Criteria in Solid Tumors ("RECIST").

EXAMPLES

Example 1: Selection of HLA-G Antibodies

[00614] HLA-G antibodies were selected from a synthetic library of human antibodies presented on the surface of yeast cells in IgG format, as generally described, e.g., in WO2009036379; WO2010105256; WO2012009568; and Xu et al., Protein Eng. Des. Sel., 2013, 26:663-670 (each incorporated by reference in its entirety), and more specifically as provided below. The sequences and characteristics of the antibodies isolated from the recombinant library are provided in Table S.

[00615] Eight naïve human synthetic yeast libraries each of ~10E+09 diversity were propagated as described in WO2009036379; WO2010105256; WO2012009568; and Xu et al., Protein Eng. Des. Sel., 2013, 26:663-670; each incorporated by reference in its entirety. For the first two rounds of selection, a magnetic bead sorting technique utilizing the Miltenyi MACS® system was performed, as described in Siegel et al., J. Immunol. Meth., 2004, 286:141-153. The following rounds of selection were performed using flow cytometry-based sorting. For all rounds of selection, the antigen was biotinylated human HLA-G, decreasing concentrations of antigen were used in each subsequent round of selection. In addition to selection on antigen, some rounds of selection were employed to reduce the number of non-specific binders utilizing soluble membrane proteins from CHO cells (see WO2014179363 and Xu et al., Protein Eng. Des. Sel., 2013, 26:663-670, each incorporated by reference in its entirety). In addition to the CHO cell proteins, deselections against recombinant HLA-A/B/C proteins were performed to maintain specific binding to HLA-G. After the final round of sorting, yeast were plated and individual colonies were picked for characterization and for nomination of clones for affinity maturation.

[00616] Antibody variable domains of interest were synthesized, with codon optimization to maximize transient expression in host cells. The variable regions were cloned into expression

vectors containing human immunoglobulin constant domains and their sequence confirmed. Antibody heavy and light chain vector pairings were transfected into Expi293 cells using the Expifectamine system (Invitrogen). Transient cultures were harvested on day 4 and clarified cell culture supernatant IgG titer was estimated using Bio-Layer Interferometry (BLI) using Octet (ForteBio) alongside standards. Antibodies were subsequently purified on a Protein A column and eluted using low pH glycine. Purified antibody samples were then buffer-exchanged or dialyzed into downstream assay-compatible buffers.

[00617] Antibody purity was assessed by running samples on SDS-PAGE and on an analytical size exclusion chromatography column.

[00618] Light Chain Shuffling: Heavy chain plasmids were extracted from naïve outputs (described herein) and transformed into a pre-made naïve light chain library with a diversity of 10E+06. Selections were performed as described above with one round of MACS sorting and three rounds of FACS sorting using decreasing amounts of biotinylated HLA-G antigen for respective rounds.

Example 2: Affinity Maturation of HLA-G Antibodies

[00619] Optimization of naïve clones was carried out utilizing four maturation strategies; diversification of CDR-H1 and CDR-H2; diversification of CDR-H3; diversification of CDR-L1, L2 and L3; shuffling of diversified heavy and light chains.

[00620] CDR-H1 and CDR-H2 Selection: The CDR-H3s from clones selected from light chain batch diversification, light chain diversification, and naive discovery efforts were independently recombined into premade libraries with CDR-H1 and CDR-H2 variants of a diversity of >10E+8. Selections were performed using HLA-G antigen. Affinity pressures were applied by using decreasing concentrations of antigen and HLA-G specificity was maintained with deselections against HLA-A/B/C antigens.

[00621] CDR-H3 Selection: After characterization of CDR-H1 and CDR-H2 variants, clones with binding to HLA antigens outside of HLA-G were removed. Chemical liabilities were also removed from the variable regions when applicable. The remaining clones obtained from the CDR-H1 and CDR-H2 selection procedure were subject to additional rounds of affinity

maturation via walking dimer mutagenesis of the CDR-H3. Selections were performed using HLA-G as antigen generally as described above, except for employing FACS sorting for all selection rounds.

[00622] CDR-L1, L2, L3 Selection: Clones obtained from the CDR-H1 and CDR-H2 selection procedure were subject to additional rounds of affinity maturation via mutagenesis of the light chain. The CDR-L1 and CDR-L2 diversity was derived from a pre-made library while CDR-L3 diversity was derived from walking monomer mutagenesis. Selections were performed using HLA-G as antigen, starting with one round of MACS followed by three rounds of FACS in the CDR-L1, L2, L3 process described here.

[00623] Diversified Heavy Chain and Light Chain Shuffling: Outputs from CDR-H3 diversification and CDR-L1, L2, L3 diversification described above were recombined and selections were performed using HLA-G as antigen generally as described above, except for employing FACS sorting for all selection rounds.

Example 3: Generation of HLA-G x CD3 Bispecific Antibody

[00624] The HLA-G x CD3 bispecific antibody was prepared using two single-chain VL–VH–Fc constructs. Anti-human CD3 VL (SEQ ID NO: 422) domain was linked on its C-terminus via a 7-amino acid linker, GGGSGGG, to the N-terminus of the anti-human HLA-G VH domain (SEQ ID NO: 192). This VL-VH sequence was linked to the 'effector-silent' human Fc region containing the "EEE" mutations in the hinge region and the CH3 domain. The resultant construct was transiently co-transfected with the single-chain anti-HLA-G VL (SEQ ID NO: 220)–anti-CD3 VH (SEQ ID NO: 413)–Fc with the "RRR" mutations in Expi-293 cells to form the bispecific antibody-Fc fusion molecules. The bispecific antibody was then purified using protein A, size-exclusion and ion exchange chromatography. This bispecific antibody generation approach is described in International Patent Application No. PCT/US2011/036419 (WO2011/143545) and Strop et al. JMB 420: 204-219, 2012, which is incorporated by reference in its entirety herein.

Example 4: HLA-G x CD3 Bispecific Antibody Binds to HLA-G Expressing Cancer Cell Lines and to Human $CD4^+$ and $CD8^+$ T cells

[00625] To evaluate binding to HLA-G^+ tumor cells, A549 lung adenocarcinoma cells engineered to express HLA-G or JEG-3 choriocarcinoma cells that endogenously express HLA-G were incubated with a titration of an HLA-G x CD3 bispecific antibody and the parental anti-HLA-G monoclonal antibody for 30 minutes at 4°C in staining buffer (Phosphate Buffered Saline (PBS), 2% Fetal bovine serum (FBS), 6% mouse serum, 1:10 human Fc block (Becton Dickinson) and 2 mM EDTA). After incubation, cells were washed in wash buffer (PBS, 2% FBS, 2 mM EDTA) followed by a 30-minute incubation with a PE-conjugated anti-human Fc secondary antibody (Biolegend). A final wash was performed followed by sample acquisition using a BD Celesta flow cytometer (Becton Dickinson). Sample data was exported as FCS files and analyzed using FlowJo software v10 (Tree Star, Inc.).

[00626] The results are shown in FIG. 1A and FIG. 1B. Negative controls included JEG-3 HLA-G KO cells generated by CRISPR-Cas9 gene editing and A549 parental cells.

[00627] Binding of an HLA-G x CD3 bispecific antibody to CD3 was evaluated on primary human T cells. Briefly, pan T cells were isolated by negative selection using a pan T cell negative isolation kit (StemCell Technologies). Similar to the method used to evaluate tumor cell binding, T cells were incubated with a titration of an HLA-G x CD3 bispecific antibody followed by a 30-minute incubation with a PE-conjugated anti-human Fc secondary antibody (Biolegend). For the parental anti-CD3 antibody, a PE-conjugated anti-mouse Fc secondary antibody (Biolegend) was used. Cells were subsequently washed twice with wash buffer and then stained with fluorescently conjugated antibodies against CD4, CD8, and CD28 for 30 minutes at 4°C. A final wash was performed followed by sample acquisition using a BD Celesta flow cytometer (Becton Dickinson). Sample data was exported as FCS files and analyzed using FlowJo software v10 (Tree Star, Inc.). Gating was performed on $CD28^+CD4^+$ T cells and $CD28^+CD8^+$ T cells. Results from 2 representative donors are shown in FIG. 2.

Example 5: HLA-G x CD3 Bispecific Antibody Induces T-Cell Mediated Cellular Cytotoxicity

[00628] To demonstrate that an HLA-G x CD3 bispecific antibody can induce killing of

HLA-G$^+$ cancer cells by human T cells, A549-HLA-G$^+$ or JEG-3 cells were co-cultured with human peripheral blood mononuclear cells (PBMC). Negative controls included JEG-3 HLA-G KO cells and A549 parental cells, neither of which express detectable levels of HLA-G. Isolated PBMC (effector cells) were plated in complete RPMI (cRPMI) in a 96-well flat bottom plate at 400,000 cells/well. The effector cells were subsequently incubated with the HLA-G x CD3 bispecific antibody for 1 hour at 37°C, 5% CO_2. Target cells (A549 parental cells, A549-HLA-G$^+$ cells, JEG-3 cells or JEG-3 HLA-G KO cells) were stained with 1:1000 CellTrace Violet at 37°C in PBS, washed and plated in cRPMI at 10,000 cells/well. The mixture of effector cells and HLA-G x CD3 bispecific antibody was then combined with the target cells and incubated for 48 hours at 37°C, 5% CO_2. The final ratio of PBMC to target cells was 40:1.

[00629] After the 48-hour incubation, cells were washed once in 4°C PBS, then resuspended in 50 µL TrypLE Express Enzyme (1x) with phenol red. The cells were incubated with TrypLE for 7 minutes at 37°C, 5% CO_2 before being quenched with 150 µL cRPMI. After quenching the enzyme, the cells were washed once in 4°C wash buffer (Phosphate Buffered Saline, 2% FBS, 2 mM EDTA), and then stained with 1:2000 Fixable Viability Dye eFluor™ 780 (Invitrogen) for 30 minutes at 4°C. Cells were washed again in 4°C wash buffer before being resuspended in wash buffer and analyzed for percent dead target cells by flow cytometry analysis on a BD LSRFortessa. Percent of dead target cells was determined by gating on CTV positive cells, then dividing the Fixable Viability Dye positive portion of these cells by the total CTV count.

[00630] FIG. 3A and FIG. 3B demonstrate the titration of an HLA-G x CD3 bispecific antibody to induce T-cell mediated cytotoxicity of A549-HLA-G$^+$ cells and JEG-3 cells, respectively.

Table S Sequences.

SEQ ID NO:	Region	Scheme/Clone	Sequence
1	CDR-H1	Chothia	GGSISSSDY
2	CDR-H1	Chothia	GGSISSSST

3	CDR-H1	Chothia	GGSISSSDT
4	CDR-H1	Chothia	GGSISSADN
5	CDR-H1	Chothia	GGSVSSSST
6	CDR-H1	Chothia	GYSISSGY
7	CDR-H1	Chothia	GYSILSGY
8	CDR-H1	Chothia	GYSISSGH
9	CDR-H1	Chothia	GYSISSGF
10	CDR-H1	Chothia	GFTFDNY
11	CDR-H1	Chothia	GFTFSDY
12	CDR-H1	Chothia	GFTFSSS
13	CDR-H1	Chothia	GGSISSSN
14	CDR-H1	Chothia	GGSISSSSY
15			
16			
17			
18	CDR-H1	Kabat	SSDYYWG
19	CDR-H1	Kabat	SSSTYWA
20	CDR-H1	Kabat	SSSTYWG
21	CDR-H1	Kabat	SSDTYWG
22	CDR-H1	Kabat	SADNYWG
23	CDR-H1	Kabat	SSSTYWS
24	CDR-H1	Kabat	SGYYWG
25	CDR-H1	Kabat	SGYYWF
26	CDR-H1	Kabat	SGHYWI

27	CDR-H1	Kabat	SGFYWT
28	CDR-H1	Kabat	SGYYWL
29	CDR-H1	Kabat	SGHYWT
30	CDR-H1	Kabat	NYAMH
31	CDR-H1	Kabat	DYYMS
32	CDR-H1	Kabat	SSAMA
33	CDR-H1	Kabat	SSNWWS
34	CDR-H1	Kabat	SSSYYWG
35			
36			
37			
38	CDR-H2	Chothia	YYSGS
39	CDR-H2	Chothia	SSSGS
40	CDR-H2	Chothia	HHSGA
41	CDR-H2	Chothia	HYSGS
42	CDR-H2	Chothia	AYSGS
43	CDR-H2	Chothia	SYNAL
44	CDR-H2	Chothia	YHSGS
45	CDR-H2	Chothia	YHSAS
46	CDR-H2	Chothia	SARAGI
47	CDR-H2	Chothia	ASSGSV
48	CDR-H2	Chothia	SGSGIT
49	CDR-H2	Chothia	SYSGS

50	CDR-H2	Chothia	SSSGST
51			
52			
53			
54	CDR-H2	Kabat	SIYYSGSTYYNPSLKS
55	CDR-H2	Kabat	SISSSGSTYYNPSLKS
56	CDR-H2	Kabat	SIHHSGATYYNPSLKS
57	CDR-H2	Kabat	SIHYSGSTLYNPSLKS
58	CDR-H2	Kabat	SIHYSGSTYYNPSLKS
59	CDR-H2	Kabat	GIAYSGSTYYNPSLKS
60	CDR-H2	Kabat	SISYNALTYYNPSLKS
61	CDR-H2	Kabat	SIYHSGSTYYNPSLKS
62	CDR-H2	Kabat	GIYHSASTAYNPSLKS
63	CDR-H2	Kabat	GIYHSGSTYYNPSLKS
64	CDR-H2	Kabat	AIYHSGSTVYNPSLKS
65	CDR-H2	Kabat	GIYHSGSTAYNPSLKS
66	CDR-H2	Kabat	AISARAGITYYADSVKG
67	CDR-H2	Kabat	YIASSGSVIYYADSVKG
68	CDR-H2	Kabat	TISGSGITTWYADSVKG
69	CDR-H2	Kabat	EIYHSGSTNYNPSLKS
70	CDR-H2	Kabat	SISYSGSTYYNPSLKS
71	CDR-H2	Kabat	YISSSGSTIYYADSVKG
72			

73			
74			
75			
76	CDR-H3		GVRRAVPFDY
77	CDR-H3		GIARAVPFDY
78	CDR-H3		GPKRAVPFDY
79	CDR-H3		GVRRAVPFVD
80	CDR-H3		GVRRAVPFQR
81	CDR-H3		GTRRAVPFDY
82	CDR-H3		GVRRAVPFAD
83	CDR-H3		GIRRAVPFDY
84	CDR-H3		GQFRAVPFDY
85	CDR-H3		GGTHTYSRGPMDV
86	CDR-H3		GGTHTYSRGPFDV
87	CDR-H3		GGTPIYSRGPLDV
88	CDR-H3		GGGQTYSRGPLDV
89	CDR-H3		GGGATYSRGPLDV
90	CDR-H3		GGTHTYSRGPLDV
91	CDR-H3		GGTVKYSRGPLDV
92	CDR-H3		GGQVTYSRGPLDV
93	CDR-H3		GGEVTYSRGPLDV
94	CDR-H3		RIGYSYGTAPPFDV

95	CDR-H3		HGTPRAFDI
96	CDR-H3		GSRHLNAFNR
97	CDR-H3		GVYHYDPYGMDV
98	CDR-H3		TELGKMHFDY
99	CDR-H3		GSPRYMQD
100	CDR-H3		HSSLGTHNWFDP
101	CDR-H3		EGALSYSWLAAFDI
102			
103			
104			
105	CDR-L1		RASQSVSSSYLA
106	CDR-L1		GASQSVSSDYLA
107	CDR-L1		QASQAVSSNYLA
108	CDR-L1		GASQSVSSAFLA
109	CDR-L1		RASQSVSSTYLA
110	CDR-L1		QASQSVSSSYLA
111	CDR-L1		KASQAVSSSYLA
112	CDR-L1		EASQSVSSSYLA
113	CDR-L1		EASQSVSASYLA
114	CDR-L1		EASQSVSSAYLA
115	CDR-L1		RVSQSVSDAYLA
116	CDR-L1		EVSQSVSASYLA
117	CDR-L1		RASQSVSSAYLA
118	CDR-L1		RASNAVSSSYLA

119	CDR-L1		RASQSINSWLA
120	CDR-L1		AASQGISSDLA
121	CDR-L1		RASQDISTYLN
122	CDR-L1		RSSQSLLHSNGYNYLD
123	CDR-L1		RASQSISSYLN
124	CDR-L1		RASQSVSSNLA
125			
126			
127			
128	CDR-L2		GASSRAT
129	CDR-L2		GAYSLAT
130	CDR-L2		GASARAT
131	CDR-L2		GASSREA
132	CDR-L2		GASNRAA
133	CDR-L2		GASSRQD
134	CDR-L2		GASNRAT
135	CDR-L2		DASSRAS
136	CDR-L2		DASTRAT
137	CDR-L2		GASDRAN
138	CDR-L2		GASYRAT
139	CDR-L2		DASSLES
140	CDR-L2		SASSTQS
141	CDR-L2		DAFNLET

142	CDR-L2		LGSNRAS
143	CDR-L2		GASRRAT
144	CDR-L2		AASSLQS
145	CDR-L2		GASTRAT
146			
147			
148			
149	CDR-L3		QQAVHSPYT
150	CDR-L3		QWAVHSPYT
151	CDR-L3		QQVVHSPYT
152	CDR-L3		QQTVHSPYT
153	CDR-L3		QQAIHSPYT
154	CDR-L3		QQHSSYPPT
155	CDR-L3		QQHSLYPPT
156	CDR-L3		QQFSSYPPT
157	CDR-L3		QQVSSYPPT
158	CDR-L3		QQHSIYPPT
159	CDR-L3		QQYDSHIT
160	CDR-L3		QQAYLYPIT
161	CDR-L3		QQLPFLPIT
162	CDR-L3		MQALGGPWT
163	CDR-L3		QQYVSDPIT
164	CDR-L3		QQVGSSPIT
165	CDR-L3		QQSHLVPRT

166	CDR-L3		QQANHHPPFT
167			
168			
169			
170	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD YYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSS
171	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWAWIRQPPGKGLEWIGSISSSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GIARAVPFDYWGQGTLVTVSS
172	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWGWIRQSPGKGLEWIGSIHHSGATYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GPKRAVPFDYWGQGTLVTVSS
173	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFVDWGQGTLVTVSS
174	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSAD NYWGWIRQPPGKGLEWIGSIHYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFQRWGQGTLVTVSS
175	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGPEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSS
176	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSS
177	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGSISYNALTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GTRRAVPFDYWGQGTLVTVSS

178	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFADWGQGTLVTVSS
179	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSVSSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSS
180	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GTRRAVPFDYWGQGTLVTVSS
181	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GIRRAVPFDYWGQGTLVTVSS
182	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GQFRAVPFDYWGQGTLVTVSS
183	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPMDVWGQGTTVTVSS
184	VH		QLQLQESGPRLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPFDVWGQGTTVTVSS
185	VH		LVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSASTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTPIYSRGPLDVWGQGTTVTVSS
186	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSISSGH YWIWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKDQFSLKLSSVTAADTAVYYCARG GGQTYSRGPLDVWGQGTTVTVSS
187	VH		QVQLQESGPGLVKPPETLSLTCAVSGYSISSGH YWIWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS

			RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GGATYSRGPLDVWGQGTTVTVSS
188	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPLDVWGQGTTVTVSS
189	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSISSGF YWTWIRQPPGKGLEWIGAIYHSGSTVYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPLDVWGQGTTVTVSS
190	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWLWIRQPPGKGLEWIGGIYHSASTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTVKYSRGPLDVWGQGTTVTVSS
191	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSISSGH YWTWIRQPPGKGLEWIGAIYHSGSTVYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GQVTYSRGPLDVWGQGTTVTVSS
192	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSGSTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GEVTYSRGPLDVWGQGTTVTVSS
193	VH		EVQLLESGGGLVQPGGSLRLSCAASGFTFDNYA MHWVRQAPGKGLEWVSAISARAGITYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARR IGYSYGTAPPFDVWGQGTTVTVSS
194	VH		QVQLVESGGGLVQPGGSLRLSCAASGFTFSDYY MSWIRQAPGKGLEWVSYIASSGSVIYYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARH GTPRAFDIWGQGTTVTVSS
195	VH		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSA MAWVRQAPGKGLEWVSTISGSGITTWYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKG SRHLNAFNRWGQGTTVTVSS
196	VH		QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSN WWSWVRQPPGKGLEWIGEIYHSGSTNYNPSLKS RVTISVDKSKNQFSLKLSSVTAADTAVYYCARG VYHYDPYGMDVWGQGTTVTVSS

197	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS YYWGWIRQPPGKGLEWIGSISYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR TELGKMHFDYWGQGTLVTVSS
198	VH		QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD YYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GSPRYMQDWGQGTLVTVSS
199	VH		QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYY MSWIRQAPGKGLEWVSYISSSGSTIYYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARH SSLGTHNWFDPWGQGTLVTVSS
200	VH		QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARE GALSYSWLAAFDIWGQGTMVTVSS
201			
202			
203			
204	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAVHSPYTF GGGTKVEIK
205	VL		EIVLTQSPGTLSLSPGERATLSCGASQSVSSDY LAWYQQKPGQAPRLLIYGAYSLATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQWAVHSPYTF GGGTKVEIK
206	VL		EIVLTQSPGTLSLSPGERATLSCQASQAVSSNY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIK
207	VL		EIVLTQSPGTLSLSPGERATLSCGASQSVSSAF LAWYQQKPGQAPRLLIYGASARATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIK

208	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVSSTY LAWYQQKPGQAPRLLIYGASSREAGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQTVHSPYTF GGGTKVEIK
209	VL		EIVLTQSPGTLSLSPGERATLSCQASQAVSSNY LAWYQQKPGQAPRLLIYGASNRAAGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAIHSPYTF GGGTKVEIK
210	VL		EIVLTQSPGTLSLSPGERATLSCQASQSVSSSY LAWYQQKPGQAPRLLIYGASNRAAGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIK
211	VL		EIVLTQSPGTLSLSPGERATLSCKASQAVSSSY LAWYQQKPGQAPRLLIYGASSRQDGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIK
212	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSSYPPTF GGGTKVEIK
213	VL		EIVLTQSPGTLSLSPGERATLSCEASQSVSSSY LAWYQQKPGQAPRLLIYGASNRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIK
214	VL		EIVLTQSPGTLSLSPGERATLSCEASQSVSASY LAWYQQKPGQAPRLLIYDASSRASGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQFSSYPPTF GGGTKVEIK
215	VL		EIVLTQSPGTLSLSPGERATLSCEASQSVSSAY LAWYQQKPGQAPRLLIYDASTRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVSSYPPTF GGGTKVEIK
216	VL		EIVLTQSPGTLSLSPGERAALSCRVSQSVSDAY LAWYQQKPGQAPRLLIYDASSRASGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVSSYPPTF GGGTKVEIK
217	VL		EIVLTQSPGTLSLSPGERATLSCEVSQSVSASY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS

			GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIK
218	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVSSAY LAWYQQKPGQAPRLLIYGASDRANGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIK
219	VL		EIVLTQSPGTLSLSPGERATLSCRASNAVSSSY LAWYQQKPGQAPRLLIYGASDRANGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSIYPPTF GGGTKVEIK
220	VL		EIVLTQSPGTLSLSPGERATLSCRASNAVSSSY LAWYQQKPGQAPRLLIYGASYRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIK
221	VL		DIQMTQSPSTLSASVGDRVTITCRASQSINSWL AWYQQKPGKAPKLLISDASSLESGVPSRFSGSG SGTEFTLTISSLQPDDFATYYCQQYDSHITFGG GTKVEIK
222	VL		DIQMTQSPSSVSASVGDRVTITCAASQGISSDL AWYQQKPGKAPKLLIYSASSTQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQAYLYPITFG GGTKVEIK
223	VL		GVQMTQSPSSLSASVGDRVTITCRASQDISTYL NWYQQKPGKAPKLLIYDAFNLETGVPSRFSGSG SGTDFTFTISSLQPEDIATYYCQQLPFLPITFG GGTKVEIK
224	VL		DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSN GYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYCMQALGG PWTFGGGTKVEIK
225	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASRRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYVSDPITF GGGTKVEIK
226	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASRRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVGSSPITF GGGTKVEIK

227	VL		DIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSHLVPRTFG GGTKVEIK
228	VL		EIVMTQSPATLSVSPGERATLSCRASQSVSSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYCQQANHHPPFTF GGGTKVEIK
229			
230			
231			
232	IGG1 AAA HC	33343	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD YYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
233	IGG1 AAA HC	37268	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWAWIRQPPGKGLEWIGSISSSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GIARAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK

234	IGG1 AAA HC	37269	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWGWIRQSPGKGLEWIGSIHHSGATYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GPKRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
235	IGG1 AAA HC	37271	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFVDWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
236	IGG1 AAA HC	37272	QLQLQESGPGLVKPSETLSLTCTVSGGSISSAD NYWGWIRQPPGKGLEWIGSIHYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFQRWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK

237	IGG1 AAA HC	37277	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGPEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
238	IGG1 AAA HC	38373	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
239	IGG1 AAA HC	38375	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGSISYNALTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GTRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK

240	IGG1 AAA HC	38379	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFADWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
241	IGG1 AAA HC	38381	QLQLQESGPGLVKPSETLSLTCTVSGGSVSSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
242	IGG1 AAA HC	38383	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GTRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK

243	IGG1 AAA HC	38386	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GIRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
244	IGG1 AAA HC	37273	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GQFRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
245	IGG1 AAA HC	33361	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPMDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK

246	IGG1 AAA HC	35624	QLQLQESGPRLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPFDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
247	IGG1 AAA HC	38410	LVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSASTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTPIYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
248	IGG1 AAA HC	38418	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGH YWIWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKDQFSLKLSSVTAADTAVYYCARG GGQTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK

249	IGG1 AAA HC	38420	QVQLQESGPGLVKPPETLSLTCAVSGYSISSGH YWIWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GGATYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
250	IGG1 AAA HC	38421	QVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
251	IGG1 AAA HC	38422	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGF YWTWIRQPPGKGLEWIGAIYHSGSTVYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK

252	IGG1 AAA HC	38424	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWLWIRQPPGKGLEWIGGIYHSASTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTVKYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
253	IGG1 AAA HC	38425	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGH YWTWIRQPPGKGLEWIGAIYHSGSTVYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GQVTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
254	IGG1 AAA HC	38426	QVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSGSTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GEVTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK

255	IGG1 AAA HC	37323	EVQLLESGGGLVQPGGSLRLSCAASGFTFDNYA MHWVRQAPGKGLEWVSAISARAGITYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARR IGYSYGTAPPFDVWGQGTTVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
256	IGG1 AAA HC	38389	QVQLVESGGGLVQPGGSLRLSCAASGFTFSDYY MSWIRQAPGKGLEWVSYIASSGSVIYYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARH GTPRAFDIWGQGTTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APEAAGAPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK
257	IGG1 AAA HC	38358	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSA MAWVRQAPGKGLEWVSTISGSGITTWYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKG SRHLNAFNRWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK

258	IGG1 AAA HC	33303	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSN WWSWVRQPPGKGLEWIGEIYHSGSTNYNPSLKS RVTISVDKSKNQFSLKLSSVTAADTAVYYCARG VYHYDPYGMDVWGQGTTVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK
259	IGG1 AAA HC	33342	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS YYWGWIRQPPGKGLEWIGSISYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR TELGKMHFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
260	IGG1 AAA HC	33299	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD YYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GSPRYMQDWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APEAAGAPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK

261	IGG1 AAA HC	33351	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYY MSWIRQAPGKGLEWVSYISSSGSTIYYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARH SSLGTHNWFDPWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK
262	IGG1 AAA HC	33357	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARE GALSYSWLAAFDIWGQGTMVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
263			
264			
265			
266	IGG4 HC	33343	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD YYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV

			SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
267	IGG4 HC	37268	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWAWIRQPPGKGLEWIGSISSSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GIARAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
268	IGG4 HC	37269	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWGWIRQSPGKGLEWIGSIHHSGATYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GPKRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
269	IGG4 HC	37271	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFVDWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP

			VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
270	IGG4 HC	37272	QLQLQESGPGLVKPSETLSLTCTVSGGSISSAD NYWGWIRQPPGKGLEWIGSIHYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFQRWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
271	IGG4 HC	37277	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGPEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
272	IGG4 HC	38373	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP

			VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
273	IGG4 HC	38375	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGSISYNALTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GTRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
274	IGG4 HC	38379	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFADWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
275	IGG4 HC	38381	QLQLQESGPGLVKPSETLSLTCTVSGGSVSSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GVRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP

			VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
276	IGG4 HC	38383	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS TYWSWIRQPPGKGLEWIGGIAYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GTRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
277	IGG4 HC	38386	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GIRRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
278	IGG4 HC	37273	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD TYWGWIRQPPGKGLEWIGSIHYSGSTLYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GQFRAVPFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP

			VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
279	IGG4 HC	33361	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPMDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
280	IGG4 HC	35624	QLQLQESGPRLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPFDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
281	IGG4 HC	38410	LVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSASTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTPIYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT

			PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
282	IGG4 HC	38418	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGH YWIWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKDQFSLKLSSVTAADTAVYYCARG GGQTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
283	IGG4 HC	38420	QVQLQESGPGLVKPPETLSLTCAVSGYSISSGH YWIWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GGATYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
284	IGG4 HC	38421	QVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT

			PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
285	IGG4 HC	38422	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGF YWTWIRQPPGKGLEWIGAIYHSGSTVYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTHTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
286	IGG4 HC	38424	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWLWIRQPPGKGLEWIGGIYHSASTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GTVKYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
287	IGG4 HC	38425	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGH YWTWIRQPPGKGLEWIGAIYHSGSTVYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GQVTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT

			PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
288	IGG4 HC	38426	QVQLQESGPGLVKPSETLSLTCAVSGYSILSGY YWFWIRQPPGKGLEWIGGIYHSGSTAYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARG GEVTYSRGPLDVWGQGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSPGK
289	IGG4 HC	37323	EVQLLESGGGLVQPGGSLRLSCAASGFTFDNYA MHWVRQAPGKGLEWVSAISARAGITYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARR IGYSYGTAPPFDVWGQGTTVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPP CPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG LPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSPGK
290	IGG4 HC	38389	QVQLVESGGGLVQPGGSLRLSCAASGFTFSDYY MSWIRQAPGKGLEWVSYIASSGSVIYYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARH GTPRAFDIWGQGTTVTVSSASTKGPSVFPLAPC SRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSI EKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL

			DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSPGK
291	IGG4 HC	38358	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSA MAWVRQAPGKGLEWVSTISGSGITTWYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKG SRHLNAFNRWGQGTTVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAP EFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSPGK
292	IGG4 HC	33303	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSN WWSWVRQPPGKGLEWIGEIYHSGSTNYNPSLKS RVTISVDKSKNQFSLKLSSVTAADTAVYYCARG VYHYDPYGMDVWGQGTTVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSPGK
293	IGG4 HC	33342	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSS YYWGWIRQPPGKGLEWIGSISYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR TELGKMHFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP

			VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSPGK
294	IGG4 HC	33329	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSD YYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLK SRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GSPRYMQDWGQGTLVTVSSASTKGPSVFPLAPC SRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSI EKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSPGK
295	IGG4 HC	33351	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYY MSWIRQAPGKGLEWVSYISSSGSTIYYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARH SSLGTHNWFDPWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSPGK
296	IGG4 HC	33357	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGY YWGWIRQPPGKGLEWIGSIYHSGSTYYNPSLKS RVTISVDTSKNQFSLKLSSVTAADTAVYYCARE GALSYSWLAAFDIWGQGTMVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPP CPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG LPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT

			TPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSPGK
297			
298			
299			
300	LC	33343	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
301	LC	37268	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
302	LC	37269	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
303	LC	37271	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
304	LC	37272	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT

			EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
305	LC	37277	EIVLTQSPGTLSLSPGERATLSCGASQSVSSDY LAWYQQKPGQAPRLLIYGAYSLATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQWAVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
306	LC	38373	EIVLTQSPGTLSLSPGERATLSCQASQAVSSNY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
307	LC	38375	EIVLTQSPGTLSLSPGERATLSCGASQSVSSAF LAWYQQKPGQAPRLLIYGASARATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
308	LC	38379	EIVLTQSPGTLSLSPGERATLSCRASQSVSSTY LAWYQQKPGQAPRLLIYGASSREAGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQTVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
309	LC	38381	EIVLTQSPGTLSLSPGERATLSCQASQAVSSNY LAWYQQKPGQAPRLLIYGASNRAAGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAIHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
310	LC	38383	EIVLTQSPGTLSLSPGERATLSCQASQSVSSSY LAWYQQKPGQAPRLLIYGASNRAAGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS

			VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
311	LC	38386	EIVLTQSPGTLSLSPGERATLSCKASQAVSSSY LAWYQQKPGQAPRLLIYGASSRQDGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
312	LC	37273	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAVHSPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
313	LC	33361	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSSYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
314	LC	35624	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSSYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
315	LC	38410	EIVLTQSPGTLSLSPGERATLSCEASQSVSSSY LAWYQQKPGQAPRLLIYGASNRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
316	LC	38418	EIVLTQSPGTLSLSPGERATLSCEASQSVSASY LAWYQQKPGQAPRLLIYDASSRASGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQFSSYPPTF

			GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
317	LC	38420	EIVLTQSPGTLSLSPGERATLSCEASQSVSSAY LAWYQQKPGQAPRLLIYDASTRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVSSYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
318	LC	38421	EIVLTQSPGTLSLSPGERAALSCRVSQSVSDAY LAWYQQKPGQAPRLLIYDASSRASGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVSSYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
319	LC	38422	EIVLTQSPGTLSLSPGERATLSCEVSQSVSASY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
320	LC	38424	EIVLTQSPGTLSLSPGERATLSCRASQSVSSAY LAWYQQKPGQAPRLLIYGASDRANGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
321	LC	38425	EIVLTQSPGTLSLSPGERATLSCRASNAVSSSY LAWYQQKPGQAPRLLIYGASDRANGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQHSIYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
322	LC	38426	EIVLTQSPGTLSLSPGERATLSCRASNAVSSSY LAWYQQKPGQAPRLLIYGASYRATGIPDRFSGS

			GSGTDFTLTISRLEPEDFAVYYCQQHSLYPPTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
323	LC	37323	DIQMTQSPSTLSASVGDRVTITCRASQSINSWL AWYQQKPGKAPKLLISDASSLESGVPSRFSGSG SGTEFTLTISSLQPDDFATYYCQQYDSHITFGG GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
324	LC	38389	DIQMTQSPSSVSASVGDRVTITCAASQGISSDL AWYQQKPGKAPKLLIYSASSTQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQAYLYPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
325	LC	38358	GVQMTQSPSSLSASVGDRVTITCRASQDISTYL NWYQQKPGKAPKLLIYDAFNLETGVPSRFSGSG SGTDFTFTISSLQPEDIATYYCQQLPFLPITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
326	LC	33303	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSN GYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYCMQALGG PWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC
327	LC	33342	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASRRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYVSDPITF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC

328	LC	33299	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASRRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQVGSSPITF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
329	LC	33351	DIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSHLVPRTFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
330	LC	33357	EIVMTQSPATLSVSPGERATLSCRASQSVSSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYCQQANHHPPFTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
331			
332			
333			
334	Fc for IGG1		ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
335	Fc region for IGG4		ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVE SKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKE

			YKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSPGK
336	Kappa region for LC		RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
337		hHLA-G1	MVVMAPRTLFLLLSGALTLTETWAGSHSMRYFS AAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSAC PRMEPRAPWVEQEGPEYWEEETRNTKAHAQTDR MNLQTLRGYYNQSEASSHTLQWMIGCDLGSDGR LLRGYEQYAYDGKDYLALNEDLRSWTAADTAAQ ISKRKCEAANVAEQRRAYLEGTCVEWLHRYLEN GKEMLQRADPPKTHVTHHPVFDYEATLRCWALG FYPAEIILTWQRDGEDQTQDVELVETRPAGDGT FQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLR WKQSSLPTIPIMGIVAGLVVLAAVVTGAAVAAV LWRKKSSD
338		hHLA-G5	MVVMAPRTLFLLLSGALTLTETWAGSHSMRYFS AAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSAC PRMEPRAPWVEQEGPEYWEEETRNTKAHAQTDR MNLQTLRGYYNQSEASSHTLQWMIGCDLGSDGR LLRGYEQYAYDGKDYLALNEDLRSWTAADTAAQ ISKRKCEAANVAEQRRAYLEGTCVEWLHRYLEN GKEMLQRADPPKTHVTHHPVFDYEATLRCWALG FYPAEIILTWQRDGEDQTQDVELVETRPAGDGT FQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLR WSKEGDGGIMSVRESRSLSEDL
339		Cyno MHC-AG	MAVMAPRTLLLVLSGVLALTQPRAGSHSMRYFY TAVSRPGRGQPRFIAVGYVDDTQFVRFDSDAES PRMEPRAPWVEQEGPEYWDRETQNMKTATQTYQ ANLRTLLRYYNQSEAGSHTFQKMYGCDLGPDGR LLRGYEQFAYDGRDYIILNEDLRSWTAADMAAQ NTQRKWEAAGAAEQHRTYLEGECLEWLRRYLEN GKETLQRADPPKTNVTHHPVSDYEATLRCWALG FYPAEITLTWQRDGEEQTEDTELVETRPTGDGT FQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLR WEPSSQSTILIVGIIAGLVLLGTVVTGAVVAAV MWRRKS

340		Rhesus MHC-AG	LLLVLSGVLALTQTRAGSHSMRYFYTSMSRPGR GQPRFIAVGYVDDTQFVRFDSDAESPRMEPRAP WVEQEGPEYWDRETQNMKTATQTYRENLRTLLR YYNQSEAGSHTIQKMYGCDLGPDGRLLRGYEQF AYDGRDYIALNEDLRSWTAADMAAQFTQRKWEA AGAAEQHRTYLEGECLEWLRRYLENGKETLQRA DPPKTNVTHHPVSDYEATLRCWALGFYPAEITL TWQRDGEEQTEDTELVETRPTGDGTFQKWAAVV VPSGEEQRYTCHVQHEGLPEPLTLRWEPSSQST ILIVGIIAGLVLLGTVVTGAVVAAVMWRRKSSD R
341		hHLA-G ECD with signal peptide	MVVMAPRTLFLLLSGALTLTETWAGSHSMRYFS AAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSAC PRMEPRAPWVEQEGPEYWEEETRNTKAHAQTDR MNLQTLRGYYNQSEASSHTLQWMIGCDLGSDGR LLRGYEQYAYDGKDYLALNEDLRSWTAADTAAQ ISKRKCEAANVAEQRRAYLEGTCVEWLHRYLEN GKEMLQRADPPKTHVTHHPVFDYEATLRCWALG FYPAEIILTWQRDGEDQTQDVELVETRPAGDGT FQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLR W
342		hHLA-G ECD without signal peptide	GSHSMRYFSAAVSRPGRGEPRFIAMGYVDDTQF VRFDSDSACPRMEPRAPWVEQEGPEYWEEETRN TKAHAQTDRMNLQTLRGYYNQSEASSHTLQWMI GCDLGSDGRLLRGYEQYAYDGKDYLALNEDLRS WTAADTAAQISKRKCEAANVAEQRRAYLEGTCV EWLHRYLENGKEMLQRADPPKTHVTHHPVFDYE ATLRCWALGFYPAEIILTWQRDGEDQTQDVELV ETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHE GLPEPLMLRW
343			
344			
345			
346	CDR-H1 CD3	Chothia	GYSFTGY
347	CDR-H1 CD3	Chothia	GYTFTRY
348	CDR-H1 CD3	Chothia	GFKFSGY

349	CDRH-1 CD3	Chothia	GYTFTNY
350			
351			
352			
353			
354	CDR-H1 CD3	Kabat	GYTMN
355	CDR-H1 CD3	Kabat	RYTMH
356	CDR-H1 CD3	Kabat	GYGMH
357	CDR-H1 CD3	Kabat	NYYIH
358			
359			
360			
361			
362	CDR-H2 CD3	Chothia	NPYKGV
363	CDR-H2 CD3	Chothia	WYDGSK
364	CDR-H2 CD3	Chothia	NPSRGY

365	CDR-H2 CD3	Chothia	YPGDGN
366			
367			
368			
369			
370			
371	CDR-H2 CD3	Kabat	LINPYKGVSTYNQKFKD
372	CDR-H2 CD3	Kabat	YINPSRGYTNYNQKFKD
373	CDR-H2 CD3	Kabat	YINPSRGYTNYNQKVKD
374	CDR-H2 CD3	Kabat	WIYPGDGNTKYNEKFKG
375	CDR-H2 CD3	Kabat	VIWYDGSKKYYVDSVKG
376			
377			
378			
379	CDR-H3 CD3		SGYYGDSDWYFDV
380	CDR-H3 CD3		DSYSNYYFDY
381	CDR-H3 CD3		QMGYWHFDL

382	CDR-H3 CD3		YYDDHYCLDY
383			
384			
385			
386			
387			
388	CDR-L1 CD3		RASQDIRNYLN
389	CDR-L1 CD3		SASSSVSYMN
390	CDR-L1 CD3		RASSSVSYMN
391	CDR-L1 CD3		KSSQSLLNSRTRKNYLA
392	CDR-L1 CD3		RASQSVSSYLA
393			
394			
395			
396	CDR-L2 CD3		YTSRLHS
397	CDR-L2 CD3		DTSKLAS
398	CDR-L2 CD3		DTSKVAS

399	CDR-L2 CD3		WASTRES
400	CDR-L2 CD3		DASNRAT
401			
402			
403			
404	CDR-L3 CD3		QQGNTLPWT
405	CDR-L3 CD3		QQWSSNPFT
406	CDR-L3 CD3		QQWSSNPLT
407	CDR-L3 CD3		TQSFILRT
408	CDR-L3 CD3		QQRSNWPPLT
409			
410			
411			
412			
413	VH CD3		EVQLQQSGPELVKPGASMKISCKASGYSFTGYT MNWVKQSHGKNLEWMGLINPYKGVSTYNQKFKD KATLTVDKSSSTAYMELLSLTSEDSAVYYCARS GYYGDSDWYFDVWGQGTTVTVSS
414	VH CD3		QVQLQQSGAELARPGASVKMSCKASGYTFTRYT MHWVKQRPGQGLEWIGYINPSRGYTNYNQKFKD

			KATLTTDKSSSTAYMQLSSLTSEDSAVYYCARY YDDHYCLDYWGQGTTLTVSS
415	ScFV CD3		DIKLQQSGAELARPGASVKMSCKTSGYTFTRYT MHWVKQRPGQGLEWIGYINPSRGYTNYNQKFKD KATLTTDKSSSTAYMQLSSLTSEDSAVYYCARY YDDHYCLDYWGQGTTLTVSS
416	VH CD3		EVQLVQSGAEVKKPGASVKVSCKASGYTFTNYY IHWVRQAPGQGLEWIGWIYPGDGNTKYNEKEKG RATLTADTSTSTAYLELSSLRSEDTAVYYCARD SYSNYYFDYWGQGTLVTVSS
417	VH CD3		QVQLVESGGGVVQPGRSLRLSCAASGFKFSGYG MHWVRQAPGKGLEWVAVIWYDGSKKYYVDSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARQ MGYWHFDLWGRGTLVTVSS
418	VH CD3		QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYT MHWVRQAPGKGLEWIGYINPSRGYTNYNQKVKD RFTISRDNSKNTAFLQMDSLRPEDTGVYFCARY YDDHYCLDYWGQGTPVTVSS
419			
420			
421			
422	VL CD3		DIQMTQTTSSLSASLGDRVTISCRASQDIRNYL NWYQQKPDGTVKLLIYYTSRLHSGVPSKFSGSG SGTDYSLTISNLEQEDIATYFCQQGNTLPWTFA GGTKLEIK
423	VL CD3		QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMN WYQQKSGTSPKRWIYDTSKLASGVPAHFRGSGS GTSYSLTISGMEAEDAATYYCQQWSSNPFTFGS GTKLEIK
424	ScFV LCVR CD3		DIQLTQSPAIMSASPGEKVTMTCRASSSVSYMN WYQQKSGTSPKRWIYDTSKVASGVPYRFSGSGS GTSYSLTISSMEAEDAATYYCQQWSSNPLTFGA GTKLELK
425	VL CD3		DIVMTQSPDSLAVSLGERATINCKSSQSLLNSR TRKNYLAWYQQKPGQPPKLLIYWASTRESGVPD

			RESGSGSGTDETLTISSLQAEDVAVYYCTQSFI LRTFGQGTKVEIK
426	VL CD3		EIVLTQSPATLSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRATGIPARFSGSG SGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTF GGGTKVEIK
427	VL CD3		DIQMTQSPSSLSASVGDRVTITCSASSSVSYMN WYQQTPGKAPKRWIYDTSKLASGVPSRFSGSGS GTDYTFTISSLQPEDIATYYCQQWSSNPFTFGQ GTKLQIT
428			
429			
430			
431	CDR-H1 CD16	Chothia	GFSLSTSGM
432	CDR-H1 CD16	Chothia	GFTFNNY
433	CDR-H1 CD16	Chothia	GFTFSNY
434	CDR-H1 CD16	Chothia	GYTFTSS
435	CDR-H1 CD16	Chothia	GFTFSNYG
436	CDR-H1 CD16	Chothia	GFTFSSYG
437	CDR-H1 CD16	Chothia	GYTFTSYY
438			
439			

440			
441	CDR-H1 CD16	Kabat	TSGMGVG
442	CDR-H1 CD16	Kabat	TSGVGVG
443	CDR-H1 CD16	Kabat	NYGMS
444	CDR-H1 CD16	Chothia	SSAMH
445			
446			
447			
448	CDR-H2 CD16	Chothia	WWDDD
449	CDR-H2 CD16	Chothia	SGGGSY
450	CDR-H2 CD16	Chothia	NHYNDG
451	CDR-H2 CD16	Chothia	IYYSGGST
452	CDR-H2 CD16	Chothia	VNHSGGST
453	CDR-H2 CD16	Chothia	IEPMYGST
454	CDR-H2 CD16	Chothia	INPSGGST

455			
456			
457			
458	CDR-H2 CD16	Kabat	YINHYNDGIKYNERFKG
459	CDR-H2 CD16	Kabat	HIWWDDDKRYNPALKS
460	CDR-H2 CD16	Kabat	HIWWDDDKRYSPSLKS
461	CDR-H2 CD16	Kabat	TISGGGSYTFYPDSVKG
462			
463			
464			
465	CDR-H3 CD16		TNPAWFAY
466	CDR-H3 CD16		INPAYFAY
467	CDR-H3 CD16		QSARAPEPY
468	CDR-H3 CD16		QSANSPVPY
469	CDR-H3 CD16		GYRYASWFAS
470	CDR-H3 CD16		ARESIDY

471	CDR-H3 CD16		ARVGSFDF
472	CDR-H3 CD16		ARGSAYYYDFADY
473			
474			
475			
476	CDR-L1 CD16		KASQSVDFDGDSFMN
477	CDR-L1 CD16		KASQNVGTHVA
478	CDR-L1 CD16		RASQNVGTHVA
479	CDR-L1 CD16		RASQNIGTSIH
480	CDR-L1 CD16		NIGSKN
481			
482			
483			
484	CDR-L2 CD16		TTSNLES
485	CDR-L2 CD16		TTSSLES
486	CDR-L2 CD16		SASYRYS

487	CDR-L2 CD16		SVSESIS
488	CDR-L2 CD16		QDN
489			
490			
491			
492	CDR-L3 CD16		QQSNEDPYT
493	CDR-L3 CD16		QQSNSDPYT
494	CDR-L3 CD16		QQYKSYPLT
495	CDR-L3 CD16		QDYTNYPLT
496	CDR-L3 CD16		QQSNSWPLT
497	CDR-L3 CD16		QVWDNYSVL
498			
499			
500			

501	VH CD16		QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSG MGVGWIRQPPGKALEWLAHIWWDDDKRYNPALK SRLTISKDTSKNQVVLTMTNMDPVDTATYYCAR TNPAWFAYWGQGTLVTVSS
502	VH CD16		QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSG MGVGWIRQPPGKALEWLAHIWWDDDKRYNPALK SRLTTSKDTSKNQVVLTNTNMDPVDTATYYCAQ TNPAWFAYWGQGTLVTVSS
503	VH CD16		QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSG VGVGWIRQPPGKALEWLAHIWWDDDKRYSPSLK SRLTISKDTSKNQVVLTMTNMDPVDTATYYCAR INPAYFAYWGQGTLVTVS
504	VH CD16		EVKLVESGGTLVKPGGSLKLSCAASGFTFNNYG MSWVRQTPEKRLEWVATISGGGSYTFYPDSVKG RFTISRDNAKNSLYLQMSSLRSEDTALYYCIRQ SARAPEPYWGQGTLVTVSS
505	VH CD16		EVQLVESGGGLVKPGGSLRLSCAASGFTFSNYG MSWVRQAPGKGLEWVATISGGGSYTFYPDSVKG RFTISRDNAKNSLYLQMNSLRTEDTALYYCVRQ SARAPEPYWGQGTLVTVSS
506	VH CD16		EVQLVESGGGLVKPGGSLRLSCAASGFTFSNYG MSWVRQAPGKGLEWVATISGGGSYTFYPDSVKG RFTISRDNAKNSLYLQMNSLRTEDTALYYCVRQ SANSPVPYWGQGTLVTVSS
507	VH CD16		EVQLQQSGPELVKPGASVKMSCKASGYTFTSSA MHWVKKNPGQGLEWIGYINHYNDGIKYNERFKG KATLTSDKSSSTAYMELSSLTSEDSAVYYCATG YRYASWFASWGQGTLVTVSS
508	VH CD16		QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSA MHWVRQAPGQGLEWMGYINHYNDGIKYNERFKG RVTITADKSTSTAYMELSSLRSEDTAVYYCATG YRYASWFASWGQGTLVTVSS
509	VH CD16		QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSA MHWVRQAPGQGLEWMGYINHYNDGIKYNERFKG RVTITADKSTSTAYMELSSLRSEDTAVYYCARG YRYASWFASWGQGTLVTVSS
510	VH CD16		EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYG MSWVRQAPGKGLEWIGSLYYSGGSTNYNPSLKG SLVISRDNSKNTLYLQMNSLAEDTATYYC ARESIDYWGQGTLVTVSS
511	VH CD16		EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYG MSWVRQAPGKGLEWIGEVNHSGGSTNYNPSLKG

			SFVISRDNSKNTLYLQMNSLAEDTAVYYCARVG SFDFWGQGTLVTVSS
512	VH CD16		QVQLVQSGAEVKKPGESLKVSCKASGYTFTSYY MHWVRQAPGQGLEWMGAIEPMYGSTSYAQKFQG RVTMTRDTSTSTVYMELSSLRSEDTAVYYCARG SAYYYDFADYWGQGTLVTVSS
513	VH CD16		QVQLVQSGAEVKKPGESLKVSCKASGYTFTSYY MHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQG RVTMTRDTSTSTVYMELSSLRSEDTAVYYCARG SAYYYDFADYWGQGTLVTVSS
514			
515			
516			
517	VL CD16		DIVMTQSPDSLAVSLGERATINCKASQSVDFDG DSFMNWYQQKPGQPPKLLIYTTSNLESGVPDRF SGSGSGTDFTLTISSLQAEDVAVYYCQQSNEDP YTFGQGTKLEIK
518	VL CD16		DIVMTQSPDSLAVSLGERATINCKSSQSVDFDG DSFMNWYQQKPGQPPKLLIYTTSSLESGVPDRF SGSGSGTDFTLTISSLQAEDVAVYYCQQSNSDP YTFGQGTKLEIK
519	VL CD16		DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTHV AWYQQKSGQSPKSLLYSASYRYSGVPDRFSGSG SGTDFTLTISNVQSEDLAEYFCQQYKSYPLTFG AGTKLELK
520	VL CD16		DIQMTQSPSFLSASVGDRVTITCRASQNVGTHV AWYQQKPGKAPKSLLYSASYRYSGVPSRFSGSG SGTDFTLTISSLQSEDIATYYCQQYKSYPLTFG QGTKLEIK
521	VL CD16		DIQMTQSPSFLSASVGDRVTITCRASQNVGTHV AWYQQKPGKAPKSLLYSASYRYSGVPSRFSGSG SGTDFTLTISSLQSEDIATYYCQDYTNYPLTFG QGTKLEIK
522	VL CD16		DILLTQSPAILSVSPGERVSFSCRASQNIGTSI HWYQQRTDGSPRLLIKSVSESISGIPSRFSGSG SGTDFTLTINGVESGDISDYYCQQSNSWPLTFG AGTKLELK
523	VL CD16		EIVLTQSPATLSVSPGERATLSCRASQNIGTSI HWYQQKPDQSPKLLIKSVSESISGVPSRFSGSG SGTDFTLTINSLEAEDFATYYCQQSNSWPLTFG QGTKLEIK

524	VL CD16		SYVLTQPSSVSVAPGQTATISCGGHNIGSKNVH WYQQRPGQSPVLVIYQDNKRPSGIPERFSGSNS GNTATLTISGTQAMDEADYYCQVWDNYSVLFGG GTKLTVL
525			
526			
527			
528	CDR-H1 NKp46	Chothia	GFSLSTYGI
529			
530			
531			
532	CDR-H1 NKp46	Kabat	TYGIGVG
533			
534			
535			
536	CDR-H2 NKp46	Chothia	WWNDN
537			
538			
539			
540	CDR-H2 NKp46	Kabat	HIWWNDNEYYNIDLKS
541			
542			
543			

544	CDR-H3 NKp46		GNYRYARGYVMDY
545			
546			
547			
548	CDR-L1 NKp46		RASESVEYYGTSLMQ
549			
550			
551			
552	CDR-L2 NKp46		AASNVES
553			
554			
555			
556	CDR-L3 NKp46		QQNRKVPWT
557			
558			
559			
560	VH NKp46		QVTLKESGPGILQPSQTLSLTCSFSGFSLSTYG IGVGWNRQPSGKGLEWLAHIWWNDNEYYNIDLK SRLTISKDTSNNQVFLKIASVDTADTATYYCVR GNYRYARGYVMDYWGQGTSVTVSS
561			
562			
563			

564	VL NKp46		DIVLTQSPASLAVSLGQRATISCRASESVEYYG TSLMQWYQQKPGQPPKLLIYAASNVESGVPARF SGSGSGTDFSLNIHPVEEDDFAMYFCQQNRKVP WTFGGGTKLEIK
565			
566			
567			
568	CDR-H1 NKp30	Chothia	GHTFTSY
569	CDR-H1 NKp30	Chothia	GGTFTSY
570	CDR-H1 NKp30	Chothia	GHTFTNY
571			
572			
573			
574	CDR-H1 NKp30	Kabat	SYFMH
575	CDR-H1 NKp30	Kabat	SYSVS
576	CDR-H1 NKp30	Kabat	NYYMH
577			
578			
579			
580	CDR-H2 NKp30	Chothia	NPSDDY

581	CDR-H2 NKp30	Chothia	VPIFGT
582	CDR-H2 NKp30	Chothia	NPNGGD
583			
584			
585			
586	CDR-H2 NKp30	Kabat	IINPSDDYANYAQKFQG
587	CDR-H2 NKp30	Kabat	GIVPIFGTADYAQKFQG
588	CDR-H2 NKp30	Kabat	VINPNGGDTSYAQKFQG
589			
590			
591			
592	CDR-H3 NKp30		AIFDY
593	CDR-H3 NKp30		GYSYGQTFDY
594	CDR-H3 NKp30		DRAWDYGGNVRAFDI
595			
596			
597			

598	CDR-L1 NKp30		RASQSISSYLN
599	CDR-L1 NKp30		RSSQSLLHSNGYNYLD
600			
601			
602			
603	CDR-L2 NKp30		AASSLQS
604	CDR-L2 NKp30		LGSNRAS
605			
606			
607			
608	CDR-L3 NKp30		QQSYSTPLT
609	CDR-L3 NKp30		MQALQTPYT
610			
611			
612			
613	VH NKp30		QVQLVQSGAEVKKPGASVKVSCKASGHTFTSYF MHWVRQAPGQGLEWMGIINPSDDYANYAQKFQG RVTMTRDTSTSTVYMELSSLRSEDTAVYYCATA IFDYWGQGTLVTVSS
614	VH NKp30		QVQLVQSGAEVKKPGASVKVSCKASGHTFTSYF MHWVRQAPGQGLEWMGIINPSDDYANYAQKFQG RVTMTRDTSTSTVYMELSSLRSEDTAVYYCATA IFDYWGQGTPVTVSS

615	VH NKp30		QVQLVQSGAEVKKPGASVKVSCKASGHTFTNYY MHWVRQAPGQGLEWMGVINPNGGDTSYAQKFQG RVTMTRDTSTSTVYMELSSLRSEDTAVYYCARD RAWDYGGNVRAFDIWGQGTMVTVSS
616	VH NKp30		QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSYS VSWVRQAPGQGLEWMGGIVPIFGTADYAQKFQG RVTITADESTSTAYMELSSLRSEDTAVYYCARG YSYGQTFDYWGQGTLVTVSS
617			
618			
619			
620			
621			
622			
623			
624	VL NKp30		DIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPLTFG GGTKVEIK
625	VL NKp30		DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSN GYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT PYTFGGGTKVEIK
626			
627			
628			
629	CD3ε Sequence		MQSGTHWRVLGLCLLSVGVWGQDGNEEMGGITQ TPYKVSISGTTVILTCPQYPGSEILWQHNDKNI GGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCY PRGSKPEDANFYLYLRARVCENCMEMDVMSVAT IVIVDICITGGLLLLVYYWSKNRKAKAKPVTRG AGAGGRQRGQNKERPPPVPNPDYEPIRKGQRDL YSGLNQRRI

630	CD16A Sequence		MWQLLLPTALLLLVSAGMRTEDLPKAVVFLEPQ WYRVLEKDSVTLKCQGAYSPEDNSTQWFHNESL ISSQASSYFIDAATVDDSGEYRCQTNLSTLSDP VQLEVHIGWLLLQAPRWVFKEEDPIHLRCHSWK NTALHKVTYLQNGKGRKYFHHNSDFYIPKATLK DSGSYFCRGL**F**GSKNVSSETVNITITQGLAVST ISSFFPPGYQVSFCLVMVLLFAVDTGLYFSVKT NIRSSTRDWKDHKFKWRKDPQDK
631	CD16B Sequence		MWQLLLPTALLLLVSAGMRTEDLPKAVVFLEPQ WYSVLEKDSVTLKCQGAYSPEDNSTQWFHNESL ISSQASSYFIDAATVNDSGEYRCQTNLSTLSDP VQLEVHIGWLLLQAPRWVFKEEDPIHLRCHSWK NTALHKVTYLQNGKDRKYFHHNSDFHIPKATLK DSGSYFCRGLVGSKNVSSETVNITITQGLAVST ISSFSPPGYQVSFCLVMVLLFAVDTGLYFSVKT NI
632	NKp46 Sequence		MSSTLPALLCVGLCLSQRISAQQQTLPKPFIWA EPHFMVPKEKQVTICCQGNYGAVEYQLHFEGSL FAVDRPKPPERINKVKFYIPDMNSRMAGQYSCI YRVGELWSEPSNLLDLVVTEMYDTPTLSVHPGP EVISGEKVTFYCRLDTATSMFLLLKEGRSSHVQ RGYGKVQAEFPLGPVTTAHRGTYRCFGSYNNHA WSFPSEPVKLLVTGDIENTSLAPEDPTFPADTW GTYLLTTETGLQKDHALWDHTAQNLLRMGLAFL VLVALVWFLVEDWLSRKRTRERASRASTWEGRR RLNTQTL
633	NKp46 Sequence		MSSTLPALLCVGLCLSQRISAQQQTLPKPFIWA EPHFMVPKEKQVTICCQGNYGAVEYQLHFEGSL FAVDRPKPPERINKVKFYIPDMNSRMAGQYSCI YRVGELWSEPSNLLDLVVTEMYDTPTLSVHPGP EVISGEKVTFYCRLDTATSMFLLLKEGRSSHVQ RGYGKVQAEFPLGPVTTAHRGTYRCFGSYNNHA WSFPSEPVKLLVTGDIENTSLAPEDPTFPDHAL WDHTAQNLLRMGLAFLVLVALVWFLVEDWLSRK RTRERASRASTWEGRRRLNTQTL

634	NKp46 Sequence		MSSTLPALLCVGLCLSQRISAQQQMYDTPTLSV HPGPEVISGEKVTFYCRLDTATSMFLLLKEGRS SHVQRGYGKVQAEFPLGPVTTAHRGTYRCFGSY NNHAWSFPSEPVKLLVTGDIENTSLAPEDPTFP ADTWGTYLLTTETGLQKDHALWDHTAQNLLRMG LAFLVLVALVWFLVEDWLSRKRTRERASRASTW EGRRRLNTQTL
635	NKp46 Sequence		MSSTLPALLCVGLCLSQRISAQQQMYDTPTLSV HPGPEVISGEKVTFYCRLDTATSMFLLLKEGRS SHVQRGYGKVQAEFPLGPVTTAHRGTYRCFGSY NNHAWSFPSEPVKLLVTGDIENTSLAPEDPTFP DHALWDHTAQNLLRMGLAFLVLVALVWFLVEDW LSRKRTRERASRASTWEGRRRLNTQTL
636	NKp46 Sequence		MSSTLPALLCVEMYDTPTLSVHPGPEVISGEKV TFYCRLDTATSMFLLLKEGRSSHVQRGYGKVQA EFPLGPVTTAHRGTYRCFGSYNNHAWSFPSEPV KLLVTGDIENTSLAPEDPTFPADTWGTYLLTTE TGLQKDHALWDHTAQNLLRMGLAFLVLVALVWF LVEDWLSRKRTRERASRASTWEGRRRLNTQTL
637	NKp46		MSSTLPALLCVGLCLSQRISAQQQTLPKPFIWA EPHFMVPKEKQVTICCQGNYGAVEYQLHFEGSL FAVDRPKPPERINKVKFYIPDMNSRMAGQYSCI YRVGELWSEPSNLLDLVVTEMYDTPTLSVHPGP EVISGEKVTFYCRLDTATSMFLLLKEGRSSHVQ RGYGKVQAEFPLGPVTTAHRGTYRCFGSYNNHA WSFPSEPVKLLVTGDIENTSLAPEDPTFPDTWG TYLLTTETGLQKDHALWDHTAQNLLRMGLAFLV LVALVWFLVEDWLSRKRTRERASRASTWEGRRR LNTQTL
638	NKp30 Sequence		MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGS SAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEV RNGTPEFRGRLAPLASSRFLHDHQAELHIRDVR GHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHP QLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGK CLTWKGPRRQLPAVVPAPLPPPCGSSAHLLPPV PGG

639	NKp30 Sequence		MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGS SAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEV RNGTPEFRGRLAPLASSRFLHDHQAELHIRDVR GHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHP QLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGK CHCHMGTHCHSSDGPRGVIPEPRCP
640	NKp30 Sequence		MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGS SAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEV RNGTPEFRGRLAPLASSRFLHDHQAELHIRDVR GHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHP QLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGK YAKSTLSGFPQL
641	NKp30		MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGS SAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEA ELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTR LVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVG STVYYQGKCLTWKGPRRQLPAVVPAPLPPPCGS SAHLLPPVPGG
642	NKp30		MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGS SAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEA ELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTR LVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVG STVYYQGKCHCHMGTHCHSSDGPRGVIPEPRCP
643	NKp30		MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGS SAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEA ELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTR LVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVG STVYYQGKYAKSTLSGFPQL

Claims:

1. A bispecific antigen binding construct comprising a binding domain capable of binding to an HLA-G epitope and an additional binding domain capable of binding to a second epitope.

2. The bispecific antigen binding construct according to claim 1, wherein the second epitope comprises a CD3ε epitope.

3. The bispecific antigen binding construct according to claim 2, wherein the CD3ε epitope comprises or consists of an amino acid sequence set forth in SEQ ID NO: 629.

4. The bispecific antigen binding construct according to any one of claims 2-3, wherein the additional binding domain capable of binding to a CD3ε epitope comprises or consists of a heavy chain variable region (VH) and a light chain variable region (VL), with VH and/or VL comprising 1, 2, 3, 4, 5, or 6 of the following:

a) a VHCDR1 having the sequence set forth in any one of SEQ ID NOS: 346-349 or 354-357,

b) a VHCDR2 having the sequence set forth in any one of SEQ ID NOS: 362-365 or 371-375,

c) a VHCDR3 having the sequence set forth in any one of SEQ ID NOS: 379-382,

d) a VLCDR1 having the sequence set forth in any one of SEQ ID NOS: 388-392,

e) a VLCDR2 having the sequence set forth in any one of SEQ ID NOS: 396-400, and

f) a VLCDR3 having the sequence set forth in any one of SEQ ID NOS: 404-408.

5. The bispecific antigen binding construct according to claim 1, wherein the additional binding domain comprises an NK cell engager, dendritic cell engager, monocyte, or macrophage engager.

6. The bispecific antigen binding construct according to claim 5, wherein the NK cell engager comprises an antibody for a CD16 epitope.

7. The bispecific antigen binding construct according to claim 5, wherein the NK cell engager comprises an antibody for NKp46.

8. The bispecific antigen binding construct according to claim 5, wherein the NK cell engager comprises an antibody for NKp30.

9. The bispecific antigen binding construct according to claim 5, wherein the monocyte or macrophage engager comprises an antibody for a CD16 epitope.

10. The bispecific antigen binding construct according to claim 1, wherein the HLA-G epitope comprises or consists of an amino acid sequence set forth in SEQ ID NO: 342.

11. The bispecific antigen binding construct according to any of claims 1-10, wherein the binding domain capable of binding to an HLA-G epitope comprises or consists of a heavy chain variable region (VH) and a light chain variable region (VL), with VH and/or VL comprising 1, 2, 3, 4, 5, or 6 of the following:

a) a VHCDR1 having the sequence set forth in any one of SEQ ID NOS: 1-14 or 18-34,

b) a VHCDR2 having the sequence set forth in any one of SEQ ID NOS: 38-50 or 54-71,

c) a VHCDR3 having the sequence set forth in any one of SEQ ID NOS: 76-101,

d) a VLCDR1 having the sequence set forth in any one of SEQ ID NOS: 105-124,

e) a VLCDR2 having the sequence set forth in any one of SEQ ID NOS: 128-145, and

f) a VLCDR3 having the sequence set forth in any one of SEQ ID NOS: 149-166.

12. The bispecific antigen binding construct according to any of claims 1-4, wherein the binding domain capable of binding to an HLA-G epitope comprises a heavy chain variable region (VH) and a light chain variable region (VL), with VH comprising, consisting of, or consisting essentially of a VH having the sequence set forth in SEQ ID NOS: 170-200 and with the VL comprising, consisting of, or consisting essentially of a VL having the sequence set forth in SEQ ID NO: 204-228 and the additional binding domain capable of binding to a CD3ε epitope comprises a heavy chain variable region (VH) and a light chain variable region (VL), with VH comprising, consisting of, or consisting essentially of a VH having the sequence set forth in SEQ ID NOS: 413-418 and with the VL comprising, consisting of, or consisting essentially of a VL having the sequence set forth in SEQ ID NOS: 422-427.

13. A pharmaceutical composition comprising or consisting of a bispecific antigen binding construct according to claims 1-12.

14. The pharmaceutical composition according to claim 13, further comprising an effective amount of one or more of:

a) an anti-PD-L1 antibody or small molecule inhibitor;

b) an anti-PD-1 antibody or small molecule inhibitor;

c) an anti-CD38 antibody or small molecule inhibitor;

d) an anti-CD39 antibody or small molecule inhibitor;

e) an anti-CD73 antibody or small molecule inhibitor;

f) an anti-A2A receptor antibody or small molecule inhibitor;

g) an anti-A2B receptor antibody or small molecule inhibitor;

h) an anti-A2A/A2B dual receptor antibody or small molecule inhibitor;

i) an anti-CD47 antibody or small molecule inhibitor;

j) an anti-CTLA-4 antibody or small molecule inhibitor;

k) an anti-LAG-3 antibody or small molecule inhibitor;

l) an anti-TIM-3 antibody or small molecule inhibitor;

m) an anti-TIGIT antibody or small molecule inhibitor;

n) an anti-VISTA antibody or small molecule inhibitor;

o) an anti-CD94 antibody or small molecule inhibitor;

p) a small molecule inhibitor;

q) an oncolytic virus;

r) a chemotherapy;

s) an adoptive cell therapy; and/or

t) ADCC capable therapies using effector competent antibodies such as anti-CD19, anti-CD20, anti-EGFR, anti-Her2, anti-SLAMF7, anti-CD52, anti-BCMA, anti-GD2, and/or anti-CCR4.

15. The pharmaceutical composition according to claim 13 or claim 14, further comprising one or both of:

a) an antibody to an immune inhibitory receptor or ligand and/or

b) an antibody to an immune stimulatory receptor or ligand.

16. One or more nucleic acids encoding the bispecific antigen binding constructs according to any one of claims 1-15.

17. One or more vectors comprising the one or more nucleic acids according to claim 16.

18. A host transformed with a vector according to claim 17.

19. A method for the production of one or more bispecific antigen binding construct comprising the steps of expressing one or more nucleic acids according to any of claims 16-18 in a prokaryotic or eukaryotic host cell and recovering the one or more bispecific antigen binding construct from the cell or the cell culture supernatant.

20. A method for treating a subject with cancer comprising administering a bispecific antigen binding construct or pharmaceutical composition according to any of claims 1-15 to the subject.

21. The method according to claim 20, wherein the cancer is a solid cancer.

22. The method according to claim 20, wherein the cancer is a hematological cancer.

23. The method according to claim 20, wherein the cancer is selected from the group consisting of a hematopeietic cancer, hepatocellular carcinoma, leukemia, colorectal cancer (CRC), breast cancer, gastric cancer, esophageal cancer, endometrial cancer, prostate cancer, bladder cancer, thyroid cancer, liver cancer, pancreatic cancer, triple negative breast cancer, cervical cancer, ovarian cancer, uterine cancer, vaginal cancer, vulvar cancer, lung cancer, head and neck cancer, melanoma, renal cell carcinoma, cutaneous squamous cell carcinoma, Hodgkin's lymphoma, a metastasis of the brain, a metastasis of the lung, a metastasis of the liver, and/or a metastasis of the bone, or an unresectable or metastatic solid tumor with DNA mismatch repair deficiencies or a microsatellite instability-high state.

24. The method according to any of claims 19-23, wherein the method further comprises one or more of the following:

a) administering chemotherapy to the subject;

b) administering radiation therapy to the subject; and/or

c) administering one or more additional therapeutic agents to the subject.

25. The method according to claim 24, wherein the one or more additional therapeutic agents comprise one or more immunomodulatory agents.

26. The method according to claim 25, wherein the one or more immunomodulatory agents comprise an antagonist to an inhibitory receptor of an immune cell.

27. The method according to claim 26, wherein the inhibitory receptor is at least one of LILRB1, LILRB2, LILRB4, KIR2DL4, CTLA-4, PD-1, PD-L1, PD-L2, LAG-3, Tim3, TIGIT, B7-H3, B7-H4, neuritin, BTLA, CECAM-1, CECAM-5, VISTA, LAIR1, CD160, 2B4, TGF-B receptor, NKG2A, and/or a Killer-cell immunoglobulin-like receptor (KIR).

28. The method according to claim 26, wherein the one or more immunomodulatory agents comprise an agonist of a co-stimulatory receptor of an immune cell.

29. The method according to claim 28, wherein the co-stimulatory receptor is at least one of OX40, CD2, CD27, ICAM-1, LFA-1, ICOS (CD278), 4-1BB (CD137), GITR, CD28, CD30, CD40, BAFFR, HVEM, CD7, LIGHT, NKG2C, SLAMF7, NKp30, NKp46, NKp80, CD160, and/or CD83.

30. The method according to claim 28, wherein the one or more immunomodulatory agents is one or more cytokines.

31. The method according to claim 30, wherein the one or more cytokines is at least one of G-CSF, GM-CSF, IFN-alpha, IFN-beta, IFN-gamma, FLt3 ligand, IL-1, IL-2, IL-5, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and/or IL-27.

32. The method according to claim 25, wherein the one or more immunomodulatory agents is one or more oncolytic viruses.

33. The method according to claim 32, wherein the one or more oncolytic viruses is a Herpes simplex virus, a Vesicular stomatitis virus, an adenovirus, a Newcastle disease virus, a vaccinia virus, and/or a maraba virus.

34. The method according to claim 25, wherein the one or more immunomodulatory agents is a chimeric antigen engineered T cell.