TREATMENT OF DISEASES RELATED TO COLONY-STIMULATING FACTOR 1 RECEPTOR DYSFUNCTION USING TREM2 AGONISTS

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of United States Provisional Application Nos. 63/061,315, filed August 5, 2020, and 63/129,852, filed December 23, 2020, the entirety of which are incorporated herein by reference.

TECHNICAL FIELD OF THE INVENTION

[0002] The present invention relates to compounds and methods of use thereof for treating diseases and disorders caused by colony-stimulating factor 1 receptor (CSF1R) dysfunction.

BACKGROUND OF THE INVENTION

[0003] Microglia are brain-resident macrophages with many homeostatic and injury responsive roles, including trophic and phagocytic functions. Mutations in a key microglia regulator, colony-stimulating factor 1 receptor (CSF1R), lead to microglia dysfunction and apoptosis and result in neurological and skeletal diseases and disorders. Adult-onset leukoencephalopathy with axonal spheroids and pigmented glia (ALSP), previously recognized as hereditary diffuse leukoencephalopathy with axonal spheroids (HDLS) or pigmentary orthochromatic leukodystrophy (POLD), is one such neurological condition characterized by cerebral white matter degeneration with demyelination and axonal spheroids leading to progressive cognitive and motor dysfunction which ultimately results in death. ALSP has been found to be caused by a heterozygous loss-of-function mutations in the CSF1R which occur predominantly in the kinase domain.

[0004] To date, there are no known treatments for diseases and disorders caused by CSF1R dysfunction, including ALSP, and patients are usually treated by managing the symptoms of the disease. Therefore, there remains a need in the art for methods of treating diseases and disorders caused by CSF1R dysfunction.

SUMMARY OF THE INVENTION

[0005] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with a dysfunction in CSF1R in a human patient, the method comprising administering to the patient an effective amount of a compound that increases the activity of triggering receptor expressed on myeloid cells 2 (TREM2). In some embodiments, the compound that increases the activity of TREM2 is an agonist of TREM2. In some embodiments, the agonist of TREM2 is a small molecule agonist of TREM2 or an antibody agonist of TREM2. In some embodiments, the disease or disorder caused by and/or associated with a dysfunction in CSF1R is ALSP.

BRIEF DESCRIPTION OF THE DRAWINGS

[0006] The drawings show embodiments of the disclosed subject matter for the purpose of illustrating the invention. However, it should be understood that the present application is not limited to the precised arrangements and embodiments shown in the drawings.

[0007] **FIGs. 1** and **2** are graphs showing a comparison of cellular confluence of human derived macrophages under M-CSF withdrawal conditions, after exposure to TREM2 agonist antibody Ab-3 or an isotype matched IgG control.

[0008] **FIGs. 3** and **4** are graphs showing a comparison of apoptosis levels in human derived macrophages under M-CSF withdrawal conditions, as measured by Caspase 3/7 staining, after exposure to TREM2 agonist antibody Ab-3 or an isotype matched IgG control.

[0009] **FIG. 5** is a graph showing a comparison of cellular confluence of human derived macrophages exposed to CSF1R small molecule inhibitor PLX5622, along with either TREM2 agonist antibody Ab-3 or an isotype matched IgG control.

[0010] **FIG. 6** is a graph showing a comparison of cellular morphology of human derived macrophages exposed to CSF1R small molecule inhibitor PLX5622, along with either TREM2 agonist antibody Ab-3 or an isotype matched IgG control.

[0011] **FIG. 7** is a graph showing a comparison of cell count for human derived macrophages exposed to CSF1R small molecule inhibitor PLX5622, along with either TREM2 agonist antibody Ab-3 or an isotype matched IgG control, showing that the changes in cellular confluence and cellular morphology observed in FIGs. 5 and 6 are not due to changes in overall cell count.

DETAILED DESCRIPTION OF CERTAIN EMBODIMENTS

TREM2, DAP12, CSF1-R and ALSP

[0012] TREM2 is a member of the Ig superfamily of receptors that is expressed on cells of myeloid lineage, including macrophages, dendritic cells, and microglia (Schmid *et al.,* Journal of Neurochemistry, Vol. 83: 1309-1320, 2002; Colonna, Nature Reviews Immunology, Vol. 3: 445-453, 2003; Kiialainen *et al.*, Neurobiology of Disease, 2005, 18: 314-322). TREM2 is an immune receptor that binds many endogenous substrates, including ApoE, LPS, exposed phospholipids, phosphatidylserine and amyloid beta and signals through a short intracellular domain that complexes with the adaptor protein DAP12, the cytoplasmic domain of which comprises an ITAM motif (Bouchon *et al.*, The Journal of Experimental Medicine, 2001, 194: 1111-1122). Upon activation of TREM2, tyrosine residues within the ITAM motif in DAP12 are phosphorylated by the Src family of kinases, providing docking sites for the tyrosine kinase ζ-chain-associated protein 70 (ZAP70) and spleen tyrosine kinase (Syk) via their SH2 domains (Colonna, Nature Reviews Immunology, 2003, 3:445-453; Ulrich and Holtzman, ACS Chem. Neurosci., 2016, 7:420-427). The ZAP70 and Syk kinases induce activation of several downstream signaling cascades, including phosphatidylinositol 3-kinase (PI3K), protein kinase C (PKC), extracellular regulated kinase (ERK), and elevation of intracellular calcium (Colonna, Nature Reviews Immunology, 2003, 3:445-453; Ulrich and Holtzman, ACS Chem. Neurosci., 2016, 7:420-427). The wild-type human TREM2 amino acid sequence is provided as SEQ ID NO: 1.

[0013] Human DAP12 is encoded by the *TYROBP* gene located on chromosome 19q13.1. The human protein is 113 amino acids in length and comprises a leader sequence (amino acids 1-27 of SEQ ID NO: 3), a short extracellular domain (amino acids 28-41 of SEQ ID NO: 3), a transmembrane domain (amino acids 42-65 of SEQ ID NO: 3) and a cytoplasmic domain (amino acids 66-113 of SEQ ID NO: 3) (Paradowska-Gorycka *et al.*, Human Immunology, 2013, 74: 730-737). DAP12 forms a homodimer through two cysteine residues in the short extracellular domain. The wild-type human DAP12 amino acid sequence (NCBI Reference Sequence: NP_003323.1) is provided as SEQ ID NO: 3.

[0014] TREM2 has been implicated in several myeloid cell processes, including phagocytosis, proliferation, survival, and regulation of inflammatory cytokine production (Ulrich

and Holtzman, ACS Chem. Neurosci., 2016, 7: 420-427). In the last few years, TREM2 has been linked to several diseases. For instance, mutations in both TREM2 and DAP12 have been linked to the autosomal recessive disorder Nasu-Hakola Disease, which is characterized by bone cysts, muscle wasting and demyelination phenotypes (Guerreiro *et al.*, New England Journal of Medicine, 2013, 368: 117-127). More recently, variants in the *TREM2* gene have been linked to increased risk for Alzheimer's disease (AD) and other forms of dementia including frontotemporal dementia and amyotrophic lateral sclerosis (Jonsson *et al.*, New England Journal of Medicine, 2013, 368:107-116; Guerreiro *et al.*, JAMA Neurology, 2013, 70:78-84; Jay *et al.*, Journal of Experimental Medicine, 2015, 212: 287-295; Cady et al, JAMA Neurol. 2014 Apr;71(4):449-53). In particular, the R47H variant has been identified in genome-wide studies as being associated with increased risk for late-onset AD with an overall adjusted odds ratio (for populations of all ages) of 2.3, second only to the strong genetic association of ApoE to Alzheimer's. The R47H mutation resides on the extracellular Ig V-set domain of the TREM2 protein and has been shown to impact lipid binding and uptake of apoptotic cells and Abeta (Wang *et al.*, Cell, 2015, 160: 1061-1071; Yeh *et al.*, Neuron, 2016, 91: 328-340), suggestive of a loss-of-function linked to disease. Further, postmortem comparison of AD patients' brains with and without the R47H mutation are supportive of a novel loss-of-microglial barrier function for the carriers of the mutation, with the R47H carrier microglia putatively demonstrating a reduced ability to compact plaques and limit their spread (Yuan *et al.*, Neuron, 2016, 90: 724-739). Impairment in microgliosis has been reported in animal models of prion disease, multiple sclerosis, and stroke, suggesting that TREM2 may play an important role in supporting microgliosis in response to pathology or damage in the central nervous system (Ulrich and Holtzman, ACS Chem. Neurosci., 2016, 7: 420-427).

[0015] CSF1R is a cell-surface receptor primarily for the cytokine colony stimulating factor 1 (CSF-1), also known until recently as macrophage colony-stimulating factor (M-CSF), which regulates the survival, proliferation, differentiation and function of mononuclear phagocytic cells, including microglia of the central nervous system. CSF1R is composed of a highly glycosylated extracellular ligand-binding domain, a trans-membrane domain and an intracellular tyrosine-kinase domain. Binding of CSF-1 to CSF1R results in the formation of receptor homodimers and subsequent auto-phosphorylation of several tyrosine residues in the cytoplasmic domain, notably Syk. In the brain, CSF1R is predominantly expressed in microglial cells. It has been found that

microglia in CSF1R +/- patients are depleted and show increased apoptosis (Oosterhof et al., 2018).

[0016] The present invention relates to the unexpected discovery that administration of a TREM2 agonist can rescue the loss of microglia in cells having mutations in CSF1R. It has been previously shown that TREM2 agonist antibody 4D9 increases ATP luminescence (a measure of cell number and activity) in a dose dependent manner when the levels of M-CSF in media are reduced to 5 ng/mL (Schlepckow et al, EMBO Mol Med., 2020) and that TREM2 agonist AL002c increases ATP luminescence when M-CSF is completely removed from the media (Wang et al, J. Exp. Med.; 2020, 217(9): e20200785). This finding suggests that TREM2 agonism can compensate for deficiency in CSF1R signaling caused by a decrease in the concentration of its ligand. In a 5xFAD murine Alzheimer's disease model of amyloid pathology, doses of a CSF1R inhibitor that almost completely eliminate microglia in the brains of wild-type animals show surviving microglia clustered around the amyloid plaques (Spangenberg et al, Nature Communications 2019). Plaque amyloid has been demonstrated in the past to be a ligand for TREM2, and it has been shown that microglial engagement with amyloid is dependent on TREM2 (Condello et al, Nat Comm., 2015). The present invention relates to the unexpected discovery that it is activation of TREM2 that rescued the microglia in the presence of the CSF1R inhibitor, and that this effect is also observed in patients suffering from loss of microglia due to CSF1R mutation. This discovery has not been previously taught or suggested in the available art.

[0017] To date, no prior study has shown that TREM2 agonism can rescue the loss of microglia in cells where mutations in the CSF1R kinase domain reduce CSF1R activity, rather than the presence of a CSF1R inhibitor or a deficiency in CSF1R ligand. Furthermore, no prior study has taught or suggested that reversal of the loss of microglia due to a CSF1R mutation through TREM2 agonism can be used to treat a disease or disorder caused by and/or associated with a CSF1R mutation.

[0018] Adult-onset leukoencephalopathy with axonal spheroids and pigmented glia (ALSP), previously recognized as hereditary diffuse leukoencephalopathy with axonal spheroids (HDLS) or pigmentary orthochromatic leukodystrophy (POLD), is an autosomal-dominant central nervous system disease that manifests in the form of variable behavioral, cognitive and motor function changes in patients suffering from the disease. ALSP is characterized by patchy cerebral white

matter abnormalities visible by magnetic resonance imaging. However, the clinical symptoms and MRI changes are not specific to ALSP and are common for other neurological conditions, including Nasu-Hakola disease (NHD) and AD, making diagnosis and treatment of ALSP very difficult.

[0019] Recent studies have discovered that ALSP is a Mendelian disorder in which patients carry a heterozygous loss of function mutation in the kinase domain of CSF1R, suggesting a reduced level of signaling on the macrophage colony-stimulating factor (M-CSF) / CSF1R axis (Rademakers et al, Nat Genet 2012; Konno et al, Neurology 2018). In one aspect, the present invention relates to the surprising discovery that activation of the TREM2 pathway can rescue the loss of microglia in CSF1R +/- ALSP patients, preventing microglia apoptosis, thereby treating the ALSP condition.

[0020] The present invention also relates to the surprising discovery that neurofilament light chain and neurofilament heavy chain proteins can serve as a therapeutic biomarker to determine treatment efficacy in patients suffering from a disease or disorder caused by and/or associated with a CSF1R dysfunction, such as ALSP. Neurofilament light chain (NfL) is highly elevated in the plasma and serum of patients with ALSP, particularly those with symptoms but also in carriers of these mutations that do not yet show symptoms (Hayer et al, American Academy of Neurology 2018). ALSP is characterized by severe and rapid myelin breakdown followed by neurodegeneration. Mice exposed to cuprizone, a model of acute demyelination, show elevations in plasma NfL (Taylor Meadows et al, European Charcot Foundation 25th Annual Meeting; November 30–December 2, 2017; Baveno, Italy). Additionally, TREM2 knockout mice exposed to cuprizone show increased neurotoxicity and further increases in plasma and CSF NfL (Nugent et al, Neuron; 2020, 105(5): 837-854; O'Loughlin et al, Poster #694 ADPD Symposium, Lisbon Portugal, April 2019.) It has also been demonstrated that microglia are indeed depleted when a CSF1R inhibitor is dosed in the cuprizone model, and that this leads to a quantitative increase in the myelin debris and axonal pathology observed in these mice (Beckmann et al. Acta Neuropathologica Communications (2018)). Patients with ALSP have quantitatively fewer microglia than healthy individuals in multiple regions of the brain (Oosterhof et al., 2018, Cell Reports 24, 1203–1217). Beckmann, et al. did not measure the plasma/serum products of neurofilament degradation, but showed reduced staining for neurofilament centrally. Central neurofilament stain was reduced in mice dosed with cuprizone and further reduced with mice

dosed with cuprizone on the background of microglia depleted by concomitant administration of a CSF1R inhibitor. The present invention relates to the unexpected discovery that neurofilament is broken down in the neurons of animals suffering from a disease or disorder caused by and/or associated with a CSF1R dysfunction, such as ALSP, resulting in an increase in neurofilament breakdown products in the plasma, serum and cerebral spinal fluid (CSF), and that efficacy of treatment of the dieasese or disorder with a TREM2 agonist can be determined by measuring central levels of neurofilament and central nervous system (CNS), plasma and serum levels of its degradation products, namely neurofilament light chain and neurofilament heavy chain proteins. In one aspect, the present invention provides methods for selecting ALSP patients that are likely to experience progression of their neurodegenerative or other disease phenotypes based on neurofilament light chain or neurofilament heavy chain levels, thereby informing the timing of treatment with a TREM2 agonist.

[0021] The present invention also relates to the surprising discovery that soluble TREM2 (sTREM2) and soluble CSF1R (sCSF1R) can serve as therapeutic biomarkers for determining treatment efficacy in patients suffering from a disease or disorder caused by and/or associated with a CSF1R dysfunction, such as ALSP. It has been shown that TREM2 agonist antibody AL002 causes a dose-dependent decrease in cerebrospinal fluid concentration of sTREM2 and an increase in sCSF1R concentration (Wang et al, J. Exp. Med.; 2020, 217(9): e20200785). In one aspect, the present invention provides methods of selecting patients that are likely to experience progression of their neurodegenerative or other disease phenotypes based on concentrations of sTREM2 and sCSF1R, thereby informing the timing of treatment with a TREM2 agonist.

Definitions

[0022] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art. Accordingly, the following terms are intended to have the following meanings.

[0023] "Agonist" or an "activating" agent, such as a compound or antibody, is an agent that induces (e.g., increases) one or more activities or functions of the target (e.g., TREM2) of the agent after the agent binds the target.

[0024] "Antagonist" or a "blocking" agent, such as a compound or antibody, is an agent that reduces or eliminates (e.g., decreases) binding of the target to one or more ligands after the agent

binds the target, and/or that reduces or eliminates (e.g., decreases) one or more activities or functions of the target after the agent binds the target. In some embodiments, antagonist agent, or blocking agent substantially or completely inhibits target binding to one or more of its ligand and/or one or more activities or functions of the target.

[0025] "Antibody" is used in the broadest sense and refers to an immunoglobulin or fragment thereof, and encompasses any such polypeptide comprising an antigen-binding fragment or region of an antibody. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon and mu constant region genes, as well as myriad immunoglobulin variable region genes. Light chains are generally classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Immunoglobulin classes may also be further classified into subclasses, including IgG subclasses IgG_1, IgG_2, IgG_3, and IgG_4; and IgA subclasses IgA_1 and IgA_2. The term includes, but is not limited to, polyclonal, monoclonal, monospecific, multispecific (e.g., bispecific antibodies), natural, humanized, human, chimeric, synthetic, recombinant, hybrid, mutated, grafted, antibody fragments (e.g., a portion of a full-length antibody, generally the antigen binding or variable region thereof, e.g., Fab, Fab', F(ab')2, and Fv fragments), and in vitro generated antibodies so long as they exhibit the desired biological activity. The term also includes single chain antibodies, e.g., single chain Fv (sFv or scFv) antibodies, in which a variable heavy and a variable light chain are joined together (directly or through a peptide linker) to form a continuous polypeptide.

[0026] "Isolated" refers to a change from a natural state, that is, changed and/or removed from its original environment. For example, a polynucleotide or polypeptide (e.g., an antibody) is isolated when it is separated from material with which it is naturally associated in the natural environment. Thus, an "isolated antibody" is one which has been separated and/or recovered from a component of its natural environment.

[0027] "Purified antibody" refers to an antibody preparation in which the antibody is at least 80% or greater, at least 85% or greater, at least 90% or greater, at least 95% or greater by weight as compared to other contaminants (e.g., other proteins) in the preparation, such as by determination using SDS-polyacrylamide gel electrophoresis (PAGE) or capillary electrophoresis- (CE) SDS under reducing or non-reducing conditions.

[0028] "Extracellular domain" and "ectodomain" are used interchangeably when used in reference to a membrane bound protein and refer to the portion of the protein that is exposed on the extracellular side of a lipid membrane of a cell.

[0029] "Binds specifically" in the context of any binding agent, e.g., an antibody, refers to a binding agent that binds specifically to an antigen or epitope, such as with a high affinity, and does not significantly bind other unrelated antigens or epitopes.

[0030] "Functional" refers to a form of a molecule which possesses either the native biological activity of the naturally existing molecule of its type, or any specific desired activity, for example as judged by its ability to bind to ligand molecules. Examples of "functional" polypeptides include an antibody binding specifically to an antigen through its antigen-binding region.

[0031] "Antigen" refers to a substance, such as, without limitation, a particular peptide, protein, nucleic acid, or carbohydrate which can bind to a specific antibody.

[0032] "Epitope" or "antigenic determinant" refers to that portion of an antigen capable of being recognized and specifically bound by a particular antibody. When the antigen is a polypeptide, epitopes can be formed from contiguous amino acids and/or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Linear epitope is an epitope formed from contiguous amino acids on the linear sequence of amino acids. A linear epitope may be retained upon protein denaturing. Conformational or structural epitope is an epitope composed of amino acid residues that are not contiguous and thus comprised of separated parts of the linear sequence of amino acids that are brought into proximity to one another by folding of the molecule, such as through secondary, tertiary, and/or quaternary structures. A conformational or structural epitope may be lost upon protein denaturation. In some embodiments, an epitope can comprise at least 3, and more usually, at least 5 or 8-10 amino acids in a unique spatial conformation. Thus, an epitope as used herein encompasses a defined epitope in which an antibody binds only portions of the defined epitope. There are many methods known in the art for mapping and characterizing the location of epitopes on proteins, including solving the crystal structure of an antibody-antigen complex, competition assays, gene fragment expression assays, mutation assays, and synthetic peptide-based assays, as described, for example, in Using Antibodies: A Laboratory Manual, Chapter 11, Harlow and Lane, eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1999).

[0033] "Protein," "polypeptide," or "peptide" denotes a polymer of at least two amino acids covalently linked by an amide bond, regardless of length or post-translational modification (e.g., glycosylation, phosphorylation, lipidation, myristoylation, ubiquitination, etc.). Included within this definition are D- and L-amino acids, and mixtures of D- and L-amino acids. Unless specified otherwise, the amino acid sequences of a protein, polypeptide, or peptide are displayed herein in the conventional N-terminal to C-terminal orientation.

[0034] "Polynucleotide" and "nucleic acid" are used interchangeably herein and refer to two or more nucleosides that are covalently linked together. The polynucleotide may be wholly comprised of ribonucleosides (i.e., an RNA), wholly comprised of 2' deoxyribonucleotides (i.e., a DNA) or mixtures of ribo- and 2' deoxyribonucleosides. The nucleosides will typically be linked together by sugar-phosphate linkages (sugar-phosphate backbone), but the polynucleotides may include one or more non-standard linkages. Non-limiting example of such non-standard linkages include phosphoramidates, phosphorothioates, and amides (see, e.g., Eckstein, F., Oligonucleotides and Analogues: A Practical Approach, Oxford University Press (1992)).

[0035] "Operably linked" or "operably associated" refers to a situation in which two or more polynucleotide sequences are positioned to permit their ordinary functionality. For example, a promoter is operably linked to a coding sequence if it is capable of controlling the expression of the sequence. Other control sequences, such as enhancers, ribosome binding or entry sites, termination signals, polyadenylation sequences, and signal sequences are also operably linked to permit their proper function in transcription or translation.

[0036] "Amino acid position" and "amino acid residue" are used interchangeably to refer to the position of an amino acid in a polypeptide chain. In some embodiments, the amino acid residue can be represented as "XN", where X represents the amino acid and the N represents its position in the polypeptide chain. Where two or more variations, e.g., polymorphisms, occur at the same amino acid position, the variations can be represented with a "/" separating the variations. A substitution of one amino acid residue with another amino acid residue at a specified residue position can be represented by XNY, where X represents the original amino acid, N represents the position in the polypeptide chain, and Y represents the replacement or substitute amino acid. When the terms are used to describe a polypeptide or peptide portion in reference to a larger polypeptide or protein, the first number referenced describes the position where the polypeptide or peptide

begins (i.e., amino end) and the second referenced number describes where the polypeptide or peptide ends (i.e., carboxy end).

[0037] "Polyclonal" antibody refers to a composition of different antibody molecules which is capable of binding to or reacting with several different specific antigenic determinants on the same or on different antigens. A polyclonal antibody can also be considered to be a "cocktail of monoclonal antibodies." The polyclonal antibodies may be of any origin, e.g., chimeric, humanized, or fully human.

[0038] "Monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Each monoclonal antibody is directed against a single determinant on the antigen. In some embodiments, monoclonal antibodies to be used in accordance with the present disclosure can be made by the hybridoma method described by Kohler et al., 1975, Nature 256:495-7, or by recombinant DNA methods. The monoclonal antibodies can also be isolated, e.g., from phage antibody libraries.

[0039] "Chimeric antibody" refers to an antibody made up of components from at least two different sources. A chimeric antibody can comprise a portion of an antibody derived from a first species fused to another molecule, e.g., a portion of an antibody derived from a second species. In some embodiments, a chimeric antibody comprises a portion of an antibody derived from a non-human animal, e.g., mouse or rat, fused to a portion of an antibody derived from a human. In some embodiments, a chimeric antibody comprises all or a portion of a variable region of an antibody derived from a non-human animal fused to a constant region of an antibody derived from a human.

[0040] "Humanized antibody" refers to an antibody that comprises a donor antibody binding specificity, e.g., the CDR regions of a donor antibody, such as a mouse monoclonal antibody, grafted onto human framework sequences. A "humanized antibody" typically binds to the same epitope as the donor antibody.

[0041] "Fully human antibody" or "human antibody" refers to an antibody that comprises human immunoglobulin protein sequences only. A fully human antibody may contain murine

carbohydrate chains if produced in a non-human cell, e.g., a mouse, in a mouse cell, or in a hybridoma derived from a mouse cell.

[0042] "Full-length antibody," "intact antibody" or "whole antibody" are used interchangeably to refer to an antibody, such as an anti-TREM2 antibody of the present disclosure, in its substantially intact form, as opposed to an antibody fragment. Specifically whole antibodies include those with heavy and light chains including an Fc region. The constant domains may be native sequence constant domains (e.g. , human native sequence constant domains) or amino acid sequence variants thereof. In some cases, the intact antibody may have one or more effector functions.

[0043] "Antibody fragment" or "antigen-binding moiety" refers to a portion of a full length antibody, generally the antigen binding or variable domain thereof. Examples of antibody fragments include Fab, Fab', F(ab')2, and Fv fragments; diabodies; linear antibodies; single-chain antibodies; and multispecific antibodies formed from antibody fragments that bind two or more different antigens. Several examples of antibody fragments containing increased binding stoichiometries or variable valencies (2, 3 or 4) include triabodies, trivalent antibodies and trimerbodies, tetrabodies, tandAbs®, di-diabodies and $(sc(Fv)2)_2$ molecules, and all can be used as binding agents to bind with high affinity and avidity to soluble antigens (see, e.g., Cuesta et al., 2010, Trends Biotech. 28:355-62).

[0044] "Single-chain Fv" or "sFv" antibody fragment comprises the VH and VL domains of an antibody, where these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, Vol. 113, pp. 269-315, Rosenberg and Moore, eds., Springer-Verlag, New York (1994).

[0045] "Diabodies" refers to small antibody fragments with two antigen-binding sites, which comprise a heavy chain variable domain (VH) connected to a light chain variable domain (VL) in the same polypeptide chain (VH - VL). By using a linker that is short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites.

[0046] "Antigen binding domain" or "antigen binding portion" refers to the region or part of the antigen binding molecule that specifically binds to and complementary to part or all of an antigen. In some embodiments, an antigen binding domain may only bind to a particular part of the antigen (e.g., an epitope), particularly where the antigen is large. An antigen binding domain may comprise one or more antibody variable regions, particularly an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH), and particularly the complementarity determining regions (CDRs) on each of the VH and VL chains.

[0047] "Variable region" and "variable domain" are used interchangeably to refer to the polypeptide region that confers the binding and specificity characteristics of each particular antibody. The variable region in the heavy chain of an antibody is referred to as "VH" while the variable region in the light chain of an antibody is referred to as "VL". The major variability in sequence is generally localized in three regions of the variable domain, denoted as "hypervariable regions" or "CDRs" in each of the VL region and VH region, and forms the antigen binding site. The more conserved portions of the variable domains are referred to as the framework region FR.

[0048] "Complementarity-determining region" and "CDR" are used interchangeably to refer to non-contiguous antigen binding regions found within the variable region of the heavy and light chain polypeptides of an antibody molecule. In some embodiments, the CDRs are also described as "hypervariable regions" or "HVR". Generally, naturally occurring antibodies comprise six CDRs, three in the VH (referred to as: CDR H1 or H1; CDR H2 or H2; and CDR H3 or H3) and three in the VL (referred to as: CDR L1 or L1; CDR L2 or L2; and CDR L3 or L3). The CDR domains have been delineated using various approaches, and it is to be understood that CDRs defined by the different approaches are to be encompassed herein. The "Kabat" approach for defining CDRs uses sequence variability and is the most commonly used (Kabat et al., 1991, "Sequences of Proteins of Immunological Interest, 5th Ed." NIH 1:688-96). "Chothia" uses the location of structural loops (Chothia and Lesk, 1987, J Mol Biol. 196:901-17). CDRs defined by "AbM" are a compromise between the Kabat and Chothia approach, and can be delineated using Oxford Molecular AbM antibody modeling software (see, Martin et al., 1989, Proc. Natl Acad Sci USA. 86:9268; see also, world wide web www.bioinf-org.uk/abs). The "Contact" CDR delineations are based on analysis of known antibody-antigen crystal structures (see, e.g.,

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MacCallum et al., 1996, J. Mol. Biol. 262, 732-45). The CDRs delineated by these methods typically include overlapping or subsets of amino acid residues when compared to each other.

[0049] It is to be understood that the exact residue numbers which encompass a particular CDR will vary depending on the sequence and size of the CDR, and those skilled in the art can routinely determine which residues comprise a particular CDR given the amino acid sequence of the variable region of an antibody.

[0050] Kabat, supra, also defined a numbering system for variable domain sequences that is applicable to any antibody. The Kabat numbering system is generally used when referring to a residue in the variable domain (approximately residues 1-107 of the light chain and residues 1-113 of the heavy chain) (e.g., Kabat et al., Sequences of Immunological Interest. 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). The "EU or, Kabat numbering system" or "EU index" is generally used when referring to a residue in an immunoglobulin heavy chain constant region (e.g. , the EU index reported in Kabat et al., supra). The "EU index as in Kabat" refers to the residue numbering of the human IgGl EU antibody. References to residue numbers in the variable domain of antibodies means residue numbering by the Kabat numbering system. References to residue numbers in the constant domain of antibodies means residue numbering by the EU or, Kabat numbering system {e.g., see United States Patent Publication No. 2010-280227). One of skill in the art can assign this system of "Kabat numbering" to any variable domain sequence. Accordingly, unless otherwise specified, references to the number of specific amino acid residues in an antibody or antigen binding fragment are according to the Kabat numbering system.

[0051] "Framework region" or "FR region" refers to amino acid residues that are part of the variable region but are not part of the CDRs (e.g., using the Kabat, Chothia or AbM definition). The variable region of an antibody generally contains four FR regions: FR1, FR2, FR3 and FR4. Accordingly, the FR regions in a VL region appear in the following sequence: FR_L1-CDR L1-FR_L2-CDR L2-FR_L3-CDR L3-FR_L4, while the FR regions in a VH region appear in the following sequence: $FR1_H$-CDR H1-FR_H2-CDR H2-FR_H3-CDR H3-FR_H4.

[0052] "Constant region" or "constant domain" refers to a region of an immunoglobulin light chain or heavy chain that is distinct from the variable region. The constant domain of the heavy chain generally comprises at least one of: a CH1 domain, a Hinge (e.g., upper, middle, and/or

lower hinge region), a CH2 domain, and a CH3 domain. In some embodiments, the antibody can have additional constant domains CH4 and/or CH5. In some embodiments, an antibody described herein comprises a polypeptide containing a CH1 domain; a polypeptide comprising a CH1 domain, at least a portion of a Hinge domain, and a CH2 domain; a polypeptide comprising a CH1 domain and a CH3 domain; a polypeptide comprising a CH1 domain, at least a portion of a Hinge domain, and a CH3 domain, or a polypeptide comprising a CH1 domain, at least a portion of a Hinge domain, a CH2 domain, and a CH3 domain. In some embodiments, the antibody comprises a polypeptide which includes a CH3 domain. The constant domain of a light chain is referred to a CL, and in some embodiments, can be a kappa or lambda constant region. However, it will be understood by one of ordinary skill in the art that these constant domains (e.g., the heavy chain or light chain) may be modified such that they vary in amino acid sequence from the naturally occurring immunoglobulin molecule.

[0053] "Fc region" or "Fc portion" refers to the C terminal region of an immunoglobulin heavy chain. The Fc region can be a native-sequence Fc region or a non-naturally occurring variant Fc region. Generally, the Fc region of an immunoglobulin comprises constant domains CH2 and CH3. Although the boundaries of the Fc region can vary, in some embodiments, the human IgG heavy chain Fc region can be defined to extend from an amino acid residue at position C226 or from P230 to the carboxy terminus thereof. In some embodiments, the "CH2 domain" of a human IgG Fc region, also denoted as "Cγ2", generally extends from about amino acid residue 231 to about amino acid residue 340. In some embodiments, N-linked carbohydrate chains can be interposed between the two CH2 domains of an intact native IgG molecule. In some embodiments, the CH3 domain" of a human IgG Fc region comprises residues C-terminal to the CH2 domain, e.g., from about amino acid residue 341 to about amino acid residue 447 of the Fc region. A "functional Fc region" possesses an "effector function" of a native sequence Fc region. Exemplary Fc "effector functions" include, among others, Clq binding; complement dependent cytotoxicity (CDC); Fc receptor binding; antibody dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell-surface receptors (e.g., LT receptor); etc. Such effector functions generally require the Fc region to be combined with a binding domain (e.g., an antibody variable domain) and can be assessed using various assays known in the art.

[0054] "Native sequence Fc region" comprises an amino acid sequence identical to the amino acid sequence of an Fc region found in nature. Native sequence human Fc regions include a native sequence human IgGl Fc region (non-A and A allotypes); native sequence human IgG2 Fc region; native sequence human IgG3 Fc region; and native sequence human IgG4 Fc region as well as naturally occurring variants thereof.

[0055] "Variant Fc region" comprises an amino acid sequence which differs from that of a native sequence Fc region by virtue of at least one amino acid modification, preferably one or more amino acid substitution(s). Preferably, the variant Fc region has at least one amino acid substitution compared to a native sequence Fc region or to the Fc region of a parent polypeptide, e.g. from about one to about ten amino acid substitutions, and preferably from about one to about five amino acid substitutions in a native sequence Fc region or in the Fc region of the parent polypeptide. The variant Fc region herein will preferably possess at least about 80% homology with a native sequence Fc region and/or with an Fc region of a parent polypeptide, and most preferably at least about 90% homology therewith, more preferably at least about 95% homology therewith.

[0056] "Affinity–matured" antibody, such as an affinity matured anti-TREM2 antibody of the present disclosure, is one with one or more alterations in one or more HVRs thereof that result in an improvement in the affinity of the antibody for antigen, compared to a parent antibody that does not possess those alteration(s). In one embodiment, an affinity-matured antibody has nanomolar or even picomolar affinities for the target antigen. Affinity-matured antibodies are produced by procedures known in the art. For example, Marks et al., Bio/Technology, 1992, 10:779-783 describes affinity maturation by VH- and VL-domain shuffling. Random mutagenesis of HVR and/or framework residues is described by, for example: Barbas et al., Proc Nat. Acad. Sci. USA., 1994, 91:3809-3813; Schier et al. Gene, 1995, 169: 147-155; Yelton et al., Immunol., 1995, 155: 1994-2004; Jackson et al., Immunol., 1995, 154(7):3310-9; and Hawkins et al, J. Mol. Biol., 1992, 226:889-896.

[0057] "Binding affinity" refers to strength of the sum total of noncovalent interactions between a ligand and its binding partner. In some embodiments, binding affinity is the intrinsic affinity reflecting a one-to-one interaction between the ligand and binding partner. The affinity is

generally expressed in terms of equilibrium association (K_A) or dissociation constant (K_D), which are in turn reciprocal ratios of dissociation (k_{off}) and association rate constants (k_{on}).

[0058] "Percent (%) sequence identity" and "percentage sequence homology" are used interchangeably herein to refer to comparisons among polynucleotides or polypeptides, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise gaps as compared to the reference sequence for optimal alignment of the two sequences. The percentage may be calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Alternatively, the percentage may be calculated by determining the number of positions at which either the identical nucleic acid base or amino acid residue occurs in both sequences or a nucleic acid base or amino acid residue is aligned with a gap to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Those of skill in the art appreciate that there are many established algorithms available to align two sequences. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman, 1981, Adv Appl Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch, 1970, J Mol Biol. 48:443, by the search for similarity method of Pearson and Lipman, 1988, Proc Natl Acad Sci USA. 85:2444-8, and particularly by computerized implementations of these algorithms (e.g., BLAST, ALIGN, GAP, BESTFIT, FASTA, and TFASTA; see, e.g., Mount, D.W., Bioinformatics: Sequence and Genome Analysis, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (2013))

[0059] Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0, FASTDB, or ALIGN algorithms, which are publically available (e.g., NCBI: National Center for Biotechnology Information). Those skilled in the art can determine appropriate parameters for aligning sequences. For example, the BLASTN program (for nucleotide sequences) can use as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. Comparison of amino acid

sequences using BLASTP can use as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff, 1989, Proc Natl Acad Sci USA. 89:10915-9).

[0060] "Amino acid substitution" refers to the replacement of one amino acid in a polypeptide with another amino acid. A "conservative amino acid substitution" refers to the interchangeability of residues having similar side chains, and thus typically involves substitution of the amino acid in the polypeptide with amino acids within the same or similar defined class of amino acids. By way of example and not limitation, an amino acid with an aliphatic side chain may be substituted with another aliphatic amino acid, e.g., alanine, valine, leucine, isoleucine, and methionine; an amino acid with hydroxyl side chain is substituted with another amino acid with a hydroxyl side chain, e.g., serine and threonine; an amino acid having aromatic side chains is substituted with another amino acid having an aromatic side chain, e.g., phenylalanine, tyrosine, tryptophan, and histidine; an amino acid with a basic side chain is substituted with another amino acid with a basic side chain, e.g., lysine, arginine, and histidine; an amino acid with an acidic side chain is substituted with another amino acid with an acidic side chain, e.g., aspartic acid or glutamic acid; and a hydrophobic or hydrophilic amino acid is replaced with another hydrophobic or hydrophilic amino acid, respectively.

[0061] "Amino acid insertion" refers to the incorporation of at least one amino acid into a predetermined amino acid sequence. An insertion can be the insertion of one or two amino acid residues; however, larger insertions of about three to about five, or up to about ten or more amino acid residues are contemplated herein.

[0062] "Amino acid deletion" refers to the removal of one or more amino acid residues from a predetermined amino acid sequence. A deletion can be the removal of one or two amino acid residues; however, larger deletions of about three to about five, or up to about ten or more amino acid residues are contemplated herein.

[0063] "Subject" refers to a mammal, including, but not limited to humans, non-human primates, and non-primates, such as goats, horses, and cows. In some embodiments, the terms "subject" and "patient" are used interchangeably herein in reference to a human subject.

[0064] "Therapeutically effective dose" or "therapeutically effective amount" or "effective dose" refers to that quantity of a compound, including a biologic compound, or pharmaceutical

composition that is sufficient to result in a desired activity upon administration to a mammal in need thereof. As used herein, with respect to the pharmaceutical compositions comprising an antibody, the term “therapeutically effective amount/dose” refers to the amount/dose of the antibody or pharmaceutical composition thereof that is sufficient to produce an effective response upon administration to a mammal.

[0065] “Pharmaceutically acceptable” refers to compounds or compositions which are generally safe, non-toxic and neither biologically nor otherwise undesirable, and includes a compound or composition that is acceptable for human pharmaceutical and veterinary use. The compound or composition may be approved or approvable by a regulatory agency or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, including humans.

[0066] “Pharmaceutically acceptable excipient, carrier or adjuvant” refers to an excipient, carrier or adjuvant that can be administered to a subject, together with at least one therapeutic agent (e.g., an antibody of the present disclosure), and which does not destroy the pharmacological activity thereof and is generally safe, nontoxic and neither biologically nor otherwise undesirable when administered in doses sufficient to deliver a therapeutic amount of the agent.

[0067] The term "treatment" is used interchangeably herein with the term "therapeutic method" and refers to both 1) therapeutic treatments or measures that cure, slow down, lessen symptoms of, and/or halt progression of a diagnosed pathologic conditions, disease or disorder, and 2) and prophylactic/ preventative measures. Those in need of treatment may include individuals already having a particular medical disease or disorder as well as those who may ultimately acquire the disorder (i.e., those at risk or needing preventive measures).

[0068] The term “subject” or “patient” as used herein refers to any individual to which the subject methods are performed. Generally, the subject is human, although as will be appreciated by those in the art, the subject may be any animal.

[0069] In some embodiments, compounds of the present invention are able to cross the blood-brain barrier (BBB). The term “blood-brain barrier” or “BBB”, as used herein, refers to the BBB proper as well as to the blood-spinal barrier. The blood-brain barrier, which consists of the endothelium of the brain vessels, the basal membrane and neuroglial cells, acts to limit penetration

of substances into the brain. In some embodiments, the brain/plasma ratio of total drug is at least approximately 0.01 after administration (e.g. oral or intravenous administration) to a patient. In some embodiments, the brain/plasma ratio of total drug is at least approximately 0.03. In some embodiments, the brain/plasma ratio of total drug is at least approximately 0.06. In some embodiments, the brain/plasma ratio of total drug is at least approximately 0.1. In some embodiments, the brain/plasma ratio of total drug is at least approximately 0.2.

[0070] The term "homologue," especially "TREM homologue" as used herein refers to any member of a series of peptides or nucleic acid molecules having a common biological activity, including antigenicity/immunogenicity and inflammation regulatory activity, and/or structural domain and having sufficient amino acid or nucleotide sequence identity as defined herein. TREM homologues can be from either the same or different species of animals.

[0071] The term "variant" as used herein refers either to a naturally occurring allelic variation of a given peptide or a recombinantly prepared variation of a given peptide or protein in which one or more amino acid residues have been modified by amino acid substitution, addition, or deletion.

[0072] The term "derivative" as used herein refers to a variation of given peptide or protein that are otherwise modified, i.e., by covalent attachment of any type of molecule, preferably having bioactivity, to the peptide or protein, including non-naturally occurring amino acids.

Description of Treatment Methods of the Present Invention

[0073] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with a CSF1R dysfunction in a human patient, the method comprising administering to the patient a compound that increases activity of TREM2. In some embodiments, the compound that increases activity of TREM2 is an agonist of TREM2. In some embodiments, the compound that increases activity of TREM2 is a compound that prevents the degradation of TREM2.

[0074] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with a CSF1R dysfunction in a human patient, the method comprising administering to the patient an effective amount of an agonist of TREM2. In some embodiments, administration of the agonist of TREM2 activates DAP12 signaling pathways in the patient, resulting in an increase in microglia proliferation, microglia survival and microglia phagocytosis,

which in turn results in a slowing of disease progression. In some embodiments, the agonist of TREM2 is an antibody or a small molecule.

[0075] In some embodiments, the agonist of TREM2 activates TREM2/DAP12 signaling in myeloid cells, including monocytes, dendritic cells, microglial cells and macrophages. In some embodiments, an agonist of TREM2 activates, induces, promotes, stimulates, or otherwise increases one or more TREM2 activities. TREM2 activities that are activated or increased by the agonist, include but are not limited to: TREM2 binding to DAP12; DAP12 binding to TREM2; TREM2 phosphorylation, DAP12 phosphorylation; PI3K activation; increased levels of soluble TREM2 (sTREM2); increased levels of soluble CSF1R (sCSF1R); increased expression of one or more anti-inflammatory mediators (e.g., cytokines) selected from the group consisting of IL-12p70, IL-6, and IL-10; reduced expression of one or more pro-inflammatory mediators selected from the group consisting of IFN-a4, IFN-b, IL-6, IL-12 p70, IL-1β, TNF, TNF-α, IL-10, IL-8, CRP, TGF-beta members of the chemokine protein families, IL-20 family members, IL-33, LIF, IFN-gamma, OSM, CNTF, TGF-beta, GM-CSF, IL-11, IL-12, IL-17, IL-18, and CRP; increased expression of one or more chemokines selected from the group consisting of CCL2, CCL4, CXCL10, CCL3 and CST7; reduced expression of TNF-α, IL-6, or both; extracellular signal-regulated kinase (ERK) phosphorylation; increased expression of C-C chemokine receptor 7 (CCR7); induction of microglial cell chemotaxis toward CCL19 and CCL21 expressing cells; an increase, normalization, or both of the ability of bone marrow-derived dendritic cells to induce antigen-specific T-cell proliferation; induction of osteoclast production, increased rate of osteoclastogenesis, or both; increasing the survival and/or function of one or more of dendritic cells, macrophages, microglial cells, M1 macrophages and/or microglial cells, activated M1 macrophages and/or microglial cells, M2 macrophages and/or microglial cells, monocytes, osteoclasts, Langerhans cells of skin, and Kupffer cells; induction of one or more types of clearance selected from the group consisting of apoptotic neuron clearance, nerve tissue debris clearance, non-nerve tissue debris clearance, bacteria or other foreign body clearance, disease-causing protein clearance, disease-causing peptide clearance, and disease-causing nucleic acid clearance; induction of phagocytosis of one or more of apoptotic neurons, nerve tissue debris, non-nerve tissue debris, bacteria, other foreign bodies, disease-causing proteins, disease-causing peptides, or disease-causing nucleic acids; normalization of disrupted TREM2/DAP12-dependent gene expression; recruitment of Syk, ZAP70, or both to the TREM2/DAP12 complex; Syk

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phosphorylation; increased expression of CD83 and/or CD86 on dendritic cells, macrophages, monocytes, and/or microglia; reduced secretion of one or more inflammatory cytokines selected from the group consisting of TNF-α, IL-10, IL-6, MCP-1, IFN-a4, IFN-b, IL-1β, IL-8, CRP, TGF-beta members of the chemokine protein families, IL-20 family members, IL-33, LIF, IFN-gamma, OSM, CNTF, TGF-beta, GM-CSF, IL-11, IL-12, IL-17, IL-18, and CRP; reduced expression of one or more inflammatory receptors; increasing phagocytosis by macrophages, dendritic cells, monocytes, and/or microglia under conditions of reduced levels of MCSF; decreasing phagocytosis by macrophages, dendritic cells, monocytes, and/or microglia in the presence of normal levels of MCSF; increasing activity of one or more TREM2-dependent genes; or any combination thereof.

[0076] In some embodiments, an agonist of TREM2 increases levels of soluble TREM2 (sTREM2). In some embodiments, an agonist of TREM2 decreases levels of soluble TREM2 (sTREM2).

[0077] In some embodiments, the agonist of TREM2 causes increased expression of one or more of IL-4, CCL8, FasL, CSF1, CSF2, FIZZ1, CD206, Arg1, Ym1, IGF-1, Chi3l3, Fzd1, and IL-34. In some embodiments, the agonist of TREM2 causes decreased expression of one or more of IL-12 p40, IL-27, CSF3, CCR5, ABCD1 and CH25H.

[0078] In another aspect, the invention provides a TREM2 agonist for the manufacture of a medicament for the treatment of a disease or disorder caused by and/or associated with a CSF1R dysfunction.

[0079] In another aspect, the invention provides a TREM2 agonist for use in treating a disease or disorder caused by and/or associated with a CSF1R dysfunction in a human patient.

I. Diseases and Disorders

[0080] The methods of the present invention can be used to treat any disease or disorder related to a dysfunction in CSF1R. In some embodiments, the patient is selected for treatment based on a diagnosis that includes the presence of a mutation in a CSF1R gene affecting the function of CSF1R. In some embodiments, the mutation in the CSF1R gene is a mutation that causes a decrease in CSF1R activity or a cessation of CSF1R activity.

[0081] In some embodiments, the disease or disorder is caused by a heterozygous CSF1R mutation. In some embodiments, the disease or disorder is caused by a homozygous CSF1R

mutation. In some embodiments, the disease or disorder is caused by a splice mutation in the csf1r gene. In some embodiments, the disease or disorder is caused by a missense mutation in the csf1r gene.

[0082] In some embodiments, the disease or disorder is caused by a mutation in the catalytic kinase domain of CSF1R. In some embodiments, the disease or disorder is caused by a mutation in an immunoglobulin domain of CSF1R. In some embodiments, the disease or disorder is caused by a mutation in the ectodomain of CSF1R.

[0083] In some embodiments, the disease or disorder is a disease or disorder resulting from a change (e.g. increase, decrease or cessation) in the activity of CSF1R. In some embodiments, the disease or disorder is a disease or disorder resulting from a decrease or cessation in the activity of CSF1R. CSF1R related activities that are changed in the disease or disorder include, but are not limited to: decrease or loss of microglia function; increased microglia apoptosis; decrease in Src signaling; decrease in Syk signaling; decreased microglial proliferation; decreased microglial response to cellular debris; decreased phagocytosis; and decreased release of cytokines in response to stimuli.

[0084] In some embodiments, the disease or disorder is caused by a loss-of-function mutation in CSF1R. In some embodiments, the loss-of-function mutation results in a complete cessation of CSF1R function. In some embodiments, the loss-of-function mutation results in a partial loss of CSF1R function, or a decrease in CSF1R activity.

[0085] In some embodiments, the disease or disorder is a neurodegenerative disorder. In some embodiments, the disease or disorder is a neurodegenerative disorder caused by and/or associated with a CSF1R dysfunction.

[0086] In some embodiments, the disease or disorder is a skeletal disorder. In some embodiments, the disease or disorder is a skeletal disorder caused by and/or associated with a CSF1R dysfunction.

[0087] In some embodiments, the disease or disorder is selected from adult-onset leukoencephalopathy with axonal spheroids and pigmented glia (ALSP), hereditary diffuse leukoencephalopathy with axonal spheroids (HDLS), pigmentary orthochromatic leukodystrophy

(POLD), pediatric-onset leukoencephalopathy, congenital absence of microglia, or brain abnormalities neurodegeneration and dysosteosclerosis (BANDDOS).

[0088] In some embodiments, the disease or disorder is selected from Nasu-Hakola disease, Alzheimer's disease, frontotemporal dementia, multiple sclerosis, Guillain-Barre syndrome, amyotrophic lateral sclerosis (ALS), Parkinson's disease, traumatic brain injury, spinal cord injury, systemic lupus erythematosus, rheumatoid arthritis, prion disease, stroke, osteoporosis, osteopetrosis, osteosclerosis, skeletal dysplasia, dysosteoplasia, Pyle disease, cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy, cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy, cerebroretinal vasculopathy, or metachromatic leukodystrophy wherein any of the aforementioned diseases or disorders are present in a patient exhibiting CSF1R dysfunction, or having a mutation in a gene affecting the function of CSF1R.

[0089] In some embodiments, the disease or disorder is ALSP, which is an encompassing and superseding name for both HDLS and POLD.

[0090] In some embodiments, the disease or disorder is a homozygous mutation in CSF1R. In some embodiments, the disease or disorder is pediatric-onset leukoencephalopathy. In some embodiments, the disease or disorder is congenital absence of microglia. In some embodiments, the disease or disorder is brain abnormalities neurodegeneration and dysosteosclerosis (BANDDOS).

[0091] In some embodiments, the disease or disorder is skeletal dysplasia wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is skeletal dysplasia, wherein the patient has a loss-of function mutation in CSF1R.

[0092] In some embodiments, the disease or disorder is osteosclerosis wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is osteosclerosis, wherein the patient has a loss-of function mutation in CSF1R.

[0093] In some embodiments, the disease or disorder is Alzheimer's disease wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function.

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In some embodiments, the patient has been diagnosed with Alzheimer's disease based on neuropathology, and also has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is Alzheimer's disease, wherein the patient has a loss-of-function mutation in CSF1R.

[0094] In some embodiments, the disease or disorder is Nasu-Hakola disease wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the patient has been diagnosed with Nasu-Hakola disease based on neuropathology, and also has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is Nasu-Hakola disease, wherein the patient has a loss-of-function mutation in CSF1R.

[0095] In some embodiments, the disease or disorder is Parkinson's disease wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the patient has been diagnosed with Parkinson's disease based on neuropathology, and also has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is Parkinson's disease, wherein the patient has a loss-of-function mutation in CSF1R.

[0096] In some embodiments, the disease or disorder is multiple sclerosis wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the patient has been diagnosed with multiple sclerosis based on neuropathology, and also has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is multiple sclerosis, wherein the patient has a loss-of-function mutation in CSF1R.

[0097] In some embodiments, the disease or disorder is ALS wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the patient has been diagnosed with ALS based on neuropathology, and also has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is ALS, wherein the patient has a loss-of-function mutation in CSF1R.

[0098] In some embodiments, the disease or disorder is Guillain-Barre syndrome wherein the patient has been found to have a mutation in one or more CSF1R genes affecting CSF1R function.

In some embodiments, the patient has been diagnosed with Guillain-Barre syndrome based on neuropathology, and also has been found to have a mutation in one or more CSF1R genes affecting CSF1R function. In some embodiments, the disease or disorder is Guillain-Barre syndrome, wherein the patient has a loss-of-function mutation in CSF1R.

[0099] In some embodiments, the patient also possesses a mutation in one or more of NOTCH3, HTRA1, TREX1, ARSA, EIF2B1, EIF2B2, EIF2B3, EIF2B4, and EIF2B5.

[00100] In some embodiments, the disease or disorder presents one or more symptoms selected from abnormal motor control, parkinsonism, slow movement (bradykinesia), involuntary trembling (tremor), muscle stiffness (rigidity), cognitive decline, dementia, inability to speak, inability to walk, memory loss, personality changes, seizures, depression, loss of executive function, loss of impulse control, loss of attention span, and incontinence.

[00101] In some embodiments, the disease or disorder causes one or more physiological abnormalities selected from, but not limited to, abnormal brain white matter, brain matter calcification, corpus callosum agenesis, Dandy-Walker malformation and bone cysts.

[00102] In one aspect, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient a compound that increases activity of TREM2. In some embodiments, the compound that increases activity of TREM2 is an agonist of TREM2. In some embodiments, the compound that increases activity of TREM2 is a compound that prevents the degradation of TREM2.

[00103] In one aspect, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of an agonist of TREM2. In some embodiments, administration of the agonist of TREM2 activates DAP12 signaling pathways in the patient, resulting in an increase in microglia proliferation, microglia survival and microglia phagocytosis, which in turn results in a slowing of disease progression in ALSP. In some embodiments, the agonist of TREM2 is an antibody or a small molecule.

[00104] In another aspect, the invention provides a TREM2 agonist for the manufacture of a medicament for the treatment of ALSP.

[00105] In another aspect, the invention provides a TREM2 agonist for use in treating ALSP in a human patient.

II. Antibodies

[00106] In one aspect, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of an antigen binding protein or an antibody, or an antigen-binding fragment thereof, which increases the activity of TREM2. In some embodiments, the antibody is an agonist of TREM2. In some embodiments, the antibody is an agonist of TREM2 that specifically binds to and activates human TREM2.

[00107] The TREM2 agonist antibodies specifically bind to human TREM2 (SEQ ID NO: 1) or an extra cellular domain (ECD) of human TREM2 (e.g. ECD set forth in SEQ ID NO: 2), for example with an equilibrium dissociation constant (K_D) less than 50 nM, less than 25 nM, less than 10 nM, or less than 5 nM. In some embodiments, the TREM2 agonist antibodies do not cross-react with other TREM proteins, such as human TREM1. In some embodiments, the TREM2 agonist antibodies do not bind to human TREM1 (SEQ ID NO: 4).

[00108] In some embodiments, the TREM2 antibody specifically binds to human TREM2 residues 19-174 (SEQ ID NO: 1). In some embodiments, the TREM2 antibody specifically binds to IgV region of human TREM2, for example human TREM2 residues 19-140 (SEQ ID NO: 1).

[00109] In certain embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 29-112 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 29-112 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 29-41 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 29-41 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 47-69 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 47-69 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 76-86 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 76-86 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 91-100 of human TREM2 (SEQ ID NO: 1),

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or within amino acid residues on a TREM2 protein corresponding to amino acid residues 91-100 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 99-115 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 99-115 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 104-112 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 104-112 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 114-118 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 114-118 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 130-171 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 130-171 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 139-153 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 139-153 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 139-146 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 139-146 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 130-144 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 130-144 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 158-171 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 158-171 of SEQ ID NO: 1.

[00110] In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 43-50 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 43-50 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 49-57 of human TREM 2 (SEQ ID NO: 1), or within

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amino acid residues on a TREM2 protein corresponding to amino acid residues 49-57 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 139-146 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 139-146 of SEQ ID NO: 1. In some embodiments, anti-TREM2 antibodies of the present disclosure bind to one or more amino acids within amino acid residues 140-153 of human TREM 2 (SEQ ID NO: 1), or within amino acid residues on a TREM2 protein corresponding to amino acid residues 140-153 of SEQ ID NO: 1. In some embodiments, the TREM2 antibody specifically binds to the stalk region of human TREM2, for example amino acid residues 145-174 of human TREM2.

[00111] In some embodiments, the antibody, or an antigen-binding fragment thereof, specifically binds TREM2 and prevents the degradation or cleavage of TREM2.

[00112] In some embodiments, the antibody is a polyclonal antibody. In some embodiments, the antibody is a monoclonal antibody. In some embodiments, the antibody is a chimeric antibody. In some embodiments, the antibody is a humanized antibody. In some embodiments, the antibody is a human antibody, particularly a fully human antibody. In some embodiments, the antibody is a bispecific or other multivalent antibody. In some embodiments, the antibody is a single chain antibody.

[00113] In some embodiments, a TREM2 activating antibody comprise a light chain variable region comprising complementarity determining regions CDRL1, CDRL2, and CDRL3 and a heavy chain variable region comprising complementarity determining regions CDRH1, CDRH2, and CDRH3 described herein.

[00114] In certain embodiments, the TREM2 agonist antigen binding proteins of the invention comprise at least one light chain variable region comprising a CDRL1, CDRL2, and CDRL3, and at least one heavy chain variable region comprising a CDRH1, CDRH2, and CDRH3 from an anti-TREM2 agonist antibody described herein.

[00115] In some embodiments, a TREM2 activating antibody comprises a light chain variable region and a heavy chain variable region described herein. The light chain and heavy chain variable regions or CDRs may be from any of the anti-TREM2 antibodies or a variant thereof described herein.

A. PCT Patent Application Publication No. WO2018/195506A1

[00116] In some embodiments, the TREM2 agonist is an antigen binding protein or an antibody, or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. WO2018/195506A1, which is incorporated by reference herein, in its entirety.

[00117] In some embodiments, the TREM2 agonist antigen binding protein comprises a CDRL1 or a variant thereof having one, two, three or four amino acid substitutions; a CDRL2, or a variant thereof having one, two, three or four amino acid substitutions; a CDRL3, or a variant thereof having one, two, three or four amino acid substitutions; a CDRH1, or a variant thereof having one, two, three or four amino acid substitutions; a CDRH2, or a variant thereof having one, two, three or four amino acid substitutions; and a CDRH3, or a variant thereof having one, two, three or four amino acid substitutions, where the amino acid sequences of the CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 are provided in **Tables 1A** and **1B** below, along with exemplary light chain and variable regions

Table 1A: Exemplary Anti-Human TREM2 Antibody Light Chain Variable Region Amino Acid Sequences

Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
12G10	LV-01	QAVPTQPSSLSASPGVLASLTCTLRSGINVGTYRIYWYQQKPGSPPQYLLRYKSDSDKQQGSGVPSRFSGSKDASANAGILLISGLQSEDEADYYCMIWYSSAVVFGGGTKLTVL (SEQ ID NO: 46)	TLRSGINVGTYRIY (SEQ ID NO: 5)	YKSDSDKQQGS (SEQ ID NO: 19)	MIWYSSAVV (SEQ ID NO: 31)
26A10	LV-02	SYELTQPPSVSVSPGQTASITCSGDKLGDKYVCWYQQKPGQSPVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSNTVVFGGGTKLTVL (SEQ ID NO: 47)	SGDKLGDKYVC (SEQ ID NO: 6)	QDSKRPS (SEQ ID NO: 20)	QAWDSNTVV (SEQ ID NO: 32)
26C10	LV-03	SFELTQPPSVSVSPGQTASITCSGDKLGDKYVCWYQQKPGQSPML	SGDKLGDKYVC (SEQ ID NO: 6)	QDTKRPS (SEQ ID NO: 21)	QAWDSSTVV (SEQ ID NO: 33)

Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
		VIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL (SEQ ID NO: 48)			
26F2	LV-04	SYELTQPPSVSVSPGQTASITCSGDKLGDKYVCWYQQKPGQSPVLVIFQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL (SEQ ID NO: 49)	SGDKLGDKYVC (SEQ ID NO: 6)	QDSKRPS (SEQ ID NO: 20)	QAWDSSTVV (SEQ ID NO: 33)
33B12	LV-05	SYELTQPPSVSVSPGQTASITCSGDKLGDKYVCWYQQKPGQSPVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL (SEQ ID NO: 50)	SGDKLGDKYVC (SEQ ID NO: 6)	QDSKRPS (SEQ ID NO: 20)	QAWDSSTVV (SEQ ID NO: 33)
24C12	LV-06	GIVMTQSPDSLAVSLGERATINCKSSRSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYNCQQYYITPITFGQGTRLEIK (SEQ ID NO: 51)	KSSRSVLYSSNNKNYLA (SEQ ID NO: 7)	WASTRES (SEQ ID NO: 22)	QQYYITPIT (SEQ ID NO: 34)
24G6	LV-07	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKHFLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAFYYCQQYYSTPLTFGGGTKVEIK (SEQ ID NO: 52)	KSSQSVLYSSNNKHFLA (SEQ ID NO: 8)	WASTRES (SEQ ID NO: 22)	QQYYSTPLT (SEQ ID NO: 35)
24A10	LV-08	DIVMTQSPDSLAVSLGERATITCKSSHNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVA	KSSHNVLYSSNNKNYLA (SEQ ID NO: 9)	WASTRES (SEQ ID NO: 22)	HQYYSTPCS (SEQ ID NO: 36)

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Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
		VYYCHQYYSTPCSFG QGTKLEIK (SEQ ID NO: 53)			
10E3	LV-09	EIVMTQSPATLSVSP GERATLSCRASQSVS SNLAWFQQKPGQAPR LLIYGASTRATGIPA RFSVSGSGTEFTLTI SSLQSEDFAFYYCLQ DNNWPPTFGPGTKVD IK (SEQ ID NO: 54)	RASQSVSSNLA (SEQ ID NO: 10)	GASTRAT (SEQ ID NO: 23)	LQDNNWPPT (SEQ ID NO: 37)
13E7 14C12	LV-10	EIVMTQSPATLSVSP GERATLSCRASQSVS SNLAWFQQKPGQAPR LLIYGASTRATGIPA RFSVSGSGTEFTLTI SSLQSEDFAVYYCLQ DNNWPPTFGPGTKVD IK (SEQ ID NO: 55)	RASQSVSSNLA (SEQ ID NO: 10)	GASTRAT (SEQ ID NO: 23)	LQDNNWPPT (SEQ ID NO: 37)
25F12	LV-11	EKVMTQSPATLSVSP GERATLSCRASQSVN NNLAWYQQKPGQAPR LLIYGASTRATGIPA RFSGSGSGTEFTLTI SSLQSEDFAVYYCQQ YNNWPRTFGQGTKVE IK (SEQ ID NO: 56)	RASQSVNNNLA (SEQ ID NO: 11)	GASTRAT (SEQ ID NO: 23)	QQYNNWPRT (SEQ ID NO: 38)
32E3	LV-12	EFVLTQSPGTLSLSP GERATLSCRASQIIS SNYLAWYQQKPGQAP RLLIYSASSRATGIP DRFSGSGSGTDFTLT ISRLEPEDFAVYYCQ QFDSSPITFGRGTRL DIK (SEQ ID NO: 57)	RASQIISSNYLA (SEQ ID NO: 12)	SASSRAT (SEQ ID NO: 24)	QQFDSSPIT (SEQ ID NO: 39)
24F4	LV-13	EIVLTQSPGTLSLSP GERATLSCRASQSVS SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGSGTDFTLT ISRLEPEDFALYYCQ QYDTSPFTFGPGTKV DIK (SEQ ID NO: 58)	RASQSVSSSYLA (SEQ ID NO: 13)	GASSRAT (SEQ ID NO: 25)	QQYDTSPFT (SEQ ID NO: 40)

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Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
16B8	LV-14	DIQMTQSPSSVSASVGDRVTVTCRASQDINSWLAWYQQKPGKAPKLLIYAASSLQTGVPSRFSGSGSGTDFTLTISSLQPEDFATYSCQQSNSFPITFGQGTRLEIK (SEQ ID NO: 59)	RASQDINSWLA (SEQ ID NO: 14)	AASSLQT (SEQ ID NO: 26)	QQSNSFPIT (SEQ ID NO: 41)
4C5	LV-15	DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWYQQKPGKAPKLLIYAASSLQVGVPLRFSGSGSGTDFTLTISSLQPEDFATYYCQQADSFPRNFGQGTKLEIK (SEQ ID NO: 60)	RASQGISNWLA (SEQ ID NO: 15)	AASSLQV (SEQ ID NO: 27)	QQADSFPRN (SEQ ID NO: 42)
6E7	LV-16	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 61)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQN (SEQ ID NO: 28)	QQADSFPRT (SEQ ID NO: 43)
5E3	LV-17	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTYPFTFGPGTKVDIK (SEQ ID NO: 62)	RASQGISNYLA (SEQ ID NO: 17)	AASSLQS (SEQ ID NO: 29)	QQYSTYPFT (SEQ ID NO: 44)
4G10	LV-18	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGNAPKRLIYAASSLPSGVPSRFSGSGSGPEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIT (SEQ ID NO: 63)	RASQGIRNDLG (SEQ ID NO: 18)	AASSLPS (SEQ ID NO: 30)	LQHNSYPWT (SEQ ID NO: 45)

Table 1B. Exemplary Anti-Human TREM2 Antibody Heavy Chain Variable Region Amino Acid Sequences

Ab ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
12G10 24C12	HV-01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAIGGGGVSTYCADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFYIAVAGSHFDYWGQGTLVTVSS (SEQ ID NO: 110)	SYAMS (SEQ ID NO: 77)	AIGGGGVSTYCADSVKG (SEQ ID NO: 87)	FYIAVAGSHFDY (SEQ ID NO: 95)
26A10	HV-02	EVQLVESGGALVQRGGSLRLSCAASRFTFSSFGMSWVRQAPGKGLEWVSYISSSSFTIYYADSVKGRFTISRDNAKNSFYLQMNSLRDEDTAVYYCAREGGLTMVRGVSSYGLDVWGQGTTVTVSS (SEQ ID NO: 111)	SFGMS (SEQ ID NO: 78)	YISSSSFTIYYADSVKG (SEQ ID NO: 88)	EGGLTMVRGVSSYGLDV (SEQ ID NO: 96)
26C10	HV-03	EVQLVESGGALVQPGGSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSYISSSSFTIYYADSVKGRFTISRDNAKNSFYLQMNSLRDEDTAVYFCVREGGITMVRGVSSYGMDVWGQGTTVTVSS (SEQ ID NO: 112)	SFGMS (SEQ ID NO: 78)	YISSSSFTIYYADSVKG (SEQ ID NO: 88)	EGGITMVRGVSSYGMDV (SEQ ID NO: 97)
26F2	HV-04	EVQLVESGGALVQPGGSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWISYISSSSFTIYYADSVKGRFTISRDNAKNSFYLQMNSLRDEDTAVYFCAREGGITMVRGVSSYGMDVWGQGTTVTVSS (SEQ ID NO: 113)	SFGMS (SEQ ID NO: 78)	YISSSSFTIYYADSVKG (SEQ ID NO: 88)	EGGITMVRGVSSYGMDV (SEQ ID NO: 97)

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Ab ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
33B12	HV-05	EVQLVESGGALVQPGGSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSYISKSSFTIYYADSVKGRFTISRDNAKNSFYLQMNSLRDEDTAVYYCAREGGLTMVRGVSSYGLDVWGQGTTVTVSS (SEQ ID NO: 114)	SFGMS (SEQ ID NO: 78)	YISKSSFTIYYADSVKG (SEQ ID NO: 89)	EGGLTMVRGVSSYGLDV (SEQ ID NO: 96)
24G6	HV-06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAYTPMAFFDYWGQGTLVTVSS (SEQ ID NO: 115)	SYAMS (SEQ ID NO: 77)	AISGSGGSTYYADSVKG (SEQ ID NO: 90)	AYTPMAFFDY (SEQ ID NO: 98)
24A10	HV-07	EVQVLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGGWELFYWGQGTLVTVSS (SEQ ID NO: 116)	NYAMS (SEQ ID NO: 79)	AISGSGGSTYYADSVKG (SEQ ID NO: 90)	GGWELFY (SEQ ID NO: 99)
10E3	HV-08	EVQLVQSGAEVKKPGESLMISCKGSGYSFTNYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARRRQGIWGDALDIWGQGTLVTVSS (SEQ ID NO: 117)	NYWIG (SEQ ID NO: 80)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	RRQGIWGDALDI (SEQ ID NO: 100)

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Ab ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
13E7 14C12	HV-09	EVQLVQSGAEVKKPGESLMISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARRRQGIWGDALDFWGQGTLVTVSS (SEQ ID NO: 118)	SYWIG (SEQ ID NO: 81)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	RRQGIWGDALDF (SEQ ID NO: 101)
25F12	HV-10	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSSYYWSWIRQPPGKGLEWIGEINHSGNTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGYYDILTGYHDAFDIWDQGTMVTVFS (SEQ ID NO: 119)	SYYWS (SEQ ID NO: 82)	EINHSGNTNYNPSLKS (SEQ ID NO: 92)	EGYYDILTGYHDAFDI (SEQ ID NO: 102)
32E3	HV-11	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSTLKASDTAIYYCARHDIIPAAPGAFDIWGQGTMVTVSS (SEQ ID NO: 120)	SYWIG (SEQ ID NO: 81)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	HDIIPAAPGAFDI (SEQ ID NO: 103)
24F4	HV-12	EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISVDKSSSTAYLQWSSLKASDTAIYYCTRQAIAVTGLGGFDPWGQGTLVTVSS (SEQ ID NO: 121)	SYWIG (SEQ ID NO: 81)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QAIAVTGLGGFDP (SEQ ID NO: 104)

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Ab ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
16B8	HV-13	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTVYMELRSLRSDDTAVYYCARRGYSYGSFDYWGQGTLVTVSS (SEQ ID NO: 122)	NYGIS (SEQ ID NO: 83)	WISAYNGNTNYAQKLQG (SEQ ID NO: 93)	RGYSYGSFDY (SEQ ID NO: 105)
4C5	HV-14	EVQLVQSGAEVKKPGESLKISCKGSGHSFTNYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAVYFCARQRTFYYDSSGYFDYWGQGTLVTVSS (SEQ ID NO: 123)	NYWIA (SEQ ID NO: 84)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSGYFDY (SEQ ID NO: 106)
6E7	HV-15	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 124)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSDYFDY (SEQ ID NO: 107)
5E3	HV-16	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGLGLEWMGWINPYSGGTTSAQKFQGRVTMTRDTSISSAYMELSRLRSDDTAVYYCARDGGYLALYGTDVWGQGTTVTVSS (SEQ ID NO: 125)	GYYIH (SEQ ID NO: 86)	WINPYSGGTTSAQKFQG (SEQ ID NO: 94)	DGGYLALYGTDV (SEQ ID NO: 108)

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Ab ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
4G10	HV-17	EVQLVQSGAEVKKPGESLKISCKGSGYSFPSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAFLKWSSLKASDTAMYFCARQGIEVTGTGGLDVWGQGTTVTVSS (SEQ ID NO: 126)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QGIEVTGTGGLDV (SEQ ID NO: 109)

[00118] As noted above, a TREM2 agonist antigen binding protein may comprise one or more of the CDRs presented in **Table 1A** (light chain CDRs; i.e. CDRLs) and **Table 1B** (heavy chain CDRs, i.e. CDRHs).

[00119] In some embodiments, the TREM2 agonist antigen binding protein comprises one or more light chain CDRs selected from (i) a CDRL1 selected from SEQ ID NOs: 5 to 18, (ii) a CDRL2 selected from SEQ ID NOs: 19 to 30, and (iii) a CDRL3 selected from SEQ ID NOs: 31 to 45, and (iv) a CDRL of (i), (ii) and (iii) that contains one or more, e.g., one, two, three, four or more amino acid substitutions (e.g., conservative amino acid substitutions), deletions or insertions of no more than five, four, three, two, or one amino acids. In these and other embodiments, the TREM2 agonist antigen binding proteins comprise one or more heavy chain CDRs selected from (i) a CDRH1 selected from SEQ ID NOs: 77 to 86, (ii) a CDRH2 selected from SEQ ID NOs: 87 to 94, and (iii) a CDRH3 selected from SEQ ID NOs: 95 to 109, and (iv) a CDRH of (i), (ii) and (iii) that contains one or more, e.g., one, two, three, four or more amino acid substitutions (e.g., conservative amino acid substitutions), deletions or insertions of no more than five, four, three, two, or one amino acids amino acids.

[00120] In some embodiments, the TREM2 agonist antigen binding protein may comprise 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in **Tables 1A** and **1B**, each having at least 80%, 85%, 90% or 95% sequence identity to a CDR sequence listed in **Tables 1A** and **1B**. In some embodiments, the TREM2 agonist antigen binding protein includes 1, 2, 3, 4, 5, or 6 of the

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CDRs listed in **Tables 1A** and **1B**, each differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables.

[00121] In some embodiments, the TREM2 agonist antigen binding protein comprises a CDRL1 comprising a sequence selected from SEQ ID NOs: 5-18 or a variant thereof having one, two, three or four amino acid substitutions; a CDRL2 comprising a sequence selected from SEQ ID NOs: 19-30 or a variant thereof having one, two, three or four amino acid substitutions; a CDRL3 comprising a sequence selected from SEQ ID NOs: 31-45 or a variant thereof having one, two, three or four amino acid substitutions; a CDRH1 comprising a sequence selected from SEQ ID NOs: 77-86 or a variant thereof having one, two, three or four amino acid substitutions; a CDRH2 comprising a sequence selected from SEQ ID NOs: 87-94 or a variant thereof having one, two, three or four amino acid substitutions; and a CDRH3 comprising a sequence selected from SEQ ID NOs: 95-109 or a variant thereof having one, two, three or four amino acid substitutions.

[00122] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a CDRL1 comprising a sequence selected from SEQ ID NOs: 5-18; a CDRL2 comprising a sequence selected from SEQ ID NOs: 19-30; a CDRL3 comprising a sequence selected from SEQ ID NOs: 31-45; a CDRH1 comprising a sequence selected from SEQ ID NOs: 77-86; a CDRH2 comprising a sequence selected from SEQ ID NOs: 87-94; and a CDRH3 comprising a sequence selected from SEQ ID NOs: 95-109.

[00123] In some embodiments, the TREM2 agonist antigen binding protein comprise a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 5, 19, and 31, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 20, and 32, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 21, and 33, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 20, and 33, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 7, 22, and 34,

respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 8, 22, and 35, respectively;

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 9, 22, and 36, respectively;

(h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 37, respectively;

(i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 11, 23, and 38, respectively;

(j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 12, 24, and 39, respectively;

(k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 13, 25, and 40, respectively;

(l) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 14, 26, and 41, respectively;

(m) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 15, 27, and 42, respectively;

(n) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively;

(o) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 17, 29, and 44, respectively, or

(p) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 18, 30, and 45, respectively.

[00124] In some embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 87, and 95, respectively;

(b) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 78, 88, and 96, respectively;

(c) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 78, 88, and 97, respectively;

(d) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 78, 89, and 96, respectively;

(e) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 90, and 98, respectively;

(f) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 79, 90, and 99, respectively;

(g) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 80, 91, and 100, respectively;

(h) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 91, and 101, respectively;

(i) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 82, 92, and 102, respectively;

(j) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 91, and 103, respectively;

(k) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 91, and 104, respectively;

(l) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 83, 93, and 105, respectively;

(m) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 84, 91, and 106, respectively;

(n) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively;

(o) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 86, 94, and 108, respectively; or

(p) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 109, respectively.

[00125] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 5, 19, and 31, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 87, and 95, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 20, and 32, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 78, 88, and 96, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 21, and 33, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 78, 88, and 97, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 20, and 33, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 78, 88, and 97, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 20, and 33, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 78, 89, and 96, respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 7, 22, and 34, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 87, and 95, respectively;

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 8, 22, and 35, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 90, and 98, respectively;

(h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 9, 22, and 36, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 79, 90, and 99, respectively;

(i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 37, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 80, 91, and 100, respectively;

(j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 37, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 91, and 101, respectively;

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(k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 11, 23, and 38, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 82, 92, and 102, respectively;

(l) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 12, 24, and 39, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 91, and 103, respectively;

(m) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 13, 25, and 40, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 91, and 104, respectively;

(n) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 14, 26, and 41, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 83, 93, and 105, respectively;

(o) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 15, 27, and 42, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 84, 91, and 106, respectively;

(p) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively;

(q) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 17, 29, and 44, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 86, 94, and 108, respectively; or

(r) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 18, 30, and 45, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 109, respectively.

[00126] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 37, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 80, 91, and 100, respectively. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region

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comprising a CDRH1, a CDRH2, and a CDRH3, wherein CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 37, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 91, and 101, respectively. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 15, 27, and 42, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 84, 91, and 106, respectively. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 17, 29, and 44, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 86, 94, and 108, respectively. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 8, 22, and 35, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 90, and 98, respectively.

[00127] In some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region comprising a sequence selected from SEQ ID NOs: 46-63 and a heavy chain variable region comprising a sequence selected from SEQ ID NOs: 110-126.In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 46 and a heavy chain variable region comprising the sequence of SEQ ID NO: 110. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 47 and a heavy chain variable region comprising the sequence of SEQ ID NO: 111. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the

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sequence of SEQ ID NO: 48 and a heavy chain variable region comprising the sequence of SEQ ID NO: 112. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 49 and a heavy chain variable region comprising the sequence of SEQ ID NO: 113. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 50 and a heavy chain variable region comprising the sequence of SEQ ID NO: 114. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 51 and a heavy chain variable region comprising the sequence of SEQ ID NO: 110. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 53 and a heavy chain variable region comprising the sequence of SEQ ID NO: 116. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 54 and a heavy chain variable region comprising the sequence of SEQ ID NO: 117. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 55 and a heavy chain variable region comprising the sequence of SEQ ID NO: 118. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 56 and a heavy chain variable region comprising the sequence of SEQ ID NO: 119. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 57 and a heavy chain variable region comprising the sequence of SEQ ID NO: 120. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 58 and a heavy chain variable region comprising the sequence of SEQ ID NO: 121. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 59 and a heavy chain variable region comprising the sequence of SEQ ID NO: 122. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 60 and a heavy chain variable region comprising the sequence of SEQ ID NO: 123. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 61 and a heavy chain variable region comprising the sequence of SEQ ID NO: 124. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable

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region comprising the sequence of SEQ ID NO: 62 and a heavy chain variable region comprising the sequence of SEQ ID NO: 125. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 63 and a heavy chain variable region comprising the sequence of SEQ ID NO: 126. In yet another embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 52 and a heavy chain variable region comprising the sequence of SEQ ID NO: 115.

[00128] In some embodiments, the TREM2 agonist antigen binding protein may comprise a light chain variable region selected from LV-01, LV-02, LV-03, LV-04, LV-05, LV-06, LV-07, LV-08, LV-09, LV-10, LV-11, LV-12, LV-13, LV-14, LV-15, LV-16, LV-17, and LV-18, as shown in **Table 1A**, and/or a heavy chain variable region selected from HV-01, HV-02, HV-03, HV-04, HV-05, HV-06, HV-07, HV-08, HV-09, HV-10, HV-11, HV-12, HV-13, HV-14, HV-15, HV-16, and HV-17, as shown in **Table 1B**, and functional fragments, derivatives, muteins and variants of these light chain and heavy chain variable regions.

[00129] In some embodiments, each of the light chain variable regions listed in **Table 1A** may be combined with any of the heavy chain variable regions listed in **Table 1B** to form an anti-TREM2 binding domain of the antigen binding proteins of the invention. Examples of such combinations include, but are not limited to: LV-01 (SEQ ID NO: 46) and HV-01 (SEQ ID NO: 110); LV-02 (SEQ ID NO: 47) and HV-02 (SEQ ID NO: 111); LV-03 (SEQ ID NO: 48) and HV-03 (SEQ ID NO: 112); LV-04 (SEQ ID NO: 49) and HV-04 (SEQ ID NO: 113); LV-05 (SEQ ID NO: 50) and HV-05 (SEQ ID NO: 114); LV-06 (SEQ ID NO: 51) and HV-01 (SEQ ID NO: 110); LV-07 (SEQ ID NO: 52) and HV-06 (SEQ ID NO: 115); LV-08 (SEQ ID NO: 53) and HV-07 (SEQ ID NO: 116); LV-09 (SEQ ID NO: 54) and HV-08 (SEQ ID NO: 117); LV-10 (SEQ ID NO: 55) and HV-09 (SEQ ID NO: 118); LV-11 (SEQ ID NO: 56) and HV-10 (SEQ ID NO: 119); LV-12 (SEQ ID NO: 57) and HV-11 (SEQ ID NO: 120); LV-13 (SEQ ID NO: 58) and HV-12 (SEQ ID NO: 121); LV-14 (SEQ ID NO: 59) and HV-13 (SEQ ID NO: 122); LV-15 (SEQ ID NO: 60) and HV-14 (SEQ ID NO: 123); LV-16 (SEQ ID NO: 61) and HV-15 (SEQ ID NO: 124); LV-17 (SEQ ID NO: 62) and HV-16 (SEQ ID NO: 125); and LV-18 (SEQ ID NO: 63) and HV-17 (SEQ ID NO: 126).

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[00130] In certain embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising the sequence of LV-09 (SEQ ID NO: 54) and a heavy chain variable region comprising the sequence of HV-08 (SEQ ID NO: 117). In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising the sequence of LV-10 (SEQ ID NO: 55) and a heavy chain variable region comprising the sequence of HV-09 (SEQ ID NO: 118). In other embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising the sequence of LV-15 (SEQ ID NO: 60) and a heavy chain variable region comprising the sequence of HV-14 (SEQ ID NO: 123). In still other embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising the sequence of LV-16 (SEQ ID NO: 61) and a heavy chain variable region comprising the sequence of HV-15 (SEQ ID NO: 124). In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising the sequence of LV-17 (SEQ ID NO: 62) and a heavy chain variable region comprising the sequence of HV-16 (SEQ ID NO: 125). In certain embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising the sequence of LV-07 (SEQ ID NO: 52) and a heavy chain variable region comprising the sequence of HV-06 (SEQ ID NO: 115).

[00131] In some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region comprising a sequence of contiguous amino acids that differs from the sequence of a light chain variable region in **Table 1A**, i.e. a VL selected from LV-01, LV-02, LV-03, LV-04, LV-05, LV-06, LV-07, LV-08, LV-09, LV-10, LV-11, LV-12, LV-13, LV-14, LV-15, LV-16, LV-17, or LV-18, at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino acid, with the deletions, insertions and/or substitutions resulting in no more than 15 amino acid changes relative to the foregoing variable domain sequences. The light chain variable region in some TREM2 agonist antigen binding proteins comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 46-63 (i.e. the light chain variable regions in **Table 1A**). In one embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence that is at least 90% identical to a sequence selected from SEQ ID NOs: 46-63. In another embodiment, the

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TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence that is at least 95% identical to a sequence selected from SEQ ID NOs: 46-63. In yet another embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence selected from SEQ ID NOs: 46-63. In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence of SEQ ID NO: 54. In other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence of SEQ ID NO: 55. In yet other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence of SEQ ID NO: 60. In still other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence of SEQ ID NO: 61. In certain embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence of SEQ ID NO: 62. In other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence of SEQ ID NO: 52.

[00132] In these and other embodiments, the TREM2 agonist antigen binding proteins comprise a heavy chain variable region comprising a sequence of contiguous amino acids that differs from the sequence of a heavy chain variable region in **Table 1B**, i.e., a VH selected from HV-01, HV-02, HV-03, HV-04, HV-05, HV-06, HV-07, HV-08, HV-09, HV-10, HV-11, HV-12, HV-13, HV-14, HV-15, HV-16, or HV-17, at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino acid, with the deletions, insertions and/or substitutions resulting in no more than 15 amino acid changes relative to the foregoing variable domain sequences. The heavy chain variable region in some TREM2 agonist antigen binding proteins comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 110-126 (i.e. the heavy chain variable regions in **Table 1B**). In one embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence that is at least 90% identical to a sequence selected from SEQ ID NOs: 110-126. In another embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence that is at least 95% identical to a sequence selected from SEQ ID NOs: 110-126. In yet another embodiment, the TREM2 agonist antigen binding protein comprises a

heavy chain variable region comprising a sequence selected from SEQ ID NOs: 110-126. In some embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence of SEQ ID NO: 117. In other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence of SEQ ID NO: 118. In yet other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence of SEQ ID NO: 123. In still other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence of SEQ ID NO: 124. In certain embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence of SEQ ID NO: 125. In other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a sequence of SEQ ID NO: 115.

[00133] In some embodiments, variants of the anti-TREM2 antibodies can be generated by substituting one or more amino acids in the light chain or heavy chain variable regions to address chemical liabilities (e.g., aspartate isomerization, asparagine deamidation, tryptophan and methionine oxidation) or correct covariance violations (see e.g., WO 2012/125495, which is hereby incorporated by reference in its entirety). Such variants can have improved biophysical, expression, and/or stability properties as compared with the parental antibody. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region and/or heavy chain variable region having one or more of the amino acid substitutions set forth in any of **Tables 2A-2F** below.

[00134] In some embodiments, additional variants of the anti-TREM2 antibodies described herein can be generated by affinity modulating any of the anti-TREM2 antibodies described herein. An "affinity-modulated antibody" is an antibody that comprises one or more amino acid substitutions in its light chain variable region sequence and/or heavy chain variable region sequence that increases or decreases the affinity of the antibody for the target antigen as compared to the parental antibody that does not contain the amino acid substitutions. Antibody affinity modulation methods are known to those of skill in the art and can include CDR walking mutagenesis (Yang et al., J. Mol. Biol., 254, 392-403, 1995), chain shuffling (Marks et al., Bio/Technology, 10, 779-783, 1992), use of mutation strains of *E. coli* (Low et al., J. Mol. Biol., 250, 350-368, 1996), DNA shuffling (Patten et al., Curr. Opin. Biotechnol., 1997, 8:724-733), phage display (Thompson et al., J. Mol. Biol., 1996, 256:7-88), PCR techniques (Crameri, et al.,

Nature, 1998, 391:288-291), and other mutagenesis strategies (Barbas et al., Proc Nat. Acad. Sci. USA 91:3809-3813, 1994; Schier et al., Gene 169:147-155, 1995; Yelton et al., J. Immunol. 155:1994-2004, 1995; Jackson et al., J. Immunol. 154(7):3310-9, 1995; and Hawkins et al., J. Mol. Biol., 1992, 226:889-896). Methods of affinity modulation are discussed in Hoogenboom, Trends in Biotechnology, 1995, 15:62-70, and Vaughan *et al.*, Nature Biotechnology, 1998, 16535-539,. One specific method for generating affinity-modulated variants of the anti-TREM2 antibodies described herein is the use of a yeast-display Fab mutagenesis library.

[00135] In some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region that is a variant of a light chain variable region of any of the anti-TREM2 antibodies described herein. Thus, in some embodiments, the light chain variable region of the TREM2 agonist antigen binding proteins comprises a sequence that is at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least 94% identical, or at least 95% identical to a sequence selected from SEQ ID NOs: 46-63. In some embodiments, the TREM2 agonist antigen binding proteins can comprise a light chain variable region from any of the engineered anti-TREM2 antibody variants set forth in **Tables 2A-2F** below.

[00136] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 54 with a mutation at one or more amino acid positions 64, 79, 80, 85, 94, and/or 100. In some such embodiments, the mutation is V64G, V64A, Q79E, Q79D, S80P, S80A, F85V, F85L, F85A, F85D, F85I, F85L, F85M, F85T, W94F, W94Y, W94S, W94T, W94A, W94H, W94I, W94Q, P100R, P100Q, P100G, or combinations thereof. In another embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 55 with a mutation at one or more amino acid positions 64, 79, 80, 94, and/or 100. Such mutations can include V64G, V64A, Q79E, Q79D, S80P, S80A, W94F, W94Y, W94S, W94T, W94A, W94H, W94I, W94Q, P100R, P100Q, P100G, or combinations thereof. In certain embodiments, the mutation is V64G, V64A, Q79E, S80P, S80A, W94Y, W94S, P100R, P100Q, or combinations thereof. In another embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 60 with a mutation at one or more amino acid positions 60, 92, and/or 93. The mutation in such embodiments can be selected from L60S, L60P, L60D, L60A, D92E, D92Q, D92T, D92N, S93A, S93N, S93Q, S93V, or combinations thereof. In yet another embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable

region comprising the sequence of SEQ ID NO: 61 with a mutation at one or more amino acid positions 56, 57, 92, and/or 93. In such embodiments, the mutation can be N56S, N56T, N56Q, N56E, G57A, G57V, D92E, D92Q, D92T, D92N, S93A, S93N, S93Q, S93V, or combinations thereof. In certain embodiments, the mutation is N56S, N56Q, G57A, D92E, D92Q, S93A, or combinations thereof. In still another embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 62 with a mutation at amino acid position 36, 46, 61 and/or 100. Such mutations can include F36Y, S46L, S46R, S46V, S46F, K61R, P100Q, P100G, P100R or combinations thereof. In particular embodiments, the mutation is F36Y, K61R, P100Q, or combinations thereof. In another embodiment, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 52 with a mutation at amino acid position 91, which can be selected from F91V, F91I, F91T, F91L, or F91D. In one embodiment, the mutation is F91V.

[00137] In some embodiments, the TREM2 agonist antigen binding proteins comprise a heavy chain variable region that is a variant of a heavy chain variable region from any of the anti-TREM2 antibodies described herein. Thus, in some embodiments, the heavy chain variable region of the TREM2 agonist antigen binding proteins comprises a sequence that is at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least 94% identical, or at least 95% identical to a sequence selected from SEQ ID NOs: 110-126. For instance, the TREM2 agonist antigen binding proteins can comprise a heavy chain variable region from any of the engineered anti-TREM2 antibody variants set forth in **Tables 2A-2F** below. In one embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 117 with a mutation at one or more amino acid positions 19, 55, 56, 57, 58, and/or 104. In some such embodiments, the mutation is M19K, M19R, M19T, M19E, M19N, M19Q, D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, W104F, W104Y, W104T, W104S, W104A, W104H, W104I, W104Q, or combinations thereof. In another embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 118 with a mutation at one or more amino acid positions 19, 55, 56, 57, 58, and/or 104. Such mutations can include M19K, M19R, M19T, M19E, M19N, M19Q, D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, W104F, W104Y, W104T, W104S, W104A, W104H, W104I, W104Q, or combinations thereof. In certain embodiments, the mutation is M19K, D55E, S56A, D57E, T58A,

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W104Y, W104T, or combinations thereof. In another embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 123 with a mutation at one or more amino acid positions 27, 55, 56, 57, 58, 105, and/or 106. In some embodiments, the mutation is selected from H27Y, H27D, H27F, H27N, D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, D105E, D105Q, D105T, D105N, D105G, S106A, S106Q, S106V, S106T, or combinations thereof. In yet another embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 124 with a mutation at one or more amino acid positions 55, 56, 57, 58, 105, and/or 106. The mutation in such embodiments can be selected from D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, D105E, D105Q, D105T, D105N, D105G, S106A, S106Q, S106V, S106T, or combinations thereof. In certain embodiments, the mutation is D55E, D55Q, S56A, D57E, T58A, D105E, D105N, S106A, or combinations thereof. In still another embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 125 with a mutation at one or more amino acid positions 43, 76, 85, 99, 100, and/or 116. Such mutations can include L43Q, L43K, L43H, I76T, R85S, R85G, R85N, R85D, D99E, D99Q, D99S, D99T, G100A, G100Y, G100V, T116L, T116M, T116P, T116R, or combinations thereof. In certain embodiments, the mutation is L43Q, R85S, D99E, G100A, G100Y, T116L, or combinations thereof. In another embodiment, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 115 with a mutation at amino acid position 62 and/or 63. In such embodiments, the mutation can be selected from D62E, D62Q, D62T, D62N, S63A, S63Q, S63V, or combinations thereof. In some embodiments, the mutation is D62E, D62Q, S63A, or combinations thereof. In some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region and/or heavy chain variable region from any of the anti-TREM2 variant antibodies set forth in Tables 2A, 2B, 3A, 3B, and 19. Accordingly, in some embodiments, the light chain variable region of the TREM2 agonist antigen binding proteins comprises a sequence that is at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least 94% identical, or at least 95% identical to a sequence selected from SEQ ID NOs: 61, 153-162, and 295-300. In these and other embodiments, the heavy chain variable region of the TREM2 agonist antigen binding proteins comprises a sequence that is at least 90% identical, at least 91% identical, at least 92% identical, at least 93% identical, at least

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94% identical, or at least 95% identical to a sequence selected from SEQ ID NOs: 124, 180-190, and 307-312.

[00138] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 54 with a mutation at one or more amino acid positions 64, 79, 80, 85, 94, and/or 100. Such mutations can include V64G, V64A, Q79E, Q79D, S80P, S80A, F85V, F85L, F85A, F85D, F85I, F85L, F85M, F85T, W94F, W94Y, W94S, W94T, W94A, W94H, W94I, W94Q, P100R, P100Q, P100G, or combinations thereof. In these and other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 117 with a mutation at one or more amino acid positions 19, 55, 56, 57, 58, and/or 104. In certain embodiments, the mutation is selected from M19K, M19R, M19T, M19E, M19N, M19Q, D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, W104F, W104Y, W104T, W104S, W104A, W104H, W104I, W104Q, or combinations thereof.

[00139] In other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 55 with a mutation at one or more amino acid positions 64, 79, 80, 94, and/or 100. In some embodiments, the mutation is selected from V64G, V64A, Q79E, Q79D, S80P, S80A, W94F, W94Y, W94S, W94T, W94A, W94H, W94I, W94Q, P100R, P100Q, P100G, or combinations thereof. In certain embodiments, the mutation is selected from V64G, V64A, Q79E, S80P, S80A, W94Y, W94S, P100R, P100Q, or combinations thereof. For instance, in some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 55 with one or more mutations selected from V64G, Q79E, S80P, W94Y, and P100Q. In these and other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 118 with a mutation at one or more amino acid positions 19, 55, 56, 57, 58, and/or 104. Such mutations can include M19K, M19R, M19T, M19E, M19N, M19Q, D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, W104F, W104Y, W104T, W104S, W104A, W104H, W104I, W104Q, or combinations thereof. In certain embodiments, the mutation is selected from M19K, D55E, S56A, D57E, T58A, W104Y, W104T, or combinations thereof.

[00140] In certain other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 60 with a mutation at one or more amino acid positions 60, 92, and/or 93. The mutation can be selected from L60S, L60P, L60D, L60A, D92E, D92Q, D92T, D92N, S93A, S93N, S93Q, S93V, or combinations thereof. In these and other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 123 with a mutation at one or more amino acid positions 27, 55, 56, 57, 58, 105, and/or 106. In some embodiments, the mutation is selected from H27Y, H27D, H27F, H27N, D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, D105E, D105Q, D105T, D105N, D105G, S106A, S106Q, S106V, S106T, or combinations thereof.

[00141] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 61 with a mutation at one or more amino acid positions 56, 57, 92, and/or 93. In certain embodiments, the mutation is selected from N56S, N56T, N56Q, N56E, G57A, G57V, D92E, D92Q, D92T, D92N, S93A, S93N, S93Q, S93V, or combinations thereof. In some embodiments, the mutation is selected from N56S, N56Q, G57A, D92E, D92Q, S93A, or combinations thereof. In particular embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 61 with one or more mutations selected from N56S, D92E, and S93A. In these and other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 124 with a mutation at one or more amino acid positions 55, 56, 57, 58, 105, and/or 106. The mutation can be selected from D55E, D55Q, D55N, D55T, S56A, S56Q, S56V, D57S, D57E, D57Q, T58A, T58V, D105E, D105Q, D105T, D105N, D105G, S106A, S106Q, S106V, S106T, or combinations thereof. In certain embodiments, the mutation is D55E, D55Q, S56A, D57E, T58A, D105E, D105N, S106A, or combinations thereof. In some embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 124 with one or more mutations selected from D55E, S56A, D57E, D105E, and S106A.

[00142] In other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 62 with a mutation at amino acid position 36, 46, 61 and/or 100. In particular embodiments, the mutation is selected from F36Y, S46L, S46R, S46V, S46F, K61R, P100Q, P100G, P100R or combinations thereof. In some

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embodiments, the mutation is F36Y, K61R, P100Q, or combinations thereof. In some embodiments, the mutation is S46L, P100Q, or combinations thereof. In these and other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 125 with a mutation at one or more amino acid positions 43, 76, 85, 99, 100, and/or 116. The mutation can be selected from L43Q, L43K, L43H, I76T, R85S, R85G, R85N, R85D, D99E, D99Q, D99S, D99T, G100A, G100Y, G100V, T116L, T116M, T116P, T116R, or combinations thereof. In certain embodiments, the mutation is L43Q, I76T, R85S, D99E, G100A, G100Y, T116L, or combinations thereof.

[00143] In still other embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 52 with a mutation at amino acid position 91. The mutation can be selected from F91V, F91I, F91T, F91L, or F91D. In one embodiment, the mutation is F91V. In these and other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 115 with a mutation at amino acid position 62 and/or 63. In particular embodiments, the mutation is selected from D62E, D62Q, D62T, D62N, S63A, S63Q, S63V, or combinations thereof. In some embodiments, the mutation is selected from D62E, D62Q, S63A, or combinations thereof.

Table 2A. Engineered Variants of 10E3 Antibody

Position in 10E3 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
Light chain variable sequence (SEQ ID NO: 54)				
64	FR3	Covariance violator	V	G, A
79	FR3	Covariance violator	Q	E, D
80	FR3	Covariance violator	S	P, A
85	FR3	Covariance violator	F	V, L, A, D, I, L, M, T
94	CDR3	Potential Tryptophan Oxidation Site	W	F, Y, S, T, A, H, I, Q
100	FR4	Covariance violator	P	R, Q, G
Heavy chain variable sequence (SEQ ID NO: 117)				
19	FR1	Covariance violator	M	K, R, T, E, N, Q

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Position in 10E3 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
55-56	CDR2	Potential Isomerization Site	DS	ES, QS, DA, NS, DQ, TS, DV
57-58	CDR2	Potential Isomerization Site	DT	ST, ET, DA, DV, QT
104	CDR3	Potential Tryptophan Oxidation Site	W	F, Y, T, S, A, H, I, Q

Table 2B. Engineered Variants of 13E7 Antibody

Position in 13E7 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
Light chain variable sequence (SEQ ID NO: 55)				
64	FR3	Covariance violator	V	G, A
79	FR3	Covariance violator	Q	E, D
80	FR3	Covariance violator	S	P, A
94	CDR3	Potential Tryptophan Oxidation Site	W	F, Y, S, T, A, H, I, Q
100	FR4	Covariance violator	P	R, Q, G
Heavy chain variable sequence (SEQ ID NO: 118)				
19	FR1	Covariance violator	M	K, R, T, E, N, Q
55-56	CDR2	Potential Isomerization Site	DS	ES, QS, DA, DQ, NS, TS, DV
57-58	CDR2	Potential Isomerization Site	DT	ST, ET, DA, DV, QT
104	CDR3	Potential Tryptophan Oxidation Site	W	F, Y, T, S, A, H, I, Q

Table 2C. Engineered Variants of 4C5 Antibody

Position in 4C5 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
Light chain variable sequence (SEQ ID NO: 60)				
60	FR3	Covariance violator	L	S, P, D, A
92-93	CDR3	Potential Isomerization Site	DS	ES, QS, DA, DN, DQ, TS, NS, DV
Heavy chain variable sequence (SEQ ID NO: 123)				

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27	FR1	Covariance violator	H	Y, D, F, N
55-56	CDR2	Potential Isomerization Site	DS	ES, QS, DA, DQ, DV, TS, NS
57-58	CDR2	Potential Isomerization Site	DT	ST, ET, DA, DV, QT
105-106	CDR3	Potential Isomerization Site	DS	ES, QS, DA, DQ, DV, TS, NS, GT

Table 2D. Engineered Variants of 6E7 Antibody

Position in 6E7 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
Light chain variable sequence (SEQ ID NO: 61)				
56-57	CDR2/FR3 boundary	Potential Deamidation Site	NG	SG, TG, QG, NA, EG, NV
92-93	CDR3	Potential Isomerization Site	DS	ES, QS, DA, DN, DQ, DV, TS, NS
Heavy chain variable sequence (SEQ ID NO: 124)				
55-56	CDR2	Potential Isomerization Site	DS	ES, QS, DA, DQ, DV, TS, NS
57-58	CDR2	Potential Isomerization Site	DT	ST, ET, DA, DV, QT
105-106	CDR3	Potential Isomerization Site	DS	ES, QS, DA, DQ, DV, TS, NS, GT

Table 2E. Engineered Variants of 5E3 Antibody

Position in 5E3 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
Light chain variable sequence (SEQ ID NO: 62)				
36	FR2	Consensus violator	F	Y
46	FR2	Covariance violator	S	L, R,V, F
61	FR3	Consensus violator	K	R
100	FR4	Covariance violator	P	Q, G, R
Heavy chain variable sequence (SEQ ID NO: 125)				
43	FR2	Covariance violator	L	Q, K, H

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76	FR3	Covariance violator	I	T
85	FR3	Covariance violator	R	S, G, N, D
99-100	CDR3	Potential Isomerization Site	DG	EG, DA, DY, DV, QG, SG, TG
116	FR4	Covariance violator	T	L, M, P, R

Table 2F. Engineered Variants of 24G6 Antibody

Position in 24G6 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
Light chain variable sequence (SEQ ID NO: 52)				
91	FR3	Covariance violator	F	V, I, T, L, D
Heavy chain variable sequence (SEQ ID NO: 115)				
62-63	CDR2	Potential Isomerization Site	DS	ES, QS, DA, DQ, TS, DV, NS

[00144] In some embodiments, the TREM2 agonist antigen binding proteins comprise one or more CDRs of a variant of the anti-TREM2 antibodies described herein. In some embodiments, the TREM2 agonist antigen binding proteins may comprise one or more CDRs of the anti-TREM2 antibody variants set forth in **Tables 3A**, **3B**, **3C**, **3D**, and **3E**, below.

[00145] In certain embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region and/or heavy chain variable region from an affinity-modulated variant of the 6E7 antibody. For instance, in some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region and/or a heavy chain variable region having one or more of the amino acid substitutions set forth in **Table 2G**.

Table 2G. 6E7 Antibody Affinity Modulation Variants

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	Substitutions with respect to 6E7 VH sequence (SEQ ID NO: 124)			Substitutions with respect to 6E7 VL sequence (SEQ ID NO: 61)			Binding Signal (fold over 6E7 parental antibody)			
Variant Ab ID	**HC FR1-CDR1**	**HC CDR2**	**HC CDR3**	**LC CDR1**	**LC CDR2**	**LC CDR3**	**1st screen 110 nM or 10nM[a]**	**2nd screen 2 nM**	**2nd screen 10 nM**	**2nd screen 100 nM**
V1	Y32S		Q99S		Q55T	F94Y	1.68	1.29	1.92	
V2	Y27S	S56G	Q99S		L54R	S93R	2.55	2.23	2.90	
V3	T30A	G66D	Q99G		L54R	S93R	1.97	1.95	2.24	
V4	T30G	Y60V	Q99S		S53R	F94Y	6.00	5.88	5.51	
V5		I50T				F94H	2.73	1.25	2.84	
V6	Y32M						0.20*			0.56
V7	Y32E						0.11*			0.32
V8		R59K					0.28*			0.77
V9			T101G				0.67*			0.54
V10					A50S		0.76*			0.70
V11						D92A	0.79*			0.42
V12	S28E	T58V	Q99G		N56R		2.29	1.04	2.58	
V13	T30G	P62A	Q99G		N56G	F94M	1.31	1.15	1.35	
V14	T30G	S56Q	Q99G		S53R		4.71	2.57	4.64	
V15	T30A	I50T	Q99S		S53W	F94Y	5.23	4.72	4.78	
V16	F29M	S56G	Q99S		S53N		4.01	3.57	4.04	
V17	T30G		Q99S		L54R	F94S	5.37	4.22	5.51	
V18	W33H						0.17*			0.42
V19	Y32S						0.59*			0.48
V20		I50R					0.18*			0.52
V21			Y109F				0.76*			0.68
V22					A50R		0.30*			0.71
V23						R96L	0.40*			0.40
V24		T58V	Q99S		N56K	R96H	2.64	1.42	2.90	
V25	T30G	I50L	Q99S		Q55A	F94M	4.23	3.15	4.70	
V26	A35G	I50T	F102M, Y112A		N56R	F94Y	3.57	2.83	3.47	
V27		S61A	Q99S		N56R		5.50	5.67	5.69	
V28	T30Q	I50T	Y103F		N56S	F94L	3.08	2.63	3.61	
V29	T30K						1.53	0.84	1.67	
V30	Y27S						0.79*			0.72
V31		D57E					0.61*			0.73
V32		P62N					0.82*			0.89

	Substitutions with respect to 6E7 VH sequence (SEQ ID NO: 124)			Substitutions with respect to 6E7 VL sequence (SEQ ID NO: 61)			Binding Signal (fold over 6E7 parental antibody)			
Variant Ab ID	**HC FR1-CDR1**	**HC CDR2**	**HC CDR3**	**LC CDR1**	**LC CDR2**	**LC CDR3**	**1st screen 110 nM or 10nM[a]**	**2nd screen 2 nM**	**2nd screen 10 nM**	**2nd screen 100 nM**
V33			Y104G				0.23*			0.34
V34					N56D		0.34*			1.02
V35						D92Y	0.21*			0.29
V36	I34L		Q99S		L54R	F94Y	3.38	4.00	3.44	
V37	F29H	Q65A	Q99S		N56W	F94Y	3.46	3.69	3.49	
V38	T30G	T58V			L54R	F94H	4.34	3.44	4.36	
V39	T30G	S61N	Q99G		Q55V	F94S	6.15	5.11	5.81	
V40	T30G	T58V	F110S		N56L	S93R	4.48	3.41	4.16	
V41		I50T					1.74	0.58	1.72	
V42	Y32A						0.45*			0.41
V43		D57G					0.20*			0.33
V44		G54S					0.65*			0.52
V45				W32F			0.43*			0.53
V46					S53T		0.83*			0.96
V47						R96M	0.42*			0.47
V48	T30G	T58V	Q99M		N56T	F94L	2.42	2.30	2.54	
V49	T30N	I50T, Y60L	Q99S		L54R	F94Y	6.51	5.02	6.58	
V50	T30G	I50V	F110L		L54R	F94L	4.10	3.39	4.16	
V51		T58V	Q99G, Y112N		L54R		2.81	1.83	3.18	
V52	T30E		Q99G		N56R	S93R	3.00	1.78	3.09	
V53		S63H					1.25	0.66	1.17	
V54	Y32Q						0.55*			0.54
V55		R59I, F64H					0.24*			0.66
V56		S61Q					0.23*			0.59
V57				R24A			0.84*			0.85
V58					A50K		0.28*			0.68
V59						Q89M	0.19*			0.60
V60	S28H	T58V	F110S		N56R	Q89G	3.26	3.35	3.63	
V61	T30S	S61N	Q99G		Q55V	F94L	5.08	3.63	5.22	
V62	T30G	S61A	D108G		N56R	Q89G	2.49	1.87	2.89	

	Substitutions with respect to 6E7 VH sequence (SEQ ID NO: 124)			Substitutions with respect to 6E7 VL sequence (SEQ ID NO: 61)			Binding Signal (fold over 6E7 parental antibody)			
Variant Ab ID	**HC FR1-CDR1**	**HC CDR2**	**HC CDR3**	**LC CDR1**	**LC CDR2**	**LC CDR3**	**1st screen 110 nM or 10nM[a]**	**2nd screen 2 nM**	**2nd screen 10 nM**	**2nd screen 100 nM**
V63	T30R		Q99S		N56R	S93R	3.76	4.91	3.71	
V64	T30Q		Q99G		Q55A	F94Y	5.41	4.88	5.48	
V65			Q99S				2.05	1.29	2.75	
V66	Y27T						0.25*			0.74
V67		I50M					0.80*			0.84
V68			Y103R				0.44*			0.43
V69				W32Y			0.41*			0.40
V70					S52G		0.79*			0.84
V71						F94E	0.37*			0.48
V72	A35G		Q99G		Q55V	F94Y	3.64	2.50	4.01	
V73	T30G	S63G	Q99G		L54R	F94Y	5.12	4.17	5.44	
V74	T30A	T58V	Q99G		N56L		3.94	2.54	4.01	
V75			Q99G		N56A	F94Y	4.64	3.74	4.52	
V76	T30G	S63E	F110S		N56K		4.57	4.34	4.93	
V77					L54R		1.43	0.83	1.38	
V78	S28R						0.86*			1.11
V79		R59N					0.70*			0.52
V80			T101N				0.59*			0.50
V81				W32L			0.17*			0.23
V82					A51G		0.30*			0.79
V83						D92V	0.20*			0.29
V84	S28G		F110S		A50G		1.44	1.45	1.62	
V85	T30R	I50T	Q99S		L54R		5.41	5.41	5.37	
V86	T30G, I34L	Q65E	Q99S		L54R		4.80	5.17	5.02	
V87	T30R	T58V, S63D	Q99S		N56W		3.84	4.86	3.93	
V88	T30G				S53R, N56R	F94S	4.92	5.57	5.30	
V89						F94H	1.33	0.94	1.46	
V90	Y32E			S31R			0.33*			0.36
V91		G54D					0.25*			0.61
V92			Y103H				0.22*			0.65

	Substitutions with respect to 6E7 VH sequence (SEQ ID NO: 124)			Substitutions with respect to 6E7 VL sequence (SEQ ID NO: 61)			Binding Signal (fold over 6E7 parental antibody)			
Variant Ab ID	**HC FR1-CDR1**	**HC CDR2**	**HC CDR3**	**LC CDR1**	**LC CDR2**	**LC CDR3**	**1st screen 110 nM or 10nM[a]**	**2nd screen 2 nM**	**2nd screen 10 nM**	**2nd screen 100 nM**
V93				S31G			0.35*			1.05
V94					S52A		0.31*			0.87

[00146] Binding signal values marked with an * were obtained with the 110 nM Ab concentration, whereas the remaining values in the column were obtained with the 10 nM Ab concentration

[00147] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the sequence of SEQ ID NO: 61 with a mutation at one or more amino acid positions 24, 31, 50, 52, 54, 56, 89, 92, 93, 94 and/or 96. In certain embodiments, the mutation is selected from R24A, S31R, A50S, A50G, S52G, L54R, N56K, N56R, N56L, N56T, Q89G, D92V, S93R, F94Y, F94L, R96H, R96L, or combinations thereof. In these and other embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising the sequence of SEQ ID NO: 124 with a mutation at one or more amino acid positions 27, 28, 30, 32, 50, 54, 58, 60, 61, 63, 66, 99, 101, 103, 104, and/or 110. In some embodiments, the mutation is selected from Y27S, S28G, S28H, T30N, T30G, T30E, T30A, Y32E, I50T, G54S, T58V, Y60L, S61A, S63G, S63E, G66D, Q99G, Q99S, Q99M, T101G, Y103R, Y104G, F110S, or combinations thereof. Amino acid sequences for light chain and heavy chain variable regions and associated CDRs of exemplary variants of the 6E7 antibody with improved affinity are set forth below in **Tables 3A** and **3B**, respectively. Amino acid sequences for light chain and heavy chain variable regions and associated CDRs of exemplary variants of the 6E7 antibody with reduced affinity are set forth below in **Tables 3C** and **3D**, respectively. The corresponding sequences for the 6E7 antibody are listed for comparison.

Table 3A. Light Chain Variable Region Amino Acid Sequences for Improved Affinity TREM2 Antibodies

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Variant Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
6E7	LV-16	DIQMTQSPSSVSASVGDR VTITCRASQGISSWLAWY QQKPGKAPKLLIYAASSL QNGVPSRFSGSGSGTDFT LTISSLQPEDFATYFCQQ ADSFPRTFGQGTKLEIK (SEQ ID NO: 61)	RASQGISSWL A (SEQ ID NO: 16)	AASSLQN (SEQ ID NO: 28)	QQADSFPRT (SEQ ID NO: 43)
V3	LV-101	DIQMTQSPSSVSASVGDR VTITCRASQGISSWLAWY QQKPGKAPKLLIYAASSR QNGVPSRFSGSGSGTDFT LTISSLQPEDFATYFCQQ ADRFPRTFGQGTKLEIK (SEQ ID NO: 153)	RASQGISSWL A (SEQ ID NO: 16)	AASSRQN (SEQ ID NO: 143)	QQADRFPRT (SEQ ID NO: 148)
V24	LV-102	DIQMTQSPSSVSASVGDR VTITCRASQGISSWLAWY QQKPGKAPKLLIYAASSL QKGVPSRFSGSGSGTDFT LTISSLQPEDFATYFCQQ ADSFPHTFGQGTKLEIK (SEQ ID NO: 154)	RASQGISSWL A (SEQ ID NO: 16)	AASSLQK (SEQ ID NO: 144)	QQADSFPHT (SEQ ID NO: 149)
V27	LV-103	DIQMTQSPSSVSASVGDR VTITCRASQGISSWLAWY QQKPGKAPKLLIYAASSL QRGVPSRFSGSGSGTDFT LTISSLQPEDFATYFCQQ ADSFPRTFGQGTKLEIK (SEQ ID NO: 155)	RASQGISSWL A (SEQ ID NO: 16)	AASSLQR (SEQ ID NO: 145)	QQADSFPRT (SEQ ID NO: 43)
V40	LV-104	DIQMTQSPSSVSASVGDR VTITCRASQGISSWLAWY QQKPGKAPKLLIYAASSL QLGVPSRFSGSGSGTDFT LTISSLQPEDFATYFCQQ ADRFPRTFGQGTKLEIK (SEQ ID NO: 156)	RASQGISSWL A (SEQ ID NO: 16)	AASSLQL (SEQ ID NO: 146)	QQADRFPRT (SEQ ID NO: 148)
V48	LV-105	DIQMTQSPSSVSASVGDR VTITCRASQGISSWLAWY QQKPGKAPKLLIYAASSL QTGVPSRFSGSGSGTDFT LTISSLQPEDFATYFCQQ ADSLPRTFGQGTKLEIK (SEQ ID NO: 157)	RASQGISSWL A (SEQ ID NO: 16)	AASSLQT (SEQ ID NO: 26)	QQADSLPRT (SEQ ID NO: 150)
V49 V73	LV-106	DIQMTQSPSSVSASVGDR VTITCRASQGISSWLAWY QQKPGKAPKLLIYAASSR QNGVPSRFSGSGSGTDFT LTISSLQPEDFATYFCQQ ADSYPRTFGQGTKLEIK (SEQ ID NO: 158)	RASQGISSWL A (SEQ ID NO: 16)	AASSRQN (SEQ ID NO: 143)	QQADSYPRT (SEQ ID NO: 151)

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Variant Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
V52	LV-107	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADRFPRTFGQGTKLEIK (SEQ ID NO: 159)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQR (SEQ ID NO: 145)	QQADRFPRT (SEQ ID NO: 148)
V60	LV-108	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCGQADSFPRTFGQGTKLEIK (SEQ ID NO: 160)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQR (SEQ ID NO: 145)	GQADSFPRT (SEQ ID NO: 152)
V76	LV-109	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQKGVPSRFSGSGSGRDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 161)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQK (SEQ ID NO: 144)	QQADSFPRT (SEQ ID NO: 43)
V84	LV-110	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYGASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 162)	RASQGISSWLA (SEQ ID NO: 16)	GASSLQN (SEQ ID NO: 147)	QQADSFPRT (SEQ ID NO: 43)

Table 3B. Heavy Chain Variable Region Amino Acid Sequences for Improved Affinity TREM2 Antibodies

Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/CDRH1 Border	CDRH1	CDRH2	CDRH3
6E7	HV-15	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSDYFDY (SEQ ID NO: 107)

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Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 Border	CDRH1	CDRH2	CDRH3
		(SEQ ID NO: 124)				
V3	HV-101	EVQLVQSGAEVKKPGESLKISCKGSGYSFASYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQDQVTISADKSISTAYLQWSSLKASDTAMYFCARGRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 180)	YSFA (SEQ ID NO: 164)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQD (SEQ ID NO: 170)	GRTFYYDSSDYFDY (SEQ ID NO: 176)
V24	HV-102	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDVRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARSRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 181)	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDVRYSPSFQG (SEQ ID NO: 171)	SRTFYYDSSDYFDY (SEQ ID NO: 177)
V27	HV-103	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCVRSRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 182)	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYAPSFQG (SEQ ID NO: 172)	SRTFYYDSSDYFDY (SEQ ID NO: 177)

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Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 Border	CDRH1	CDRH2	CDRH3
V40	HV-104	EVQLVQSGAEVKKPGESLKISCKGSGYSFGSYWIAWVRQMPGKGLEWMGIIYPGDSDVRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYSDYWGQGTLVTVSS (SEQ ID NO: 183)	YSFG (SEQ ID NO: 165)	SYWIA (SEQ ID NO: 85)	IIYPGDSDVRYSPSFQG (SEQ ID NO: 171)	QRTFYYDSSDYSDY (SEQ ID NO: 178)
V48	HV-105	EVQLVQSGAEVKKPGESLKISCKGSGYSFGSYWIAWVRQMPGKGLEWMGIIYPGDSDVRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARMRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 184)	YSFG (SEQ ID NO: 165)	SYWIA (SEQ ID NO: 85)	IIYPGDSDVRYSPSFQG (SEQ ID NO: 171)	MRTFYYDSSDYFDY (SEQ ID NO: 179)
V49	HV-106	EVQLVQSGAEVKKPGESLKISCKGSGYSFNSYWIAWVRQMPGKGLEWMGTIYPGDSDTRLSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARSRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 185)	YSFN (SEQ ID NO: 166)	SYWIA (SEQ ID NO: 85)	TIYPGDSDTRLSPSFQG (SEQ ID NO: 173)	SRTFYYDSSDYFDY (SEQ ID NO: 177)
V52	HV-107	EVQLVQSGAEVKKPGESLKISCKGSGYSFESYW	YSFE (SEQ ID	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG	GRTFYYDSSDYFDY (SEQ ID NO: 176)

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Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 Border	CDRH1	CDRH2	CDRH3
		IAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARGRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 186)	NO: 167)		(SEQ ID NO: 91)	
V60	HV-108	EVQLVQSGAEVKKPGESLKISCKGSGYHFTSYWIAWVRQMPGKGLEWMGIIYPGDSDVRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYSDYWGQGTLVTVSS (SEQ ID NO: 187)	YHFT (SEQ ID NO: 168)	SYWIA (SEQ ID NO: 85)	IIYPGDSDVRYSPSFQG (SEQ ID NO: 171)	QRTFYYDSSDYSDY (SEQ ID NO: 178)
V73	HV-109	EVQLVQSGAEVKKPGESLKISCKGSGYSFGSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPGFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARGRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 188)	YSFG (SEQ ID NO: 165)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPGFQG (SEQ ID NO: 174)	GRTFYYDSSDYFDY (SEQ ID NO: 176)
V76	HV-110	EVQLVQSGAEVKKPGESLKISCKGSGYSFGSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPEFQG	YSFG (SEQ ID NO: 165)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPEFQG (SEQ ID NO: 175)	QRTFYYDSSDYSDY (SEQ ID NO: 178)

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Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 Border	CDRH1	CDRH2	CDRH3
		QVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYSDYWGQGTLVTVSS (SEQ ID NO: 189)				
V84	HV-111	EVQLVQSGAEVKKPGESLKISCKGSGYGFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYSDYWGQGTLVTVSS (SEQ ID NO: 190)	YGFT (SEQ ID NO: 169)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSDYSDY (SEQ ID NO: 178)

[00148] In some embodiments, the TREM2 agonist antigen binding proteins of the invention may comprise one or more of the CDRs from the improved affinity variants presented in **Table 3A** (light chain CDRs; i.e. CDRLs) and **Table 3B** (heavy chain CDRs, i.e. CDRHs). In some embodiments, the TREM2 agonist antigen binding proteins comprise a consensus CDR sequence derived from the improved affinity variants. For instance, in some embodiments, the TREM2 agonist antigen binding proteins comprise a CDRL2 consensus sequence of $X_1ASSX_2QX_3$ (SEQ ID NO: 139), where X_1 is A or G; X_2 is L or R; and X_3 is N, K, R, L, or T. In another embodiment, the TREM2 agonist antigen binding proteins comprise a CDRL3 consensus sequence of $X_1QADX_2X_3PX_4T$ (SEQ ID NO: 140), where X_1 is Q or G; X_2 is S or R; X_3 is F, L, or Y; and X_4 is R or H. In yet another embodiment, the TREM2 agonist antigen binding proteins comprise a CDRH2 consensus sequence of $X_1IYPGDSDX_2RX_3X_4PX_5FQX_6$ (SEQ ID NO: 141), where X_1 is I or T; X_2 is T or V; X_3 is Y or L; X_4 is S or A; X_5 is S, G, or E; and X_6 is G or D. In some embodiments, the TREM2 agonist antigen binding proteins comprise a CDRH3 consensus

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sequence of X_1RTFYYDSSDYX_2DY (SEQ ID NO: 142), where X_1 is Q, G, S, or M; and X_2 is F or S.

[00149] In some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region comprising complementarity determining regions CDRL1, CDRL2, and CDRL3 and a heavy chain variable region comprising complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein CDRL1 comprises the sequence of SEQ ID NO: 16, CDRL2 comprises the consensus sequence of SEQ ID NO: 139, CDRL3 comprises the consensus sequence of SEQ ID NO: 140, CDRH1 comprises the sequence of SEQ ID NO: 85, CDRH2 comprises the consensus sequence of SEQ ID NO: 141, and CDRH3 comprises the consensus sequence of SEQ ID NO: 142.

[00150] In some embodiments, the TREM2 agonist antigen binding protein comprises a CDRL1 comprising the sequence of SEQ ID NO: 16; a CDRL2 comprising a sequence selected from SEQ ID NOs: 26 and 143-147; a CDRL3 comprising a sequence selected from SEQ ID NOs: 43 and 148-152; a CDRH1 comprising the sequence of SEQ ID NO: 85; a CDRH2 comprising a sequence selected from SEQ ID NOs: 91 and 170-175; and a CDRH3 comprising a sequence selected from SEQ ID NOs: 176-179.

[00151] In particular embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 143, and 148, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 144, and 149, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 145, and 43, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 146, and 148, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 26, and 150, respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 143, and

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151, respectively;

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 145, and 148, respectively;

(h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 145, and 152, respectively;

(i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 144, and 43, respectively; or

(j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 147, and 43, respectively.

[00152] In related embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein: (a) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 170, and 176, respectively;

(b) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 171, and 177, respectively;

(c) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 172, and 177, respectively;

(d) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 171, and 178, respectively;

(e) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 171, and 179, respectively;

(f) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 173, and 177, respectively;

(g) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 176, respectively;

(h) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 174, and 176, respectively;

(i) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 175, and 178, respectively; or

(j) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 178, respectively.

[00153] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 143, and 148, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 170, and 176, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 144, and 149, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 171, and 177, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 145, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 172, and 177, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 146, and 148, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 171, and 178, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 26, and 150, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 171, and 179, respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 143, and 151, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 173, and 177, respectively;

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 145, and 148, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 176, respectively;

(h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 145, and 152, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 171, and 178, respectively;

(i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 143, and 151, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 174, and 176, respectively;

(j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 144, and

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43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 175, and 178, respectively; or

(k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 147, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 178, respectively.

[00154] In some embodiments, the TREM2 agonist antigen binding proteins of the invention may comprise a light chain variable region selected from LV-101, LV-102, LV-103, LV-104, LV-105, LV-106, LV-107, LV-108, LV-109, and LV-110, as shown in **Table 3A**, and/or a heavy chain variable region selected from HV-101, HV-102, HV-103, HV-104, HV-105, HV-106, HV-107, HV-108, HV-109, HV-110, and HV-111, as shown in **Table 3B**, or sequences that are at least 80% identical, at least 85% identical, at least 90% identical, or at least 95% identical to any of the sequences in **Tables 3A** and **3B**. For instance, in some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region comprising (i) a sequence that is at least 90% identical to a sequence selected from SEQ ID NOs: 153-162, (ii) a sequence that is at least 95% identical to a sequence selected from SEQ ID NOs: 153-162, or (iii) a sequence selected from SEQ ID NOs: 153-162. In related embodiments, the TREM2 agonist antigen binding proteins comprise a heavy chain variable region comprising (i) a sequence that is at least 90% identical to a sequence selected from SEQ ID NOs: 180-190, (ii) a sequence that is at least 95% identical to a sequence selected from SEQ ID NOs: 180-190, or (iii) a sequence selected from SEQ ID NOs: 180-190.

[00155] Each of the light chain variable regions listed in **Table 3A** may be combined with any of the heavy chain variable regions listed in **Table 3B** to form an anti-TREM2 binding domain of the antigen binding proteins of the invention. Examples of such combinations include, but are not limited to: LV-101 (SEQ ID NO: 153) and HV-101 (SEQ ID NO: 180); LV-102 (SEQ ID NO: 154) and HV-102 (SEQ ID NO: 181); LV-103 (SEQ ID NO: 155) and HV-103 (SEQ ID NO: 182); LV-104 (SEQ ID NO: 156) and HV-104 (SEQ ID NO: 183); LV-105 (SEQ ID NO: 157) and HV-105 (SEQ ID NO: 184); LV-106 (SEQ ID NO: 158) and HV-106 (SEQ ID NO: 185); LV-107 (SEQ ID NO: 159) and HV-107 (SEQ ID NO: 186); LV-108 (SEQ ID NO: 160) and HV-108 (SEQ ID NO: 187); LV-106 (SEQ ID NO: 158) and HV-109 (SEQ ID NO: 188); LV-109 (SEQ ID NO: 161) and HV-110 (SEQ ID NO: 189); and LV-110 (SEQ ID NO: 162) and HV-111 (SEQ ID NO: 190).

Table 3C. Light Chain Variable Region Amino Acid Sequences for Reduced Affinity TREM2 Antibodies

Variant Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
6E7	LV-16	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 61)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQN (SEQ ID NO: 28)	QQADSFPRT (SEQ ID NO: 43)
V9 V30 V33 V44 V68	LV-16	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 61)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQN (SEQ ID NO: 28)	QQADSFPRT (SEQ ID NO: 43)
V10	LV-201	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYSASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 295)	RASQGISSWLA (SEQ ID NO: 16)	SASSLQN (SEQ ID NO: 292)	QQADSFPRT (SEQ ID NO: 43)
V23	LV-202	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPLTFGQGTKLEIK (SEQ ID NO: 296)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQN (SEQ ID NO: 28)	QQADSFPLT (SEQ ID NO: 294)
V57	LV-203	DIQMTQSPSSVSASVGDRVTITCAASQGISSWLAWYQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 297)	AASQGISSWLA (SEQ ID NO: 290)	AASSLQN (SEQ ID NO: 28)	QQADSFPRT (SEQ ID NO: 43)
V70	LV-204	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAAGSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 298)	RASQGISSWLA (SEQ ID NO: 16)	AAGSLQN (SEQ ID NO: 293)	QQADSFPRT (SEQ ID NO: 43)

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Variant Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
V83	LV-205	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQAVSFPRTFGQGTKLEIK (SEQ ID NO: 299)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQN (SEQ ID NO: 28)	QQAVSFPRT (SEQ ID NO: 271)
V90	LV-206	DIQMTQSPSSVSASVGDRVTITCRASQGISRWLAWYQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKLEIK (SEQ ID NO: 300)	RASQGISRWLA (SEQ ID NO: 291)	AASSLQN (SEQ ID NO: 28)	QQADSFPRT (SEQ ID NO: 43)

Table 3D. Heavy Chain Variable Region Amino Acid Sequences for Reduced Affinity TREM2 Antibodies

Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/CDRH1 border	CDRH1	CDRH2	CDRH3
6E7	HV-15	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 124)	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSDYFDY (SEQ ID NO: 107)
V9	HV-201	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRGFYYDSSDYFDYWGQGTLVTV	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRGFYYDSSDYFDY (SEQ ID NO: 304)

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Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 border	CDRH1	CDRH2	CDRH3
		SS (SEQ ID NO: 307)				
V10 V23 V57 V70 V83	HV-15	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 124)	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSDYFDY (SEQ ID NO: 107)
V30	HV-202	EVQLVQSGAEVKKPGESLKISCKGSGSSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 308)	SSFT (SEQ ID NO: 301)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSDYFDY (SEQ ID NO: 107)
V33	HV-203	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYGDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 309)	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYGDSSDYFDY (SEQ ID NO: 305)
V44	HV-204	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPSDSDTRYSPSFQG	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPSDSDTRYSPSFQG (SEQ ID NO: 303)	QRTFYYDSSDYFDY (SEQ ID NO: 107)

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Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/CDRH1 border	CDRH1	CDRH2	CDRH3
		QVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 310)				
V68	HV-205	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFRYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 311)	YSFT (SEQ ID NO: 163)	SYWIA (SEQ ID NO: 85)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFRYDSSDYFDY (SEQ ID NO: 306)
V90	HV-206	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSEWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 312)	YSFT (SEQ ID NO: 163)	SEWIA (SEQ ID NO: 302)	IIYPGDSDTRYSPSFQG (SEQ ID NO: 91)	QRTFYYDSSDYFDY (SEQ ID NO: 107)

[00156] In some embodiments, the TREM2 agonist antigen binding proteins of the invention may comprise one or more of the CDRs from the reduced affinity variants presented in **Table 3C** (light chain CDRs; i.e. CDRLs) and **Table 3D** (heavy chain CDRs, i.e. CDRHs). In some embodiments, the TREM2 agonist antigen binding proteins comprise a consensus CDR sequence derived from the reduced affinity variants. For instance, in one embodiment, the TREM2 agonist antigen binding proteins comprise a CDRL1 consensus sequence of X_1ASQGISX_2WLA (SEQ ID NO: 284), where X_1 is R or A; and X_2 is S or R. In another embodiment, the TREM2 agonist antigen binding proteins comprise a CDRL2 consensus sequence of X_1AX_2SLQN (SEQ ID NO:

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285), where X_1 is A or S; and X_2 is S or G. In another embodiment, the TREM2 agonist antigen binding proteins comprise a CDRL3 consensus sequence of QQAX_1SFPX_2T (SEQ ID NO: 286), where X_1 is D or V; and X_2 is R or L. In another embodiment, the TREM2 agonist antigen binding proteins comprise a CDRH1 consensus sequence of SX_1WIA (SEQ ID NO: 287), where X_1 is Y or E. In yet another embodiment, the TREM2 agonist antigen binding proteins comprise a CDRH2 consensus sequence of IIYPX_1DSDTRYSPSFQG (SEQ ID NO: 288), where X_1 is G or S. In still another embodiment, the TREM2 agonist antigen binding proteins comprise a CDRH3 consensus sequence of QRX_1FX_2X_3DSSDYFDY (SEQ ID NO: 289), where X_1 is T or G; X_2 is Y or R; and X_3 is Y or G. In some embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region comprising complementarity determining regions CDRL1, CDRL2, and CDRL3 and a heavy chain variable region comprising complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein CDRL1 comprises the sequence of SEQ ID NO: 284, CDRL2 comprises the consensus sequence of SEQ ID NO: 285, CDRL3 comprises the consensus sequence of SEQ ID NO: 286, CDRH1 comprises the sequence of SEQ ID NO: 287, CDRH2 comprises the consensus sequence of SEQ ID NO: 288, and CDRH3 comprises the consensus sequence of SEQ ID NO: 289.

[00157] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a CDRL1 comprising a sequence selected from SEQ ID NOs: 16, 290, and 291; a CDRL2 comprising a sequence selected from SEQ ID NOs: 28, 292, and 293; a CDRL3 comprising a sequence selected from SEQ ID NOs: 43, 294, and 271; a CDRH1 comprising the sequence of SEQ ID NO: 85 or SEQ ID NO: 302; a CDRH2 comprising the sequence of SEQ ID NO: 91 or SEQ ID NO: 303; and a CDRH3 comprising a sequence selected from SEQ ID NOs: 107 and 304-306.

[00158] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 292, and 43, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 294, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 290, 28, and 43, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 293, and 43, respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 271, respectively; or

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 291, 28, and 43, respectively.

[00159] In related embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 304, respectively;

(b) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively;

(c) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 305, respectively;

(d) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 303, and 107, respectively;

(e) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 306, respectively; or

(f) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 302, 91, and 107, respectively.

[00160] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 304, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 292, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91,

and 107, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 294, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 305, respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 303, and 107, respectively;

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 290, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively;

(h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 306, respectively;

(i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 293, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively;

(j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 28, and 271, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 91, and 107, respectively; or

(k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 291, 28, and 43, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 302, 91, and 107, respectively.

[00161] In some embodiments, the TREM2 agonist antigen binding proteins of the invention may comprise a light chain variable region selected from LV-16, LV-201, LV-202, LV-203, LV-204, LV-205, and LV-206, as shown in **Table 3C**, and/or a heavy chain variable region selected

from HV-15, HV-201, HV-202, HV-203, HV-204, HV-205, and HV-206, as shown in **Table 3D**, or sequences that are at least 80% identical, at least 85% identical, at least 90% identical, or at least 95% identical to any of the sequences in **Tables 3C** and **3D**. For instance, in certain embodiments, the TREM2 agonist antigen binding proteins comprise a light chain variable region comprising (i) a sequence that is at least 90% identical to a sequence selected from SEQ ID NOs: 61 and 295-300, (ii) a sequence that is at least 95% identical to a sequence selected from SEQ ID NOs: 61 and 295-300, or (iii) a sequence selected from SEQ ID NOs: 61 and 295-300. In related embodiments, the TREM2 agonist antigen binding proteins comprise a heavy chain variable region comprising (i) a sequence that is at least 90% identical to a sequence selected from SEQ ID NOs: 124 and 307-312, (ii) a sequence that is at least 95% identical to a sequence selected from SEQ ID NOs: 124 and 307-312, or (iii) a sequence selected from SEQ ID NOs: 124 and 307-312.

[00162] In some embodiments, each of the light chain variable regions listed in **Table 3C** may be combined with any of the heavy chain variable regions listed in **Table 3D** to form an anti-TREM2 binding domain of the antigen binding proteins of the invention. Examples of such combinations include, but are not limited to: LV-16 (SEQ ID NO: 61) and HV-201 (SEQ ID NO: 307); LV-201 (SEQ ID NO: 295) and HV-15 (SEQ ID NO: 124); LV-202 (SEQ ID NO: 296) and HV-15 (SEQ ID NO: 124); LV-16 (SEQ ID NO: 61) and HV-202 (SEQ ID NO: 308); LV-16 (SEQ ID NO: 61) and HV-203 (SEQ ID NO: 309); LV-16 (SEQ ID NO: 61) and HV-204 (SEQ ID NO: 310); LV-203 (SEQ ID NO: 297) and HV-15 (SEQ ID NO: 124); LV-16 (SEQ ID NO: 61) and HV-205 (SEQ ID NO: 311); LV-204 (SEQ ID NO: 298) and HV-15 (SEQ ID NO: 124); LV-205 (SEQ ID NO: 299) and HV-15 (SEQ ID NO: 124); and LV-206 (SEQ ID NO: 300) and HV-206 (SEQ ID NO: 312).

[00163] In some embodiments, the TREM2 agonist antigen binding proteins comprise one or more CDRs of the anti-TREM2 antibody variants set forth in **Table 3E**. In some embodiments, the TREM2 agonist antigen binding proteins comprise the light chain variable region and heavy chain variable region of the anti-TREM2 antibody variants set forth in **Table 3E**.

Table 3E. Exemplary Variable Region Amino Acid Sequences of Engineered Antibodies

Ab ID.	LC variable region	CDRL1	CDRL2	CDRL3

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24G6 (SST28347 and SST204812)	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKHFLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVEIK (SEQ ID NO: 326)	KSSQSVLYSSNNKHFLA (SEQ ID NO: 8)	WASTRES (SEQ ID NO: 22)	QQYYSTPLT (SEQ ID NO: 35)
6E7 (SST29857)	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADAFPRTFGQGTKLEIK (SEQ ID NO: 328)	RASQGISSWLA (SEQ ID NO: 16)	AASSLQS (SEQ ID NO: 369)	QQADAFPRT (SEQ ID NO: 370)
13E7 (SST202443)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQDNNFPPTFGQGTKVDIK (SEQ ID NO: 330)	RASQSVSSNLA (SEQ ID NO: 10)	GASTRAT (SEQ ID NO: 23)	LQDNNFPPT (SEQ ID NO: 372)
5E3 (SST29825)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTYPFTFGQGTKVDIK (SEQ ID NO: 332)	RASQGISNYLA (SEQ ID NO: 17)	AASSLQS (SEQ ID NO: 29)	QQYSTYPFT (SEQ ID NO: 44)
Ab ID.	**HC variable region**	**CDRH1**	**CDRH2**	**CDRH3**
24G6 (SST28347 and SST204812)	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAYTPMAFFDYWGQGTLVTVSS (SEQ ID NO: 327)	SYAMS (SEQ ID NO: 77)	AISGSGGSTYYAESVKG (SEQ ID NO: 368)	AYTPMAFFDY (SEQ ID NO: 98)
6E7	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKG	SYWIA	IIYPGDADARYSPSFQG	QRTFYYDSSDYFDY

2 4

(SST29857)	LEWMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS (SEQ ID NO: 329)	(SEQ ID NO: 85)	(SEQ ID NO: 371)	(SEQ ID NO: 107)
13E7 (SST202443)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFCARRRQGIFGDALDFWGQGTLVTVSS (SEQ ID NO: 331)	SYWIG (SEQ ID NO: 81)	IIYPGDADARYSPSFQG (SEQ ID NO: 373)	RRQGIFGDALDF (SEQ ID NO: 374)
	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINPYSGGTTSAQKFQGRVTMTRDTSTSSAYMELSRLRSDDTAVYYCARDAGYLALYGTDVWGQGTLVTVSS (SEQ ID NO: 333)	GYYIH (SEQ ID NO: 86)	WINPYSGGTTSAQKFQG (SEQ ID NO: 94)	DAGYLALYGTDV (SEQ ID NO: 375)

[00164] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 369, and 370, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 372, respectively; or

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 21, and 33, respectively; (d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 20, and 33, respectively.

[00165] In some embodiments, the TREM2 agonist antigen binding protein comprises a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 368, and 98, respectively;

(b) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 371, and 107, respectively;

(c) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 373, and 374, respectively; or

(d) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 86, 94, and 375, respectively.

[00166] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 8, 22, and 35, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 77, 368, and 98, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 16, 369, and 370, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 85, 371, and 107, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 372, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 373, and 374, respectively; or

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 17, 29, and 44, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 86, 94, and 375, respectively.

[00167] Accordingly, in some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3, and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein the CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 23, and 372, respectively, and the CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 81, 373, and 374, respectively.

[00168] In some embodiments therefore, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a CDRL1, CDRL2, and CDRL3

having the sequence of SEQ ID NOs: 10, 23, and 372, respectively, and a CDRH1, CDRH2, and CDRH3 having the sequence of SEQ ID NOs: 81, 373, and 374, respectively. In certain embodiments, the antibody is human.In some embodiments, the TREM2 agonist antigen binding protein comprises

(a) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 326 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 327;

(b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 328 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 329;

(c) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 330 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 331; or

(d) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 332 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 333.

[00169] In some embodiments, the TREM2 agonist antigen binding protein comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 330 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 331.

[00170] In some embodiments therefore, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain variable region comprising the amino acid sequence of SEQ ID NO: 330 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 331. In certain embodiments, the antibody is human.

[00171] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 326, 328, 330 or 332. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a heavy chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 327, 329, 331 or 333. In a specific embodiment, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region and a heavy chain variable region, wherein the light chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 326 and

the heavy chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 327. In a specific embodiment, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region and a heavy chain variable region, wherein the light chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 328 and the heavy chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 329. In a specific embodiment, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region and a heavy chain variable region, wherein the light chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 330 and the heavy chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 331. In a specific embodiment, the TREM2 agonist antigen binding proteins of the invention comprise a light chain variable region and a heavy chain variable region, wherein the light chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 332 and the heavy chain variable region consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 333.

[00172] In some embodiments, each of the light chain variable regions disclosed in **Tables 1A, 3A, 3C, and 3E** and each of the heavy chain variable regions disclosed in **Tables 1B, 3B, 3D, and 3E** may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

[00173] In some embodiments, exemplary TREM2 agonist antibody having a light chain variable region with a light chain constant domain and a heavy chain variable region with a heavy chain constant region are disclosed in **Table 3F**.

Table 3F. Light Chain and Heavy Chain Amino Acid Sequences of Exemplary Antibodies

Ab ID.		Sequence
24G6 (SST28347)	LC	MDMRVPAQLLGLLLLWLRGARCDIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNKHFLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSG

2 4

Ab ID.		Sequence
		TDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC (SEQ ID NO: 334)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAYTPMAFFDYWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 335)
24G6 (SST204812)	LC	MDMRVPAQLLGLLLLWLRGARCDIVMTQSPDSLAVSLGERATINCKSS QSVLYSSNNKHFLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSG TDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC (SEQ ID NO: 334)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAYTPMAFFDYWGQGTLVTVSSAST KGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVE RKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 336)

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Ab ID.		Sequence
6E7 (SST29857)	LC	MDMRVPAQLLGLLLLWLRGARCDIQMTQSPSSVSASVGDRVTITCRAS QGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLT ISSLQPEDFATYFCQQADAFPRTFGQGTKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 337)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLVQSGAEVKKPGESLKISCKGSG YSFTSYWIAWVRQMPGKGLEWMGIIYPGDADARYSPSFQGQVTISADK SISTAYLQWSSLKASDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVS SASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVD KTVERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 338)
13E7 (SST202443)	LC	MDMRVPAQLLGLLLLWLRGARCEIVMTQSPATLSVSPGERATLSCRAS QSVSSNLAWFQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLT ISSLQPEDFAVYYCLQDNNFPPTFGQGTKVDIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 339)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLVQSGAEVKKPGESLKISCKGSG YSFTSYWIGWVRQMPGKGLEWMGIIYPGDADARYSPSFQGQVTISADK SISTAYLQWSSLKASDTAMYFCARRRQGIFGDALDFWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL

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Ab ID.		Sequence
		YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 340)
5E3 (SST29825)	LC	MDMRVPAQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRAS QGISNYLAWYQQKPGKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLT ISSLQPEDFATYYCQQYSTYPFTFGQGTKVDIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 341)
	HC	MDMRVPAQLLGLLLLWLRGARCQVQLVQSGAEVKKPGASVKVSCKASG YTFTGYYIHWVRQAPGQGLEWMGWINPYSGGTTSAQKFQGRVTMTRDT STSSAYMELSRLRSDDTAVYYCARDAGYLALYGTDVWGQGTLVTVSSA STKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKT VERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 342)
24G6-1 (SST28347-1)	LC	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKHFLAWYQQKPGQ PPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2768)
	HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWV SAISGSGGSTYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC AKAYTPMAFFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE

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Ab ID.		Sequence
		SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK (SEQ ID NO: 2769)
24G6-1 (SST28347-1)	LC	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKHFLAWYQQKPGQ PPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2768)
	HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWV SAISGSGGSTYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC AKAYTPMAFFDYWGQGTLVTVSSASTKGPSVFPLAPSSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG (SEQ ID NO: 2770)
6E7-1 (SST29857-1)	LC	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLI YAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQADAFPR TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2771)
	HC	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWM GIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFC ARQRTFYYDSSDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPG (SEQ ID NO: 2772)

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Ab ID.		Sequence
13E7-1 (SST202443-1)	LC	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLI YGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQDNNFPP TFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2773)
	HC	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWM GIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFC ARRRQGIFGDALDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG (SEQ ID NO: 2774)
5E3-1 (SST29825-1)	LC	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKSLI YAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTYPF TFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2775)
	HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWM GWINPYSGGTTSAQKFQGRVTMTRDTSTSSAYMELSRLRSDDTAVYYC ARDAGYLALYGTDVWGQGTLVTVSSASTKGPSVFPLAPSSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPG (SEQ ID NO: 2776)
13E7 Variant	LC	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLI YGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQDNNFPP TFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA

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Ab ID.		Sequence
		KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC(SEQ ID NO: 2777)
	HC	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWM GIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYFC ARRRQGIFGDALDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK(SEQ ID NO: 2778)

[00174] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 334 and a heavy chain comprising the sequence of SEQ ID NO: 335. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 334 and a heavy chain comprising the sequence of SEQ ID NO: 336. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 337 and a heavy chain comprising the sequence of SEQ ID NO: 338. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 339 and a heavy chain comprising the sequence of SEQ ID NO: 340. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 341 and a heavy chain comprising the sequence of SEQ ID NO: 342. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 2768 and a heavy chain comprising the sequence of SEQ ID NO: 2769. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 2768 and a heavy chain comprising the sequence of SEQ ID NO: 2770. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence

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of SEQ ID NO: 2771 and a heavy chain comprising the sequence of SEQ ID NO: 2772. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 2773 and a heavy chain comprising the sequence of SEQ ID NO: 2774. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain comprising the sequence of SEQ ID NO: 2775 and a heavy chain comprising the sequence of SEQ ID NO: 2776.

[00175] In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 334 and a heavy chain comprising the sequence of SEQ ID NO: 335. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 334 and a heavy chain comprising the sequence of SEQ ID NO: 336. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 337 and a heavy chain comprising the sequence of SEQ ID NO: 338. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 339 and a heavy chain comprising the sequence of SEQ ID NO: 340. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 341 and a heavy chain comprising the sequence of SEQ ID NO: 342. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 2768 and a heavy chain comprising the sequence of SEQ ID NO: 2769. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen

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binding protein comprising a light chain comprising the sequence of SEQ ID NO: 2768 and a heavy chain comprising the sequence of SEQ ID NO: 2770. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 2771 and a heavy chain comprising the sequence of SEQ ID NO: 2772. In some embodiments therefore, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 2773 and a heavy chain comprising the sequence of SEQ ID NO: 2774. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 2775 and a heavy chain comprising the sequence of SEQ ID NO: 2776. In some embodiments, the present invention provides a method of treating ALSP in a human patient, the method comprising administering to the patient an effective amount of a TREM2 agonist antigen binding protein comprising a light chain comprising the sequence of SEQ ID NO: 2777 and a heavy chain comprising the sequence of SEQ ID NO: 2778.

[00176] In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 334, 337, 339 or 341. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2768, 2771, 2773, or 2775. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 335, 336, 338, 340, or 342. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2769, 2770, 2772, 2774, or 2776. In a specific embodiment, the TREM2 agonist antigen binding proteins of the invention comprise a light chain and a heavy chain, wherein:

(a) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 334 and the heavy chain consisting of or consisting essentially of the amino acid

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sequence of SEQ ID NO: 335;

(b) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 334 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 336;

(c) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 337 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 338;

(d) the light chain consisting of or consisting of essentially of the amino acid sequence of SEQ ID NO: 339 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 340; or

(e) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 341 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 342.

[00177] In a specific embodiment, the TREM2 agonist antigen binding proteins of the invention comprise a light chain and a heavy chain, wherein:

(a) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2768 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2769;

(b) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2768 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2770;

(c) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2771 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2772;

(d) the light chain consisting of or consisting of essentially of the amino acid sequence of SEQ ID NO: 2773 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2774;

(e) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2775 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2776; or

(f) the light chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2777 and the heavy chain consisting of or consisting essentially of the amino acid sequence of SEQ ID NO: 2778.

[00178] Unless indicated otherwise by reference to a specific sequence in Tables 1A, 1B, 3A, 3B, 3C, 3D, 3E and in related discussions, the numbering of the amino acid residues in an immunoglobulin heavy chain or light chain is according to Kabat-EU numbering as described in Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed., US Department of Health and Human Services, NIH publication No. 91-3242, pp 662,680,689 (1991) and Edelman *et al.*, Proc. Natl. Acad. USA, Vol. 63: 78-85 (1969). The Kabat numbering scheme is typically used when referring to the position of an amino acid within the variable regions, whereas the EU numbering scheme is generally used when referring to the position of an amino acid with an immunoglobulin constant region.

[00179] In some embodiments, the TREM2 antigen binding protein comprise an antibody that competes with an antibody comprising CDRL1, CDRL2, CDRL3 or light chain variable region disclosed in **Tables 1A, 3A, 3C and 3E**, and a heavy chain variable region disclosed in **Tables 1B, 3B, 3D and 3E**. In some embodiments, a suitable assay for detecting competitive binding employs kinetic sensors used with Octet® systems (Pall ForteBio), which measures binding interactions using bio-layer interferometry methodology. One group of antibodies, antibodies 10E3, 13E7, 24F4, 4C5, 4G10, 32E3, and 6E7, competed with each other for binding to human TREM2, indicating that they share the same or similar epitope on human TREM2. Antibodies 16B8, 26A10, 26C10, 26F2, 33B12, and 5E3 compete with each other for TREM2 binding, but does not compete with antibodies in the first group or antibodies 24A10, 24G6, or 25F12, indicating that this second group of antibodies bind to a distinct epitope on human TREM2. Antibodies 24A10 and 24G6 share a similar epitope on human TREM2 as these two antibodies compete with each other for human TREM2 binding, but did not compete with any other antibody. Antibody 25F12 did not compete with any of the other tested antibodies for human TREM2 binding, indicating that this antibody binds to yet another epitope.

[00180] In some embodiments, a TREM2 agonist antigen binding protein competes with a reference antibody for binding to human TREM2, wherein the reference antibody comprises a light chain variable region comprising a sequence selected from SEQ ID NOs: 46-63 and a heavy

chain variable region comprising a sequence selected from SEQ ID NOs: 110-126. In other embodiments, a TREM2 agonist antigen binding protein of the invention competes with a reference antibody for binding to human TREM2, wherein the reference antibody comprises a light chain variable region comprising a sequence selected from SEQ ID NOs: 153-162 and a heavy chain variable region comprising a sequence selected from SEQ ID NOs: 180-190. In still other embodiments, a TREM2 agonist antigen binding protein of the invention competes with a reference antibody for binding to human TREM2, wherein the reference antibody comprises a light chain variable region comprising a sequence selected from SEQ ID NOs: 61 and 295-300 and a heavy chain variable region comprising a sequence selected from SEQ ID NOs: 124 and 307-312. In certain embodiments, a TREM2 agonist antigen binding protein of the invention competes for binding to human TREM2 with one or more of the anti-TREM2 antibodies described herein, including 12G10, 26A10, 26C10, 26F2, 33B12, 24C12, 24G6, 24A10, 10E3, 13E7, 14C12, 25F12, 32E3, 24F4, 16B8, 4C5, 6E7, 5E3, 4G10, V3, V9, V10, V23, V24, V27, V30, V33, V40, V44, V48, V49, V52, V57, V60, V68, V70, V73, V76, V83, V84, and V90.

[00181] In some embodiments, the TREM2 agonist antigen binding protein competes with a reference antibody for binding to human TREM2, wherein the reference antibody comprises a light chain variable region comprising the sequence of SEQ ID NO: 61 and a heavy chain variable region comprising the sequence of SEQ ID NO: 124. In such embodiments, antigen binding proteins that compete with this reference antibody for binding to human TREM2 would bind the same or similar epitope as antibody 6E7 or any of the other antibodies 10E3, 13E7, 24F4, 4C5, 4G10, and 32E3.

[00182] In some embodiments, the TREM2 agonist antigen binding protein competes with a reference antibody for binding to human TREM2, wherein the reference antibody comprises a light chain variable region comprising the sequence of SEQ ID NO: 62 and a heavy chain variable region comprising the sequence of SEQ ID NO: 125. In such embodiments, antigen binding proteins that compete with this reference antibody for binding to human TREM2 would bind the same or similar epitope as antibody 5E3 or any of the other antibodies 16B8, 26A10, 26C10, 26F2, and 33B12.

[00183] In some embodiments, the TREM2 agonist antigen binding protein competes with a reference antibody for binding to human TREM2, wherein the reference antibody comprises a

light chain variable region comprising the sequence of SEQ ID NO: 52 and a heavy chain variable region comprising the sequence of SEQ ID NO: 115. In such embodiments, antigen binding proteins that compete with this reference antibody for binding to human TREM2 would bind the same or similar epitope as antibody 24G6 or antibody 24A10.

[00184] In some embodiments, the TREM2 agonist antigen binding protein competes with a reference antibody for binding to human TREM2, wherein the reference antibody comprises a light chain variable region comprising the sequence of SEQ ID NO: 56 and a heavy chain variable region comprising the sequence of SEQ ID NO: 119. In such embodiments, antigen binding proteins that compete with this reference antibody for binding to human TREM2 would bind the same or similar epitope as antibody 25F12.

[00185] In some embodiments, isolated nucleic acids encoding the anti-TREM2 binding domain of the antigen binding proteins of the invention can be used to synthesize the antigen binding protein or used to generate variants. In some embodiments, the polynucleotide may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the nucleotide sequences listed in **Table 3G**.

Table 3G. Exemplary Anti-TREM2 Antibody Variable Region Nucleic Acid Sequences

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		Light chain variable regions	
12G10	LV-01	CAGGCTGTGCCGACTCAGCCGTCTTCCCTCTCTGCATCTCCTGGAGTATT AGCCAGTCTCACCTGCACCTTACGCAGTGGCATCAATGTTGGTACCTACA GGATATACTGGTACCAGCAGAAGCCAGGGAGTCCTCCCCAGTATCTCCTG AGGTACAAATCAGACTCAGATAAGCAGCAGGGCTCTGGAGTCCCCAGCCG CTTCTCTGGATCCAAGGATGCTTCGGCCAATGCAGGGATTTTACTCATCT CTGGGCTCCAGTCTGAGGATGAGGCTGACTATTACTGTATGATTTGGTAC AGCAGTGCTGTGGTATTCGGCGGAGGGACCAAACTGACCGTCCTA	208
26A10	LV-02	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGAC AGCCAGCATCACCTGCTCTGGAGATAAATTGGGAGATAAGTATGTTTGCT GGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGCTGGTCATCTATCAAGAT AGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGG GAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTG ACTATTACTGTCAGGCGTGGGACAGTAACACTGTGGTATTCGGCGGAGGG ACCAAGCTGACCGTCCTA	209
26C10	LV-03	TCCTTTGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGAC AGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAGTATGTTTGCT GGTATCAGCAGAAGCCAGGCCAGTCCCCTATGTTGGTCATCTATCAAGAT	210

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		ACCAAGCGGCCCTCAGGGATCCCTGAACGATTCTCTGGCTCCAACTCTGG GAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTG ACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTCTTCGGCGGAGGG ACCAAGCTGACCGTCCTA	
26F2	LV-04	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGAC AGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAGTATGTTTGCT GGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGTTGGTCATCTTTCAAGAT AGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGG GAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTG ACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGG ACCAAGCTGACCGTCCTA	211
33B12	LV-05	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGAC AGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAGTATGTTTGCT GGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGTTGGTCATCTATCAAGAT AGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGG GAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTG ACTATTACTGTCAGGCGTGGGACAGTAGCACTGTGGTATTCGGCGGAGGG ACCAAGCTGACCGTCCTA	212
24C12	LV-06	GGCATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGA GAGGGCCACCATCAACTGCAAGTCCAGCCGGAGTGTTTTGTACAGCTCCA ACAATAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCT AAGGTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCG ATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGCAGGCTGAAGATGTGGCAGTTTATAACTGTCAGCAATATTATATTACT CCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA	213
24G6	LV-07	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGA GAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCA ACAATAAGCACTTCTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCT AAGCTGCTCATTTACTGGGCATCTACCCGGGAGTCCGGGGTCCCTGACCG ATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGCAGGCTGAAGATGTGGCATTTTATTACTGTCAGCAATATTATAGTACT CCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	214
24A10	LV-08	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGA GAGGGCCACCATCACCTGCAAGTCCAGCCACAATGTTTTATACAGCTCCA ACAATAAGAACTACTTAGCTTGGTATCAGCAGAAACCAGGACAGCCTCCT AAACTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCG ATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGCAGGCTGAAGATGTGGCAGTTTATTACTGTCACCAATATTATAGTACT CCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAA	215
10E3	LV-09	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAG CCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT GCTTCCACCAGGGCCACTGGTATTCCAGCCAGGTTCAGTGTCAGTGGGTC TGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTG CATTTTATTACTGTCTGCAGGATAATAATTGGCCTCCCACTTTCGGCCCT GGGACCAAAGTGGATATCAAA	216

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
13E7	LV-10	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAG CCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT GCTTCCACCAGGGCCACTGGTATTCCAGCCAGGTTCAGTGTCAGTGGGTC TGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTG CAGTTTATTACTGTCTGCAGGATAATAATTGGCCTCCCACTTTCGGCCCT GGGACCAAAGTGGATATCAAA	217
25F12	LV-11	GAAAAAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAACAACAACTTAG CCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT GCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTC TGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTG CAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCGGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAA	218
32E3	LV-12	GAATTTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCGGGGGA AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGATTATTAGCAGCAACTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT AGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGG GTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATT TTGCAGTGTATTACTGTCAGCAGTTTGATAGCTCACCGATCACCTTCGGC CGAGGGACACGACTGGACATTAAA	219
24F4	LV-13	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT GGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGG GTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATT TTGCACTGTATTACTGTCAGCAGTATGATACCTCACCATTCACTTTCGGC CCTGGGACCAAAGTGGATATCAAA	220
16B8	LV-14	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCGTCACTTGTCGGGCGAGTCAGGATATTAACAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCTCTTTGCAAACTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTCTTGTCAACAGTCTAACAGTTTCCCGATCACCTTCGGCCAA GGGACACGACTGGAGATTAAA	221
4C5	LV-15	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAACTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAGTTGGGGTCCCATTAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTATTGTCAACAGGCTGACAGTTTCCCTCGCAATTTTGGCCAG GGGACCAAGCTGGAGATCAAA	222
6E7 V9 V30 V33	LV-16	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC	223

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
V44 V68		TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	
5E3	LV-17	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGCATTAGCAATTATTTAG CCTGGTTTCAGCAGAAACCAGGGAAAGCCCCTAAATCCCTGATCTATGCT GCATCCAGTTTGCAAAGTGGGGTCCCATCAAAGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTATTACTGCCAACAGTATAGTACTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAA	224
4G10	LV-18	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATAAGAAATGATTTAG GCTGGTATCAGCAGAAACCAGGGAATGCCCCTAAGCGCCTGATCTATGCT GCATCCAGTTTGCCAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGCCAGAATTCACTCTCACAATCAGCAGTCTGCAGCCTGAAGATTTTG CAACTTATTACTGTCTACAGCATAATAGTTACCCGTGGACGTTCGGCCAA GGGACCAAGGTGGAAATCACA	225
V3	LV-101	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTAGGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGGTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	226
V24	LV-102	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAAGGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCATACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	227
V27	LV-103	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAACGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	228
V40	LV-104	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAACTTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACCGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	229

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
V48	LV-105	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAACGGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTGCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	230
V49	LV-106	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTCGGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTATCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	231
V52	LV-107	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAGGGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACCGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	232
V60	LV-108	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAGGGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTGGGCAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	233
V73	LV-106	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTCGTCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTATCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	234
V76	LV-109	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAAGGGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGAGAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	235
V84	LV-110	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGT GCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC	236

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCGCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	
V10	LV-201	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTCT GCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	313
V23	LV-202	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCTTACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	314
V57	LV-203	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTGCGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	315
V70	LV-204	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCAGGGAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	316
V83	LV-205	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGTGAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	317
V90	LV-206	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA CAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGATGGTTAG CCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGCGGCAGTGGATC TGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTG CAACTTACTTTTGTCAACAGGCTGACAGTTTCCCTCGCACTTTTGGCCAG GGGACCAAGCTGGAGATCAAA	318
Heavy chain variable regions			

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
12G10 24C12	HV-01	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT ATTGGTGGTGGTGGTGTTAGCACATACTGCGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCCAAGAATACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAATTTTAT ATAGCAGTGGCTGGTTCTCACTTTGACTACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCA	237
26A10	HV-02	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCGGGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTAGATTCACCTTCAGTAGCTTTGGCA TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATAC ATTAGTAGTAGTAGTTTTACCATATATTACGCAGACTCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAATGCCAAGAATTCATTCTATCTGCAAATGA ACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTGTGCGAGAGAGGGG GGTCTTACTATGGTTCGGGGAGTCTCTTCCTACGGTTTGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCA	238
26C10	HV-03	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTTTGGCA TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATAC ATTAGTAGTAGTAGTTTTACCATATACTACGCAGACTCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAATGCCAAGAATTCGTTCTATCTGCAAATGA ACAGCCTGAGAGACGAGGACACGGCTGTGTATTTCTGTGTGAGAGAGGGG GGTATAACTATGGTTCGGGGAGTCTCTTCCTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCA	239
26F2	HV-04	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTTTGGCA TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATTTCATAC ATTAGTAGTAGTAGTTTTACCATATACTACGCAGACTCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAATGCCAAGAATTCATTCTATCTGCAAATGA ACAGCCTGAGAGACGAGGACACGGCTGTGTATTTCTGTGCGAGAGAGGGG GGTATTACTATGGTTCGGGGAGTCTCTTCCTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCA	240
33B12	HV-05	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTTTGGCA TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCCTGGAGTGGGTTTCATAC ATTAGTAAAAGTAGTTTTACCATATACTACGCAGACTCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAATGCCAAGAATTCATTCTATCTGCAAATGA ACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTGTGCGAGAGAGGGG GGTCTTACTATGGTTCGGGGAGTCTCTTCCTACGGTTTGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCCTCA	241
24G6	HV-06	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAGGCGTAT	242

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		ACACCTATGGCATTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGT CTCCTCA	
24A10	HV-07	GAGGTGCAGGTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAACTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGGAGGG TGGGAGCTATTTTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA	243
10E3	HV-08	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGATGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAACTACTGGA TCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGAGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACGGAGA CAGGGGATCTGGGGTGATGCTCTTGATATCTGGGGCCAAGGGACATTGGT CACCGTCTCTTCA	244
13E7	HV-09	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGATGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGA TCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGAGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACGGAGA CAGGGGATCTGGGGTGATGCTCTTGATTTCTGGGGCCAAGGGACATTGGT CACCGTCTCTTCA	245
25F12	HV-10	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTAGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGGAA ATCAATCATAGTGGAAACACCAACTACAACCCGTCCCTCAAGAGTCGAGT CACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCT CTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGAGGGGTAT TACGATATCTTGACTGGTTATCATGATGCTTTTGATATTTGGGACCAAGG GACAATGGTCACCGTNTTTTCA	246
32E3	HV-11	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGA TCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGA GCACCCTGAAGGCCTCGGACACCGCCATATATTACTGTGCGCGACATGAC ATTATACCAGCAGCCCCTGGTGCTTTTGATATCTGGGGCCAAGGGACAAT GGTCACCGTCTCTTCA	247
24F4	HV-12	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACACCTTTACCAGCTACTGGA TCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGTCGACAAGTCCAGCAGCACCGCCTACCTGCAGTGGA	248

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		GCAGCCTGAAGGCCTCGGACACCGCCATATATTACTGTACGAGACAGGCC ATAGCAGTGACTGGTTTGGGGGGTTTCGACCCCTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA	
16B8	HV-13	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAACTATGGTA TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG ATCAGCGCTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAG AGTCACCATGACCACAGACACATCCACGAGTACAGTCTACATGGAGCTGA GGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGACGGGGA TACAGCTATGGTTCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGT CTCCTCA	249
4C5	HV-14	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAAGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGACACAGTTTTACCAACTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCGTGTATTTCTGTGCGAGACAAAGG ACGTTTTACTATGATAGTAGTGGTTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCA	250
6E7	HV-15	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCA	251
5E3	HV-16	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGGCTACTATA TACACTGGGTGCGACAGGCCCCTGGACTAGGGCTTGAGTGGATGGGATGG ATCAACCCTTACAGTGGTGGCACAACCTCTGCACAGAAGTTTCAGGGCAG GGTCACCATGACCAGGGACACGTCCATCAGCTCAGCCTACATGGAACTGA GCAGGCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATGGA GGCTACCTGGCCCTCTACGGTACGGACGTCTGGGGCCAAGGGACCACGGT CACCGTCTCCTCA	252
4G10	HV-17	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTCCCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTTTTTGAAGTGGA GTAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGCGACAGGGT ATAGAAGTGACTGGTACGGGAGGTTTGGACGTCTGGGGCCAAGGGACCAC GGTCACCGTCTCCTCA	253
V3	HV-101	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGCGAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC	254

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGATCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGAGGGAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	
V24	HV-102	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TTGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATGTGAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGATCTAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	255
V27	HV-103	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACGCTCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGTGAGAAGTAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	256
V40	HV-104	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGGAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATGTTAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATTCGGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	257
V48	HV-105	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGTAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATGTGAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGAATGAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	258
V49	HV-106	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTAATAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGACG ATCTATCCTGGTGACTCTGATACCAGACTGAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGAAGTAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	259

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
V52	HV-107	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGAGAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGAGGGAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	260
V60	HV-108	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACCATTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATGTGAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATAGTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	261
V73	HV-109	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGTAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGGGGTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGAGGGAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	262
V76	HV-110	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGGAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGGAGTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATAGTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	263
V84	HV-111	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACGGGTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACAGTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATTCGGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	264
V9	HV-201	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG	319

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		GGGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	
V10 V23 V57 V70 V83	HV-15	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	320
V30	HV-202	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATCGAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	321
V33	HV-203	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATGGGGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	322
V44	HV-204	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTAGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	323
V68	HV-205	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCTACTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTAGGTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	324
V90	HV-206	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGCGAGTGGA TCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA	325

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Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence	SEQ ID NO:
		GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTACAGTGGA GCAGCCTGAAGGCCTCGGACACCGCCATGTATTTCTGTGCGAGACAAAGG ACGTTTTATTATGATAGTAGTGATTATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTGTCCTCA	

[00186] In some embodiments, an isolated nucleic acid encoding an anti-TREM2 antibody light chain variable region comprises a sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to a sequence selected from SEQ ID NOs: 208-236 and 313-318. In certain embodiments, an isolated nucleic acid encoding an anti-TREM2 antibody light chain variable region comprises a sequence selected from SEQ ID NOs: 208-236 and 313-318. In related embodiments, an isolated nucleic acid encoding an anti-TREM2 antibody heavy chain variable region comprises a sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to a sequence selected from SEQ ID NOs: 237-264 and 319-325. In other related embodiments, an isolated nucleic acid encoding an anti-TREM2 antibody heavy chain variable region comprises a sequence selected from SEQ ID NOs: 237-264 and 319-325.

[00187] In some embodiments, the polynucleotide encodes the full length light chain and full length heavy chain. Exemplary polynucleotide sequences are provided in **Table 3F**.

B. U.S. Patent No. 8,231,878

[00188] In some embodiments, the TREM2 agonist is antibody, or an antigen-binding fragment thereof, as described in U.S. Patent Nos. 8,231,878, which is incorporated by reference herein, in its entirety. In some embodiments, the TREM2 antibody is monoclonal antibody 29E3, or a fragment, homologue, derivative or variant thereof.

[00189] In some embodiments, the TREM2 antigen bind protein comprises a CDRL1, CDRL2, and CDRL3 of the light chain variable region, and a CDRH1, CDRH2, and CDRH3 of the heavy chain variable region of monoclonal antibody 29E3. Monoclonal antibody 29E3 is further described in Bouchon et al., J Exp Med., 2001, 194(8):1111-1122.

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[00190] In some embodiments, the TREM2 antigen bind protein comprises a light chain variable region and a heavy chain variable region of monoclonal antibody 29E3.

[00191] In some embodiments, the TREM2 antigen bind protein is a chimeric antibody containing the light chain variable region and the heavy chain variable region of monoclonal antibody 29E3, and a human heavy chain constant region, such as a human Fc region, or an engineered variant thereof.

[00192] In some embodiments, the TREM2 antigen bind protein, e.g., a TREM2 antibody, competes with binding of monoclonal antibody 29E3 to TREM2.

C. U.S. Patent Application Publication No. US2019/0010230A1

[00193] In some embodiments, the TREM2 agonist is an antibody, or an antigen-binding fragment thereof, as described in U.S. Patent Application Publication No. US2019/0010230A1 ("the '230 application"), which is incorporated by reference herein, in its entirety.

[00194] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3 (also referred to as HVR-L1, HVR-L2, and HVR-L3, respectively), and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 (also referred to as HVR-H1, HVR-H2, and HVR-H3, respectively) disclosed in the '230 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '230 application specification.

[00195] In some embodiments, the antibody comprises a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises the HVR-H1, HVR-H2, and/or HVR-H3 of the monoclonal antibody Ab52; and/or wherein the light chain variable domain comprises the HVR-L1, HVR-L2, and/or HVR-L3 of the monoclonal antibody Ab52. In some embodiments, the HVR-H1 comprises the amino acid sequence of SEQ ID NO:772. In some embodiments, the HVR-H2 comprises the amino acid sequence of SEQ ID NO:773. In some embodiments, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:774. In some embodiments, the HVR-L1 comprises the amino acid sequence of SEQ ID NO:775. In some embodiments, the HVR-L2 comprises the amino acid sequence of SEQ ID NO:776. In some embodiments, the HVR-L3 comprises the amino acid sequence of SEQ ID NO:777. In some embodiments, the antibody comprises a heavy chain variable domain and a light

chain variable domain, wherein the heavy chain variable domain comprises: (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:772, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:772; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:773, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:773; and; and/or (c) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:774, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:774; and/or wherein the light chain variable domain comprises: (a) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:775, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:775; (b) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:776, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:776; and/or (c) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:777, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:777. In some embodiments, the antibody comprises a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises the HVR-H1, HVR-H2, and/or HVR-H3 of the monoclonal antibody Ab21; and/or wherein the light chain variable domain comprises the HVR-L1, HVR-L2, and/or HVR-L3 of the monoclonal antibody Ab21. In some embodiments, the HVR-H1 comprises the amino acid sequence of SEQ ID NO:778. In some embodiments, the HVR-H2 comprises the amino acid sequence of SEQ ID NO:779. In some embodiments, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:780. In some embodiments, the HVR-L1 comprises the amino acid sequence of SEQ ID NO:781. In some embodiments, the HVR-L2 comprises the amino acid sequence of SEQ ID NO:782. In some embodiments, the HVR-L3 comprises the amino acid sequence of SEQ ID NO:783. In some embodiments, the antibody comprises a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises: (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:778, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:778; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:779, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:779; and/or (c) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:780, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:780, and/or wherein the light chain variable domain

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comprises: (a) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:781, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:781; (b) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:782, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:782; and/or (c) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:783, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:783.

[00196] In some embodiments, the heavy chain variable domain comprises the HVR-H1, HVR-H2, and/or HVR-H3 of the monoclonal antibody Ab52; and/or wherein the light chain variable domain comprises the HVR-L1, HVR-L2, and/or HVR-L3 of the monoclonal antibody Ab52. In some embodiments, the HVR-H1 comprises the amino acid sequence of SEQ ID NO:772. In some embodiments, the HVR-H2 comprises the amino acid sequence of SEQ ID NO:773. In some embodiments, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:774. In some embodiments, the HVR-L1 comprises the amino acid sequence of SEQ ID NO:775. In some embodiments, the HVR-L2 comprises the amino acid sequence of SEQ ID NO:776. In some embodiments, the HVR-L3 comprises the amino acid sequence of SEQ ID NO:777. In some embodiments, the antibody comprises a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO:772, an HVR-H2 comprising the amino acid sequence of SEQ ID NO:773, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO:774, and/or wherein the light chain variable domain comprises an HVR-L1 comprising the amino acid sequence of SEQ ID NO:775, an HVR-L2 comprising the amino acid sequence of SEQ ID NO:776, and an HVR-L3 comprising the amino acid sequence of SEQ ID NO:777.

[00197] In some embodiments, the heavy chain variable domain comprises: (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:772, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:772; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:773, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:773; and; and/or (c) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:774, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:774; and/or wherein the light chain variable domain comprises: (a) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:775, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID

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NO:775; (b) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:776, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:776; and/or (c) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:777, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:777.

[00198] In some embodiments, the heavy chain variable domain comprises the HVR-H1, HVR-H2, and/or HVR-H3 of the monoclonal antibody Ab21; and/or wherein the light chain variable domain comprises the HVR-L1, HVR-L2, and/or HVR-L3 of the monoclonal antibody Ab21. In some embodiments, the HVR-H1 comprises the amino acid sequence of SEQ ID NO:778. In some embodiments, the HVR-H2 comprises the amino acid sequence of SEQ ID NO:779. In some embodiments, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:780. In some embodiments, the HVR-L1 comprises the amino acid sequence of SEQ ID NO:781. In some embodiments, the HVR-L2 comprises the amino acid sequence of SEQ ID NO:782. In some embodiments, the HVR-L3 comprises the amino acid sequence of SEQ ID NO:783. In some embodiments, the antibody comprises a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO:778, an HVR-H2 comprising the amino acid sequence of SEQ ID NO:779, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO:780, and/or wherein the light chain variable domain comprises an HVR-L1 comprising the amino acid sequence of SEQ ID NO:781, an HVR-L2 comprising the amino acid sequence of SEQ ID NO:782, and an HVR-L3 comprising the amino acid sequence of SEQ ID NO:783.

[00199] In some embodiments, the heavy chain variable domain comprises: (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:778, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:778; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:779, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:779; and/or (c) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:780, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:780, and/or wherein the light chain variable domain comprises: (a) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:781, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:781; (b) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:782, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:782;

and/or (c) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:783, or an amino acid sequence with at least about 95% homology to the amino acid sequence of SEQ ID NO:783.

[00200] In some embodiments, the antibody comprises a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises: (a) an HVR-H1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:3-24, 772, and 778; an HVR-H2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:25-49, 773, and 779; and (c) an HVR-H3 c comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:50-119, 774, and 780; and/or wherein the light chain variable domain comprises: (a) an HVR-L1 c comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:120-137, 775, and 781; (b) an HVR-L2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:138-152, 776, and 782; and (c) an HVR-L3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:153-236, 777, and 783. In any of the above embodiments, the light chain variable domain and/or heavy chain variable domain comprises an amino acid sequence with at least about 90% homology to the amino acid sequence indicated.

[00201] In some embodiments, the antibody is an antibody disclosed in Tables 1A, 1B and 8 and Figures 20A and 20B of U.S. Patent Application Publication No. US2019/0010230A1, reproduced below as **Tables 6A-6E**.

Table 6A: Kabat heavy chain CDR sequences

Antibody Name	CDR Ll	CDR L2	CDR L3
Ab21	YSFTTYWIG (SEQ ID NO:778)	IIYPGDSDTRYSPSFQG (SEQ ID NO:779)	ARAGHYDGGHLGMDV (SEQ ID NO:780)
Ab52	YTFTSYYIH (SEQ ID NO:772)	IINPSGGSTSYAQKFQG (SEQ ID NO:773)	AREADDSSGYPLGLDV (SEQ ID NO:774)

Table 6B: Kabat light chain CDR sequences

Antibody Name	CDR Ll	CDR L2	CDR L3
Ab21	RASQSVSSSYLA (SEQ ID NO:781)	GASNRAT (SEQ ID NO:782)	QQDDSAPYT (SEQ ID NO:783)
Ab52	RASQSVSSNLA (SEQ ID NO:775)	GASTRAT (SEQ ID NO:776)	QQVNSLPPT (SEQ ID NO:777)

Table 6C: Kabat CDR sequences

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab1	FTFSSYAMS	VISGSGGSTYYADSVKG	AKGTPTLLFQH	RASQSVSSNLA	GASTRAT	QQLPYWPPT
	(SEQ ID NO:377)	(SEQ ID NO:399)	(SEQ ID NO:424)	(SEQ ID NO:494)	(SEQ ID NO:512)	(SEQ ID NO:527)
Ab2	FTFSSSAMS	AISGSGGSTYYADSVKG	AKVPSYDYWSGYSNYYYYMDV	RASQSVGSNLA	GASTRAT	QQYI-1-YPPT
	(SEQ ID NO:378)	(SEQ ID NO:400)	(SEQ ID NO:425)	(SEQ ID NO:495)	(SEQ ID NO:512)	(SEQ ID NO:528)
Ab3	GTFSSYAIS	GIIPIFGTANYAQKFQG	AREQYHVGMDV	QASQDISNYLN	DASNLAT	QQPFNFPYT
	(SEQ ID NO:379)	(SEQ ID NO:401)	(SEQ ID NO:426)	(SEQ ID NO:496)	(SEQ ID NO:513)	(SEQ ID NO:529)
Ab4	GTFSSYAIS	GIIPIFGTASYAQKFQG	ARGVDSIMDY	RASQSVSSNLA	SASTRAT	QQDHDYPFT
	(SEQ ID NO:379)	(SEQ ID NO:402)	(SEQ ID NO:427)	(SEQ ID NO:494)	(SEQ ID NO:514)	(SEQ ID NO:530)
Ab5	YTFTSYYIH	IINPSGGSTSYAQKFQG	ARAPQESPYVFDI	RASQSVSSSYLA	GASSRAT	QQYFSSPFT
	(SEQ ID NO:380)	(SEQ ID NO:403)	(SEQ ID NO:428)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:531)
Ab6	YTFTSYYMH	IINPGGGSTSYAQKFQG	ARGSPTYGYLYDP	RASQSVSSYLA	DASKRAT	QQRVNLPPT
	(SEQ ID NO:381)	(SEQ ID NO:404)	(SEQ ID NO:429)	(SEQ ID NO:498)	(SEQ ID NO:516)	(SEQ ID NO:532)
Ab7	YTFTSYYMH	IINPSGGSTTYAQKFQG	ARTSSKERDY	RASQSVSSYLA	DASKRAT	QQRISYPIT
	(SEQ ID NO:381)	(SEQ ID NO:405)	(SEQ ID NO:430)	(SEQ ID NO:498)	(SEQ ID NO:516)	(SEQ ID NO:533)
Ab8	GSISSSSYYWG	SISYSGSTYYNPSLKS	ARGPYRLLLGMDV	RASQSISSYLN	GASSLQS	QQIDDTPIT
	(SEQ ID NO:382)	(SEQ ID NO:406)	(SEQ ID NO:431)	(SEQ ID NO:499)	(SEQ ID NO:517)	(SEQ ID NO:534)
Ab9	YSFTSYWIG	IIYPGDSDTTYSPSFQG	ARLHISGEVNWFDP	RASQSVSSYLA	DASNRAT	QQFSYWPWT

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
	(SEQ ID NO:383)	(SEQ ID NO:407)	(SEQ ID NO:432)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:535)
Ab10	YSFTSNWIG	IIYPGDSDTRYSPSFQG	AREAGYDYGELAFDI	RASQSVSSSYLA	GASSRAT	QQHDSSPPT
	(SEQ ID NO:384)	(SEQ ID NO:408)	(SEQ ID NO:433)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:536)
Abl11	YSFTTYWIG	IIYPGDSDTRYSPSFQG	ARAGHYDGGHLGMDV	RASQSVSSDYLA	GASSRAT	QQDYSYPWT
	(SEQ ID NO:385)	(SEQ ID NO:408)	(SEQ ID NO:434)	(SEQ ID NO:500)	(SEQ ID NO:515)	(SEQ ID NO:537)
Ab12	YSFTSYWIG	IIYPGDSDTRYSPSFQG	ARLGHYSGTVSSYGMDV	RASQSISSYLN	AASSLQS	QQEYAVPYT
	(SEQ ID NO:383)	(SEQ ID NO:408)	(SEQ ID NO:435)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:538)
Ab13	YTFTSYGIS	WISAYNGNTNYAQKLQG	ARGPSHYYDLA	RASQSVSSYLA	DASNRAT	QQVSNYPIT
	(SEQ ID NO:386)	(SEQ ID NO:409)	(SEQ ID NO:436)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:539)
Ab14	GSISSGGYYWS	NIYYSGSTVYNPSLKS	ARGLYGYGVLDV	QASQDISNYLN	DASNLET	QQVDNIPPT
	(SEQ ID NO:387)	(SEQ ID NO:410)	(SEQ ID NO:437)	(SEQ ID NO:496)	(SEQ ID NO:520)	(SEQ ID NO:540)
Ab15	GSISSGGYYWS	NIYYSGSTVYNPSLKS	ARGLYGYGVLDV	QASQDISNYLN	DASNLET	QQFDTYPT
	(SEQ ID NO:387)	(SEQ ID NO:410)	(SEQ ID NO:437)	(SEQ ID NO:496)	(SEQ ID NO:520)	(SEQ ID NO:541)
Ab16	GSISSNSYYWG	SIYYSGSTYYNPSKS	ARGVLGYGVFDY	QASQDISNYLN	DASNLET	QQFLNFPT
	(SEQ ID NO:388)	(SEQ ID NO:411)	(SEQ ID NO:438)	(SEQ ID NO:496)	(SEQ ID NO:520)	(SEQ ID NO:542)
Abl7	GSISSNSYYWG	SIYYSGSTYYNPSLKS	ARGVLGYGVFDY	QASQDISNYLN	DASNLET	QQFFNFPT
	(SEQ ID NO:388)	(SEQ ID NO:411)	(SEQ ID NO:438)	(SEQ ID NO:496)	(SEQ ID NO:520)	(SEQ ID NO:543)
Ab18	GSISSYYWS	SIYYSGSTNYNPSLKS	ARDGGGEYPSGTPFDI	QASQDISNYLN	DASNLET	QQFIDLPFT
	(SEQ ID NO:389)	(SEQ ID NO:412)	(SEQ ID NO:439)	(SEQ ID NO:496)	(SEQ ID NO:520)	(SEQ ID NO:544)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab19	GSISSYYWS	SIYYSGSTNYNPSLKS	ARDGGGEYPSGTPFDI	QASQDISNYLN	DASNLET	QQYYDLPFT
	(SEQ ID NO:389)	(SEQ ID NO:412)	(SEQ ID NO:439)	(SEQ ID NO:496)	(SEQ ID NO:520)	(SEQ ID NO:545)
Ab20	GSISSYYWS	SIYYSGSTNYNPSLKS	ARSGMASFFDY	RASQSVSSDYLA	GASSRAT	QQFSSHPFT
	(SEQ ID NO:389)	(SEQ ID NO:412)	(SEQ ID NO:440)	(SEQ ID NO:500)	(SEQ ID NO:515)	(SEQ ID NO:546)
Ab22	YSFTTYWIG	IIYPGDSDTRYSPSFQG	ARAGHYDGGHLGMDV	RASQSVSSSYLA	GASSRAT	QQDDRSPYT
	(SEQ ID NO:385)	(SEQ ID NO:408)	(SEQ ID NO:434)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:547)
Ab23	FTFSSYAMS	AISGSGGSTYYADSVKG	AKLGGHSMDV	KSSQSVLYSSNNKNYLA	WASTRES	QQAYLPPIT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:441)	(SEQ ID NO:501)	(SEQ ID NO:521)	(SEQ ID NO:548)
Ab24	FTFSSYAMS	AISGSGGSTYYADSVKG	AKPLKRGRGFY	RASQSISSYLN	AASSLQS	QQAFSPPPWT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:442)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:549)
Ab25	FTFSSYAMS	VISGSGGSTYYADSVKG	AKEGRTITMD	RASQSVSSSYLA	GASSRAT	QQDDRSPT
	(SEQ ID NO:337)	(SEQ ID NO:399)	(SEQ ID NO:443)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:550)
Ab26	FTFSSYAMS	VISGSGGSTYYADSVKG	AKDQYSVLDY	RASQSVSSYLA	DASNRAT	QQEFDLPFT
	(SEQ ID NO:337)	(SEQ ID NO:399)	(SEQ ID NO:444)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:551)
Ab27	FTFSSYAMS	AISGSGGSTYYADSVKG	AKKYSSRGVYFDY	RASQSVSSYLA	DASNRAT	QQYNNFPPT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:445)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:552)
Ab28	FTFSSYAMS	AISGSGGSTYYADSVKG	ARLGGAVGARHVTY FDY	RASQSVSSYLA	DASKRAT	QQRYLRPIT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:446)	(SEQ ID NO:498)	(SEQ ID NO:516)	(SEQ ID NO:553)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab29	FTFSSYGMH	VISYDGSNKYYADS VKG	ARGQYYGGSGWFD P	RASQSVSSSYLA	GASSRAT	QQPGAVPT
	(SEQ ID NO:390)	(SEQ ID NO:413)	(SEQ ID NO:447)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:554)
Ab30	FTFSSYAMS	AISGSGGSTYYADS VKG	ARLGQEYAYFQH	RASQSISSYLN	GASSLQS	QQVYITPIT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:448)	(SEQ ID NO:499)	(SEQ ID NO:517)	(SEQ ID NO:555)
Ab31	FTFSSYGMH	LIWYDGSNKYYAD S VKG	ARRRDGYYDEVFDI	QASQDISNFLN	DASNLET	QQPVDLPEI
	(SEQ ID NO:390)	(SEQ ID NO:414)	(SEQ ID NO:449)	(SEQ ID NO:502)	(SEQ ID NO:520)	(SEQ ID NO:556)
Ab32	FTFSSYAMS	AISGSGGSTYYADS VKG	ARVPKHYVVLDY	RASQSVSSYLA	DASNRAT	QQYSH-PPT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:450)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:557)
Ab33	FTFSSYGMH	VISYDGSNKYYADS VKG	ARAGGHLFDY	RASQSVSSYLA	DASNRAT	QQDSSFPPT
	(SEQ ID NO:390)	(SEQ ID NO:413)	(SEQ ID NO:451)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:558)
Ab34	FTFSSYGMH	VISYDGSNKYYADS VKG	ARDRGGEYVDFAFD I	RASQSISSYLN	AASSLQS	QQSDFPPWT
	(SEQ ID NO:390)	(SEQ ID NO:413)	(SEQ ID NO:452)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:559)
Ab35	FTFSSYAMS	AISGSGGSTYYADS VKG	ARTRSGYGASNYFD Y	RASQSISSYLN	AASSLQS	QQGYSAPIT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:453)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:560)
Ab36	FTFSTYGMH	VIWYDGSNKYYA DS VKG	ARGTGAAAASPAFDI	RASQSVSSYLA	DASNRAT	QQLFDWPT
	(SEQ ID NO:391)	(SEQ ID NO:415)	(SEQ ID NO:454)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:561)
Ab37	FTFSSYAMS	AISGSGGSTYYADS VKG	ARVGQYMLGMDV	RASQSVSSYLA	DASNRAT	QQRAFLFT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:455)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:562)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab38	FTFSTYGMH	VIWYDGSNKYYADS VKG	ARGAPVDYGGIEPEYFQH	RASQSVSSYLA	DASNRAT	QQIDFLPYT
	(SEQ ID NO:391)	(SEQ ID NO:415)	(SEQ ID NO:456)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:563)
Ab39	FTFSSYAMS	AISGSGGSTYYADSVKG	AKHYHVGIAFDI	RASQSISSYLN	AASSLQS	QQVYSPPIT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:457)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:564)
Ab40	FTFSSYAMS	AISGSGGSTYYADSVKG	ARTRSGYGASNYFDY	RASQSISSYLN	AASSLQS	QQGYAAPIT
	(SEQ ID NO:337)	(SEQ ID NO:400)	(SEQ ID NO:453)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:565)
Ab41	FTFSTYAMS	AISGSGGSTYYADSVKG	ARAMARKSVAFDI	RASQSVSSYLA	DASNRAT	QQRYALPIT
	(SEQ ID NO:392)	(SEQ ID NO:400)	(SEQ ID NO:458)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:566)
Ab42	FTFSSSAMS	AISGSGGSTYYADSVKG	AKVPSYQRGTAFDP	RASQSVSSSYLA	GASSRAT	QQYASPPIT
	(SEQ ID NO:378)	(SEQ ID NO:400)	(SEQ ID NO:459)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:567)
Ab43	FTFSSSAMS	AISGSGGSTYYADSVKG	AKSPAVAGIYRADY	RASQSISRYLN	AASSLQS	QQVYSTPIT
	(SEQ ID NO:378)	(SEQ ID NO:400)	(SEQ ID NO:460)	(SEQ ID NO:503)	(SEQ ID NO:519)	(SEQ ID NO:568)
Ab44	FTFSTYGMH	VIWYDGSNKYYADS VKG	ARGTGAAAASPAFDI	RASQSVSSYLA	DSSNRAT	QQLVHWPT
	(SEQ ID NO:391)	(SEQ ID NO:415)	(SEQ ID NO:454)	(SEQ ID NO:498)	(SEQ ID NO:522)	(SEQ ID NO:569)
Ab45	YTFTSYYMH	IINPSGGSTSYAQKFQG	ARGPGYTTALDYYY MDV	RASQSVSSNLA	GASTRAT	QQLDDWFT
	(SEQ ID NO:381)	(SEQ ID NO:403)	(SEQ ID NO:461)	(SEQ ID NO:494)	(SEQ ID NO:512)	(SEQ ID NO:570)
Ab46	YTFTSYYMH	IINPSGGSTSYAQKFQG	ARPAKTADY	RASQSVSSYLA	DSSNRAT	QQRSNYPIT
	(SEQ ID NO:381)	(SEQ ID NO:403)	(SEQ ID NO:462)	(SEQ ID NO:498)	(SEQ ID NO:522)	(SEQ ID NO:571)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab47	YTFTSYYMH	IINPSGGSTTYAQKFQG	ARPGKSMDV	RASQSVSSYLA	DASNRAT	QQRILYPIT
	(SEQ ID NO:381)	(SEQ ID NO:405)	(SEQ ID NO:463)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:572)
Ab48	YTFTSYYMH	IINPSGGSTTYAQKFQG	ARPGKSMDV	RASQSVSSYLA	DASNRAT	QQRAAYPIT
	(SEQ ID NO:381)	(SEQ ID NO:405)	(SEQ ID NO:463)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:573)
Ab49	YTFTSYYMH	IINPSGGSTSYAQKFQG	ARPAKTADY	RASQSVSSYLA	DASKRAT	QQRTSHPIT
	(SEQ ID NO:381)	(SEQ ID NO:403)	(SEQ ID NO:462)	(SEQ ID NO:498)	(SEQ ID NO:516)	(SEQ ID NO:574)
Ab50	YTFTSYYIH	IINPSGGSTSYAQKFQG	ARAPQESPYVFDI	RASQSVSSSYLA	GASSRAT	QQYAGSPFT
	(SEQ ID NO:380)	(SEQ ID NO:403)	(SEQ ID NO:428)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:575)
Ab51	YTFTSYYMH	IINPSGGSTSYAQKFQG	ARGVGGQDYYYMDV	RASQSISSYLN	AASSLQS	QQFDDVFT
	(SEQ ID NO:381)	(SEQ ID NO:403)	(SEQ ID NO:464)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:576)
Ab53	YTFTSYYIH	IINPSGGSTSYAQKFQG	ARAPQESPYVFDI	RASQSVSSSYLA	GASSRAT	QQYVNSPFT
	(SEQ ID NO:380)	(SEQ ID NO:403)	(SEQ ID NO:428)	(SEQ ID NO:497)	(SEQ ID NO:515)	(SEQ ID NO:577)
Ab54	YTFTSYYMH	IINPSGGSTSYAQKFQG	ARGPGYTTALDYYY MDV	RASQSINSYLN	AASSLQS	QQSDDDPFT
	(SEQ ID NO:381)	(SEQ ID NO:403)	(SEQ ID NO:461)	(SEQ ID NO:504)	(SEQ ID NO:519)	(SEQ ID NO:578)
Ab55	YTFTGSYMH	WINPNSGGTNYAQK FQG	ARGPLYHPMIFDY	RASQSVSSYLA	DASNRAT	QQLSTYPLT
	(SEQ ID NO:393)	(SEQ ID NO:416)	(SEQ ID NO:465)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:579)
Ab56	YTFTGYYMH	SINPNSGGTNYAQKFQG	ARASSVDN	RASQSVSSYLA	DASNRAT	QQRSVYPIT
	(SEQ ID NO:394)	(SEQ ID NO:417)	(SEQ ID NO:466)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:580)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab57	YTFTNYGIS	WISAYNGNTNYAQ KLQG	ARGPTKAYYGSGS Y VVFDP	RASQSVSSYLA	DASKRAT	QQVSLFPLT
	(SEQ ID NO:395)	(SEQ ID NO:409)	(SEQ ID NO:467)	(SEQ ID NO:498)	(SEQ ID NO:516)	(SEQ ID NO:581)
Ab58	YSFTSYWIG	IIYPGDSDTRYSPSF QG	ARLGIYSTGATAFDI	RASQSISSWLA	DASSLES	LDYNSYSPIT
	(SEQ ID NO:383)	(SEQ ID NO:408)	(SEQ ID NO:468)	(SEQ ID NO:505)	(SEQ ID NO:523)	(SEQ ID NO:582)
Ab59	YTFTGSYMH	WINPNSGGTNYAQ K FQG	ARGGVWYSLFDI	QASQDISNYLN	DASNLET	QQHIALPFT
	(SEQ ID NO:393)	(SEQ ID NO:416)	(SEQ ID NO:469)	(SEQ ID NO:496)	(SEQ ID NO:520)	(SEQ ID NO:583)
Ab60	YTFTGYYMH	WINPNSGGTSYAQ K FQG	ARASKMGDD	RASQSVSSYLA	DASKRAT	QQRASMPIT
	(SEQ ID NO:394)	(SEQ ID NO:418)	(SEQ ID NO:470)	(SEQ ID NO:498)	(SEQ ID NO:516)	(SEQ ID NO:584)
Ab61	YTFTSYGIH	WISAYNGNTNYAQ KLQG	ARGGVPRVSYFQH	RASQSVSSYLA	DSSNRAT	QQAFNRPPT
	(SEQ ID NO:396)	(SEQ ID NO:409)	(SEQ ID NO:471)	(SEQ ID NO:498)	(SEQ ID NO:522)	(SEQ ID NO:585)
Ab62	YSFTSYWIG	IIYPGDSDTRYSPSF QG	ARAGHYDDWSGLG LDV	RASQSVSSYLA	DASKRAT	QQSSVHPYT
	(SEQ ID NO:383)	(SEQ ID NO:408)	(SEQ ID NO:472)	(SEQ ID NO:498)	(SEQ ID NO:516)	(SEQ ID NO:586)
Ab63	YTFTSYGIS	WISTYNGNTNYAQ K LQG	ARGSGSGYDSWYD	RASQGIDSWLA	AASSLQS	QQAYSLPPT
	(SEQ ID NO:386)	(SEQ ID NO:419)	(SEQ ID NO:473)	(SEQ ID NO:506)	(SEQ ID NO:519)	(SEQ ID NO:587)
Ab64	YSFTSYWIG	IIYPGDSDTRYSPSF QG	ARLGRWSSGSTAFDI	RASQSVSSNLA	GASTRAT	QQDDDGYT
	(SEQ ID NO:383)	(SEQ ID NO:408)	(SEQ ID NO:474)	(SEQ ID NO:494)	(SEQ ID NO:512)	(SEQ ID NO:588)
Ab65	YSFTSYWIG	IIYPGDSDTRYSPSF QG	ARLGRKPSGSVAFDI	RASQSVSSYLA	DASNRAT	QQDYSWPYT
	(SEQ ID NO:383)	(SEQ ID NO:408)	(SEQ ID NO:475)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:589)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab66	YTFTGSYMH	WINPNSGGTNYAQK FQG	ARAGHKTHDY	RASQSVSSYLA	DASNRAT	QQRSAYPIT
	(SEQ ID NO:393)	(SEQ ID NO:416)	(SEQ ID NO:476)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:590)
Ab67	YTFTSYYMH	IINPSGGSTTYAQKFQG	ARPGKSMDV	RASQSVSSYLA	DASNRAT	QQRSTFPIT
	(SEQ ID NO:381)	(SEQ ID NO:405)	(SEQ ID NO:463)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:591)
Ab68	FTFSSYGMH	LIWYDGSNKYYADSVKG	AKPGSMTDY	RASQSVSSYLA	DASNRAT	QQRANYPIT
	(SEQ ID NO:390)	(SEQ ID NO:414)	(SEQ ID NO:477)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:592)
Ab69	YTFTGSYMH	WINPNSGGTNYAQK FQG	ARAKSVDHDY	RASQSVSSYLA	DASNRAT	QQRADYPIT
	(SEQ ID NO:393)	(SEQ ID NO:416)	(SEQ ID NO:478)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:593)
Ab70	YTFTGYYMH	WINPNSGGTSYAQK FQG	ARASKMGDD	RASQSVSSYLA	DASNRAT	QQRSVYPIT
	(SEQ ID NO:394)	(SEQ ID NO:418)	(SEQ ID NO:470)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:580)
Ab71	YTFTSYYMH	IINPSGGSTSYAQKFQG	ARDISTHDYDLAFDI	RASQSVSSSYLA	GASNRAT	QQAGSHPFT
	(SEQ ID NO:381)	(SEQ ID NO:403)	(SEQ ID NO:479)	(SEQ ID NO:497)	(SEQ ID NO:524)	(SEQ ID NO:594)
Ab72	GSISSYYWS	SIYYSGSTNYNPSLKS	ARSGTETLFDY	QASQDITNYLN	DASNLET	QQDVNYPPT
	(SEQ ID NO:389)	(SEQ ID NO:412)	(SEQ ID NO:480)	(SEQ ID NO:507)	(SEQ ID NO:520)	(SEQ ID NO:595)
Ab73	YSFTSYWIG	IIYPGDSDTTYSPSFQG	ARAKMLDDGYAFDI	RASQSVSSNLA	GASTRAT	QQDDNYPYT
	(SEQ ID NO:383)	(SEQ ID NO:407)	(SEQ ID NO:481)	(SEQ ID NO:494)	(SEQ ID NO:512)	(SEQ ID NO:596)
Ab74	YTFTGSYMH	WINPNSGGTNYAQK FQG	ARAGHKTHDY	RASQSVSSYLA	DASNRAT	QQRSTFPIT
	(SEQ ID NO:393)	(SEQ ID NO:416)	(SEQ ID NO:476)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:597)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab75	YTFTGYYMH	WINPNSGGTNYAQK FQG	ARDLGYSSLLALDI	RASQSVSSYLA	DASNRAT	QQVSNYPFI
	(SEQ ID NO:394)	(SEQ ID NO:416)	(SEQ ID NO:482)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:598)
Ab76	FTFSSYSMN	SISSSSSYIYYADSVKG	ARGGGRRGDNNWFDP	KSSQSVLYSSNNKNYLA	WASTRES	QQYHDAPIT
	(SEQ ID NO:397)	(SEQ ID NO:420)	(SEQ ID NO:483)	(SEQ ID NO:501)	(SEQ ID NO:521)	(SEQ ID NO:599)
Ab77	FTFSSYGMH	VISYDGSNKYYADSVKG	ARGPPHEMDY	KSSQSVLYSSNNKNYLA	WASTRES	QQAYVVPPT
	(SEQ ID NO:390)	(SEQ ID NO:413)	(SEQ ID NO:484)	(SEQ ID NO:501)	(SEQ ID NO:521)	(SEQ ID NO:600)
Ab78	FTFSSYGMH	VIWYDGSNKYYADS VKG	ARTPYPWIYFDL	RASQSVSSYLA	DASNRAT	QQADNWPFT
	(SEQ ID NO:390)	(SEQ ID NO:415)	(SEQ ID NO:485)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:601)
Ab79	FTFSSYSMN	YISGSSSTIYYADSVKG	ARGGRRHYGGMDV	RSSQSLLHSNGYNYLD	LGSHRAS	MQALESPRT
	(SEQ ID NO:397)	(SEQ ID NO:421)	(SEQ ID NO:486)	(SEQ ID NO:508)	(SEQ ID NO:525)	(SEQ ID NO:602)
Ab80	GTFSSYAIS	GIIPIFGTANYAQKFQG	ARGGGTFWSGSWALY	RASQSVSSYLA	DASNRAT	QQYVNWPFT
	(SEQ ID NO:379)	(SEQ ID NO:401)	(SEQ ID NO:487)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:603)
Ab81	GTFSSYAIS	GIIPIFGTANYAQKFQG	ARDSGNYDYWSGALRY	RASQSVSSYLA	DASNRAT	QQSSNWPWT
	(SEQ ID NO:379)	(SEQ ID NO:401)	(SEQ ID NO:488)	(SEQ ID NO:498)	(SEQ ID NO:518)	(SEQ ID NO:604)
Ab82	GSISSGGYYWS	YIYYSGSTVYNPSLKS	ARVSSSWYKA	RASQGISSWLA	AASSLQS	QQASTFPIT
	(SEQ ID NO:387)	(SEQ ID NO:422)	(SEQ ID NO:489)	(SEQ ID NO:509)	(SEQ ID NO:519)	(SEQ ID NO:605)
Ab83	GSFSGYYWS	EIDHSGSTKYNPSLKS	ARVGVVVGRPGYSAFDI	RASQGISSWLA	AASSLQS	QQRNSLPLT
	(SEQ ID NO:398)	(SEQ ID NO:423)	(SEQ ID NO:490)	(SEQ ID NO:509)	(SEQ ID NO:519)	(SEQ ID NO:606)

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab84	YTFTSYGIS	WISTYNGNTNYAQK LQG	ARGSGSGYDSWYD	RASQSISSYLN	AASSLQS	QQSYDFPIT
	(SEQ ID NO:386)	(SEQ ID NO:419)	(SEQ ID NO:473)	(SEQ ID NO:499)	(SEQ ID NO:519)	(SEQ ID NO:607)
Ab85	FTFSSYGMH	VIWYDGSNKYYADSVKG	AKDLGGYYGGAAYGMDV	RASQDISSWLA	AASSLQS	QQEVDYPPLT
	(SEQ ID NO:390)	(SEQ ID NO:415)	(SEQ ID NO:491)	(SEQ ID NO:510)	(SEQ ID NO:519)	(SEQ ID NO:608)
Ab86	FTFSSYGMH	VISYDGSNKYYADSVKG	AKDGVYYGLGNWFDP	RASQSISSWLA	KASSLES	QQLNSYSPT
	(SEQ ID NO:390)	(SEQ ID NO:413)	(SEQ ID NO:492)	(SEQ ID NO:505)	(SEQ ID NO:526)	(SEQ ID NO:609)
Ab87	GSISSYYWS	SIYYSGSTNYNPSLKS	ARHGWDRVGWFDP	RASQSVSRYLA	DASNRAT	QQYIFWPPT
	(SEQ ID NO:389)	(SEQ ID NO:412)	(SEQ ID NO:493)	(SEQ ID NO:511)	(SEQ ID NO:518)	(SEQ ID NO:610)

Table 6D – Heavy chain variable regions

Ab 1	SEQ ID NO: 616	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGTPTLLFQHWGQGTLVTVSS
Ab 2	SEQ ID NO: 618	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVPSYDYWSGYSNYYYYMDVWGK GTTVTVSS
Ab 3	SEQ ID NO: 620	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREQYHVGMDVWGKGTTVTVSS
Ab 4	SEQ ID NO: 622	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTASY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGVDSIMDYWGQGTLVTVSS
Ab 5	SEQ ID NO: 624	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARAPQESPYVFDIWGQGTMVTVSS
Ab 6	SEQ ID NO: 626	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPGGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGSPTYGYLYDPWGQGTLVTVSS
Ab 7	SEQ ID NO: 628	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTTY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARTSSKERDYWGQGTLVTVSS
Ab 8	SEQ ID NO: 630	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSISYSGSTY YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPYRLLLGMDVWGQGTTVTVSS
Ab 9	SEQ ID NO: 632	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTTY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLHISGEVNWFDPWGQGTLVTVSS
Ab 10	SEQ ID NO: 634	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSNWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAREAGYDYGELAFDIWGQGTMVTVSS
Ab 11	SEQ ID NO: 636	EVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAGHYDGGHLGMDVWGQGTTVTVSS
Ab 12	SEQ ID NO: 638	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGHYSGTVSSYGMDVWGQGTTV TVSS
Ab 13	SEQ ID NO: 640	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGPSHYYDLAWGQGTLVTVSS
Ab 14	SEQ ID NO: 642	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGNIYYSGSTV YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGLYGYGVLDVWGQGTMVTVSS
Ab 15	SEQ ID NO: 642	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGNIYYSGSTV YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGLYGYGVLDVWGQGTMVTVSS
Ab 16	SEQ ID NO: 645	QLQLQESGPGLVKPSETLSLTCTVSGGSISSNSYYWGWIRQPPGKGLEWIGSIYYSGSTY YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGVLGYGVFDYWGQGTLVTVSS
Ab 17	SEQ ID NO: 645	QLQLQESGPGLVKPSETLSLTCTVSGGSISSNSYYWGWIRQPPGKGLEWIGSIYYSGSTY YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGVLGYGVFDYWGQGTLVTVSS
Ab 18	SEQ ID NO: 648	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGGGEYPSGTPFDIWGQGTMVTV SS
Ab 19	SEQ ID NO: 648	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGGGEYPSGTPFDIWGQGTMVTV SS
Ab 20	SEQ ID NO: 651	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSGMASFFDYWGQGTLVTVSS
Ab 22	SEQ ID NO: 636	EVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAGHYDGGHLGMDVWGQGTTVTVSS
Ab 23	SEQ ID NO: 654	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLGGHSMDVWGQGTTVTVSS
Ab 24	SEQ ID NO: 656	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPLKRGRGFYWGQGTLVTVSS
Ab 25	SEQ ID NO: 658	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEGRTITMDWGQGTLVTVSS
Ab 26	SEQ ID NO: 660	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDQYSVLDYWGQGTLVTVSS
Ab 27	SEQ ID NO: 662	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKKYSSRGVYFDYWGQGTLVTVSS
Ab 28	SEQ ID NO: 664	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLGGAVGARHVTYFDYWGQGTLV TVSS
Ab 29	SEQ ID NO: 666	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGQYYGGSGWFDPWGQGTLVTVSS
Ab 30	SEQ ID NO: 668	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLGQEYAYFQHWGQGTLVTVSS
Ab 31	SEQ ID NO: 670	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVALIWYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRRDGYYDEVFDIWGQGTMVTVSS

Ab 32	SEQ ID NO: 672	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPKHYVVLDYWGQGTLVTVSS
Ab 33	SEQ ID NO: 674	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAGGHLFDYWGQGTLVTVSS
Ab 34	SEQ ID NO: 676	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGGEYVDFAFDIWGQGTMVTVSS
Ab 35	SEQ ID NO: 678	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTRSGYGASNYFDYWGQGTLVTVSS
Ab 36	SEQ ID NO: 680	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTGAAAASPAFDIWGQGTMVTVSS
Ab 37	SEQ ID NO: 682	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVGQYMLGMDVWGQGTTVTVSS
Ab 38	SEQ ID NO: 684	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGAPVDYGGIEPEYFQHWGQGTL VTVSS
Ab 39	SEQ ID NO: 686	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHYHVGIAFDIWGQGTMVTVSS
Ab 40	SEQ ID NO: 678	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTRSGYGASNYFDYWGQGTLVTVSS
Ab 41	SEQ ID NO: 689	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAMARKSVAFDIWGQGTMVTVSS
Ab 42	SEQ ID NO: 691	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVPSYQRGTAFDPWGQGTLVTVSS
Ab 43	SEQ ID NO: 693	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSPAVAGIYRADYWGQGTLVTVSS
Ab 44	SEQ ID NO: 680	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTGAAAASPAFDIWGQGTMVTVSS
Ab 45	SEQ ID NO: 696	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGPGYTTALDYYYMDVWGKGTTV TVSS
Ab 46	SEQ ID NO: 698	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPAKTADYWGQGTLVTVSS
Ab 47	SEQ ID NO: 700	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTTY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPGKSMDVWGQGTTVTVSS
Ab 48	SEQ ID NO: 700	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTTY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPGKSMDVWGQGTTVTVSS
Ab 49	SEQ ID NO: 698	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPAKTADYWGQGTLVTVSS
Ab 50	SEQ ID NO: 624	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARAPQESPYVFDIWGQGTMVTVSS
Ab 51	SEQ ID NO: 705	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGVGGQDYYYMDVWGKGTTVTVSS
Ab 53	SEQ ID NO: 624	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARAPQESPYVFDIWGQGTMVTVSS
Ab 54	SEQ ID NO: 696	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGPGYTTALDYYYMDVWGKGTTV TVSS
Ab 55	SEQ ID NO: 709	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGPLYHPMIFDYWGQGTLVTVSS
Ab 56	SEQ ID NO: 711	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGSINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARASSVDNWGQGTLVTVSS
Ab 57	SEQ ID NO: 713	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGISWVRQAPGQGLEWMGWISAYNGNTNY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGPTKAYYGSGSYVVFDPWGQGT LVTVSS
Ab 58	SEQ ID NO: 715	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGIYSTGATAFDIWGQGTMVTVSS
Ab 59	SEQ ID NO: 717	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGVWYSLFDIWGQGTMVTVSS
Ab 60	SEQ ID NO: 719	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTSY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARASKMGDDWGQGTLVTVSS
Ab 61	SEQ ID NO: 721	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGIHWVRQAPGQGLEWMGWISAYNGNTNY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGGVPRVSYFQHWGQGTLVTVSS
Ab 62	SEQ ID NO: 723	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAGHYDDWSGLGLDVWGQGTMVTVSS
Ab 63	SEQ ID NO: 725	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISTYNGNTNY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGSGSGYDSWYDWGQGTLVTVSS
Ab 64	SEQ ID NO: 727	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGRWSSGSTAFDIWGQGTMVTVSS

Ab 65	SEQ ID NO: 729	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGRKPSGSVAFDIWGQGTMVTVSS
Ab 66	SEQ ID NO: 731	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARAGHKTHDYWGQGTLVTVSS
Ab 67	SEQ ID NO: 700	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTTY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPGKSMDVWGQGTTVTVSS
Ab 68	SEQ ID NO: 734	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVALIWYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPGSMTDYWGQGTLVTVSS
Ab 69	SEQ ID NO: 736	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARAKSVDHDYWGQGTLVTVSS
Ab 70	SEQ ID NO: 719	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTSY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARASKMGDDWGQGTLVTVSS
Ab 71	SEQ ID NO: 739	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDISTHDYDLAFDIWGQGTMVTVSS
Ab 72	SEQ ID NO: 741	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSGTETLFDYWGQGTLVTVSS
Ab 73	SEQ ID NO: 743	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTTY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAKMLDDGYAFDIWGQGTMVTVSS
Ab 74	SEQ ID NO: 731	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARAGHKTHDYWGQGTLVTVSS
Ab 75	SEQ ID NO: 746	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDLGYSSLLALDIWGQGTMVTVSS
Ab 76	SEQ ID NO: 748	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYY ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGGRRGDNNWFDPWGQGTLVTVSS
Ab 77	SEQ ID NO: 750	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGPPHEMDYWGQGTLVTVSS
Ab 78	SEQ ID NO: 752	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTPYPWIYFDLWGRGTLVTVSS
Ab 79	SEQ ID NO: 754	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISGSSSTIYY ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGRRHYGGMDVWGQGTTVTVSS
Ab 80	SEQ ID NO: 756	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGGGTFWSGSWALYWGQGTLVTVSS
Ab 81	SEQ ID NO: 758	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDSGNYDYWSGALRYWGQGTLVTVSS
Ab 82	SEQ ID NO: 760	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTV YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVSSSWYKAWGQGTMVTVSS
Ab 83	SEQ ID NO: 762	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEIDHSGSTKYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVGVVVGRPGYSAFDIWGQGTMVTVSS
Ab 84	SEQ ID NO: 725	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISTYNGNTNY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGSGSGYDSWYDWGQGTLVTVSS
Ab 85	SEQ ID NO: 765	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGGYYGGAAYGMDVWGQGTTV TVSS
Ab 86	SEQ ID NO: 767	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDGVYYGLGNWFDPWGQGTLVTVSS
Ab 87	SEQ ID NO: 769	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHGWDRVGWFDPWGQGTLVTVSS

Table 6E – Light chain variable regions

Ab 1	SEQ ID NO: 617	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA RFSGSGSGTEFTLTISSLQSEDFAVYYCQQLPYWPPTFGGGTKVEIK
Ab 2	SEQ ID NO: 619	EIVLTQSPATLSVSPGERATLSCRASQSVGSNLAWYQQKPGQAPRLLIYGASTRATGIPA RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYFFYPPTFGGGTKVEIK
Ab 3	SEQ ID NO: 621	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLATGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQPFNFPYTFGGGTKVEIK
Ab 4	SEQ ID NO: 623	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYSASTRATGIPA RFSGSGSGTEFTLTISSLQSEDFAVYYCQQDHDYPFTFGGGTKVEIK
Ab 5	SEQ ID NO: 625	EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYFSSPFTFGGGTKVEIK
Ab 6	SEQ ID NO: 627	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVNLPPTFGGGTKVEIK
Ab 7	SEQ ID NO: 629	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRISYPITFGGGTKVEIK
Ab 8	SEQ ID NO: 631	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQIDDTPITFGGGTKVEIK
Ab 9	SEQ ID NO: 633	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQFSYWPWTFGGGTKVEIK

Ab 10	SEQ ID NO: 635	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQHDSSPPTFGGGTKVEIK
Ab 11	SEQ ID NO: 637	EIVLTQSPGTLSLSPGERATLSCRASQSVSSDYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQDYSYPWTFGGGTKVEIK
Ab 12	SEQ ID NO: 639	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQEYAVPYTFGGGTKVEIK
Ab 13	SEQ ID NO: 641	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQVSNYPITFGGGTKVEIK
Ab 14	SEQ ID NO: 643	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQVDNIPPTFGGGTKVEIK
Ab 15	SEQ ID NO: 644	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQFDTYPTFGGGTKVEIK
Ab 16	SEQ ID NO: 646	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQFLNFPTFGGGTKVEIK
Ab 17	SEQ ID NO: 647	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQFFNFPTFGGGTKVEIK
Ab 18	SEQ ID NO: 649	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQFIDLPFTFGGGTKVEIK
Ab 19	SEQ ID NO: 650	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQYYDLPFTFGGGTKVEIK
Ab 20	SEQ ID NO: 652	EIVLTQSPGTLSLSPGERATLSCRASQSVSSDYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFSSHPFTFGGGTKVEIK
Ab 22	SEQ ID NO: 653	EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQDDRSPYTFGGGTKVEIK
Ab 23	SEQ ID NO: 655	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLISWASTR ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQAYLPPITFGGGTKVEIK
Ab 24	SEQ ID NO: 657	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQAFSPPPWTFGGGTKVEIK
Ab 25	SEQ ID NO: 659	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQDDRSPTFGGGTKVEIK
Ab 26	SEQ ID NO: 661	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQEFDLPFTFGGGTKVEIK
Ab 27	SEQ ID NO: 663	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQYNNFPPTFGGGTKVEIK
Ab 28	SEQ ID NO: 665	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRYLRPITFGGGTKVEIK
Ab 29	SEQ ID NO: 667	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQPGAVPTFGGGTKVEIK
Ab 30	SEQ ID NO: 669	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQVYITPITFGGGTKVEIK
Ab 31	SEQ ID NO: 671	DIQLTQSPSSLSASVGDRVTITCQASQDISNFLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQPVDLPFTFGGGTKVEIK
Ab 32	SEQ ID NO: 673	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSFFPPTFGGGTKVEIK
Ab 33	SEQ ID NO: 675	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQDSSFPPTFGGGTKVEIK
Ab 34	SEQ ID NO: 677	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSDFPPWTFGGGTKVEIK
Ab 35	SEQ ID NO: 679	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSAPITFGGGTKVEIK
Ab 36	SEQ ID NO: 681	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQLFDWPTFGGGTKVEIK
Ab 37	SEQ ID NO: 683	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRAFLFTFGGGTKVEIK
Ab 38	SEQ ID NO: 685	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQIDFLPYTFGGGTKVEIK
Ab 39	SEQ ID NO: 687	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSPPITFGGGTKVEIK
Ab 40	SEQ ID NO: 688	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQGYAAPITFGGGTKVEIK
Ab 41	SEQ ID NO: 690	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFTVYYCQQRYALPITFGGGTKVEIK
Ab 42	SEQ ID NO: 692	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYASPPITFGGGTKVEIK
Ab 43	SEQ ID NO: 694	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPITFGGGTKVEIK
Ab 44	SEQ ID NO: 695	EIVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDSSNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQLVHWPTFGGGTKVEIK

Ab 45	SEQ ID NO: 697	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA RFSGSGSGTEFTLTISSLQSEDFAVYYCQQLDDWFTFGGGTKVEIK
Ab 46	SEQ ID NO: 699	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDSSNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNYPITFGGGTKVEIK
Ab 47	SEQ ID NO: 701	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRILYPITFGGGTKVEIK
Ab 48	SEQ ID NO: 702	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRAAYPITFGGGTKVEIK
Ab 49	SEQ ID NO: 703	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTSHPITFGGGTKVEIK
Ab 50	SEQ ID NO: 704	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYAGSPFTFGGGTKVEIK
Ab 51	SEQ ID NO: 706	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQFDDVFTFGGGTKVEIK
Ab 53	SEQ ID NO: 707	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYVNSPFTFGGGTKVEIK
Ab 54	SEQ ID NO: 708	DIQMTQSPSSLSASVGDRVTITCRASQSINSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSDDDPFTFGGGTKVEIK
Ab 55	SEQ ID NO: 710	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQLSTYPLTFGGGTKVEIK
Ab 56	SEQ ID NO: 712	EIVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSVYPITFGGGTKVEIK
Ab 57	SEQ ID NO: 714	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQVSLFPLTFGGGTKVEIK
Ab 58	SEQ ID NO: 716	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCLDYNSYSPITFGGGTKVEIK
Ab 59	SEQ ID NO: 718	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQQHIALPFTFGGGTKVEIK
Ab 60	SEQ ID NO: 720	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRASMPITFGGGTKVEIK
Ab 61	SEQ ID NO: 722	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDSSNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQAFNRPPTFGGGTKVEIK
Ab 62	SEQ ID NO: 724	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSSVHPYTFGGGTKVEIK
Ab 63	SEQ ID NO: 726	DIQMTQSPSSVSASVGDRVTITCRASQGIDSWLAWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQAYSLPPTFGGGTKVEIK
Ab 64	SEQ ID NO: 728	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA RFSGSGSGTEFTLTISSLQSEDFAVYYCQQDDDGYTFGGGTKVEIK
Ab 65	SEQ ID NO: 730	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQDYSWPYTFGGGTKVEIK
Ab 66	SEQ ID NO: 732	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSAYPITFGGGTKVEIK
Ab 67	SEQ ID NO: 733	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSHFPITFGGGTKVEIK
Ab 68	SEQ ID NO: 735	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRANYPITFGGGTKVEIK
Ab 69	SEQ ID NO: 737	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRADYPITFGGGTKVEIK
Ab 70	SEQ ID NO: 738	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSVYPITFGGGTKVEIK
Ab 71	SEQ ID NO: 740	EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQAGSHPFTFGGGTKVEIK
Ab 72	SEQ ID NO: 742	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSRSGTDFTFTISSLQPEDIATYYCQQDVNYPPTFGGGTKVEIK
Ab 73	SEQ ID NO: 744	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA RFSGSGSGTEFTLTISSLQSEDFAVYYCQQDDNYPYTFGGGTKVEIK
Ab 74	SEQ ID NO: 745	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSTFPITFGGGTKVEIK
Ab 75	SEQ ID NO: 747	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQVSNYPFTFGGGTKVEIK
Ab 76	SEQ ID NO: 749	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYHDAPITFGGGTKVEIK
Ab 77	SEQ ID NO: 751	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQAYVVPPTFGGGTKVEIK
Ab 78	SEQ ID NO: 753	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQADNWPFTFGGGTKVEIK
Ab 79	SEQ ID NO: 755	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSHRA SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALESPRTFGGGTKVEIK

Ab 80	SEQ ID NO: 757	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQYVNWPFTFGGGTKVEIK
Ab 81	SEQ ID NO: 759	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSSNWPWTFGGGTKVEIK
Ab 82	SEQ ID NO: 761	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQASTFPITFGGGTKVEIK
Ab 83	SEQ ID NO: 763	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQRNSLPLTFGGGTKVEIK
Ab 84	SEQ ID NO: 764	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYDFPITFGGGTKVEIK
Ab 85	SEQ ID NO: 766	DIQLTQSPSSVSASVGDRVTITCRASQDISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQEVDYPPLTFGGGTKVEIK
Ab 86	SEQ ID NO: 768	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCQQLNSYSPTFGGGTKVEIK
Ab 87	SEQ ID NO: 770	EIVLTQSPATLSLSPGERATLSCRASQSVSRYLAWYQQKPGQAPRLLIYDASNRATGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQQYIFWPPTFGGGTKVEIK

[00202] In some embodiments, anti-TREM2 antibodies of the present disclosure comprise (a) a heavy chain variable region comprising at least one, two, or three HVRs selected from HVR-Hl, HVR-H2, and HVR-H3 of any one of the antibodies listed in **Table 6C** or selected from Abl, Ab2, Ab3, Ab4, Ab5, Ab6, Ab7, Ab8, Ab9, Ab10, Abl11, Ab12, Ab13, Ab14, Ab15, Ab16, Ab17, Ab18, Ab19, Ab20, Ab21, Ab22, Ab23, Ab24, Ab25, Ab26, Ab27, Ab28, Ab29, Ab30, Ab31, Ab32, Ab33, Ab34, Ab35, Ab36, Ab37, Ab38, Ab39, Ab40, Ab41, Ab42, Ab43, Ab44, Ab45, Ab46, Ab47, Ab48, Ab49, Ab50, Ab51, Ab52, Ab53, Ab54, Ab55, Ab56, Ab57, Ab58, Ab59, Ab60, Ab61, Ab62, Ab63, Ab64, Ab65, Ab66, Ab67, Ab68, Ab69, Ab70, Ab71, Ab72, Ab73, Ab74, Ab75, Ab76, Ab77, Ab78, Ab79, Ab80, Ab81, Ab82, Ab83, Ab84, Ab85, Ab86, and Ab87; and/or (b) a light chain variable region comprising at least one, two, or three HVRs selected from HVR-Ll, HVR-L2, and HVR-L3 of any one of the antibodies selected from Abl, Ab2, Ab3, Ab4, Ab5, Ab6, Ab7, Ab8, Ab9, Ab10, Ab11, Ab12, Ab13, Ab14, Ab15, Ab16, Ab17, Ab18, Ab19, Ab20, Ab21, Ab22, Ab23, Ab24, Ab25, Ab26, Ab27, Ab28, Ab29, Ab30, Ab31, Ab32, Ab33, Ab34, Ab35, Ab36, Ab37, Ab38, Ab39, Ab40, Ab41, Ab42, Ab43, Ab44, Ab45, Ab46, Ab47, Ab48, Ab49, Ab50, Ab51, Ab52, Ab53, Ab54, Ab55, Ab56, Ab57, Ab58, Ab59, Ab60, Ab61, Ab62, Ab63, Ab64, Ab65, Ab66, Ab67, Ab68, Ab69, Ab70, Ab71, Ab72, Ab73, Ab74, Ab75, Ab76, Ab77, Ab78, Ab79, Ab80, Ab81, Ab82, Ab83, Ab84, Ab85, Ab86, and Ab87.

[00203] In some embodiments, the anti-TREM2 antibody comprises a light chain variable domain and a heavy chain variable region, wherein the light chain variable region comprises a HVR-L1, HVR-L2, and HVR-L3, and the heavy chain variable domain comprises a HVR-H1, HVR-H2, and HVR-H3 of an antibody listed in **Table 6C** or selected from the group consisting of: Abl, Ab2, Ab3, Ab4, Ab5, Ab6, Ab7, Ab8, Ab9, Ab10, Ab11, Ab12, Ab13, Ab14, Ab15, Ab16, Ab17, Ab18, Ab19, Ab20, Ab21, Ab22, Ab23, Ab24, Ab25, Ab26, Ab27, Ab28, Ab29, Ab30, Ab31, Ab32, Ab33, Ab34, Ab35, Ab36,

Ab37, Ab38, Ab39, Ab40, Ab41, Ab42, Ab43, Ab44, Ab45, Ab46, Ab47, Ab48, Ab49, Ab50, Ab51, Ab52, Ab53, Ab54, Ab55, Ab56, Ab57, Ab58, Ab59, Ab60, Ab61, Ab62, Ab63, Ab64, Ab65, Ab66, Ab67, Ab68, Ab69, Ab70, Ab71, Ab72, Ab73, Ab74, Ab75, Ab76, Ab77, Ab78, Ab79, Ab80, Ab81, Ab82, Ab83, Ab84, Ab85, Ab86, and Ab87.

[00204] In some embodiments, an anti-human TREM2 antibody is an antibody which competes with a monoclonal antibody selected from the group consisting of: Abl, Ab2, Ab3, Ab4, Ab5, Ab6, Ab7, Ab8, Ab9, Ab10, A11, Ab12, Ab13, Ab14, Ab15, Ab16, Ab17, Ab18, Ab19, Ab20, Ab21, Ab22, Ab23, Ab24, Ab25, Ab26, Ab27, Ab28, Ab29, Ab30, Ab31, Ab32, Ab33, Ab34, Ab35, Ab36, Ab37, Ab38, Ab39, Ab40, Ab41, Ab42, Ab43, Ab44, Ab45, Ab46, Ab47, Ab48, Ab49, Ab50, Ab51, Ab52, Ab53, Ab54, Ab55, Ab56, Ab57, Ab58, Ab59, Ab60, Ab61, Ab62, Ab63, Ab64, Ab65, Ab66, Ab67, Ab68, Ab69, Ab70, Ab71, Ab72, Ab73, Ab74, Ab75, Ab76, Ab77, Ab78, Ab79, Ab80, Ab81, Ab82, Ab83, Ab84, Ab85, Ab86, and Ab87 for binding to TREM2.

In some embodiments, each of the light chain variable regions disclosed in **Tables 6A-6C** and each of the heavy chain variable regions disclosed in **Tables 6A-6C** may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

D. PCT Patent Application Publication No. WO2017/062672A1

[00205] In some embodiments, the TREM2 agonist is an antibody or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. WO2017/062672A1 ("the '672 application"), which is incorporated by reference herein, in its entirety.

[00206] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3 (also referred to as HVR-L1, HVR-L2, and HVR-L3, respectively), and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 (also referred to as HVR-H1, HVR-H2, and HVR-H3, respectively) disclosed in the '672 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '672 application specification.

[00207] In some embodiments, the antibody comprises a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain, or the heavy chain variable domain, or both comprise at least one, two, three, four, five, or six HVRs selected from HVR-L1, HVR-L2, HVR-L3, HVR-Hl, HVR-H2, and HVR-H3 such that: (a) the HVR-L1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 829-843, 1401, 1510-1514, 1554-1558, and 1646-1648; (b) the HVR-L2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 844-853, 1515-1517, and 1559-1563; (c) the HVR-L3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 854-867, 1402, 1403, 1518-1522, and 1564-1566; (d) the HVR-Hl comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 868-885, 1404, 1523-1525, 1567-1574, and 1649-1655; (e) the HVR-H2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 886-904, 1405-1407, 1526-1528, 1575-1582, 1656-1662, and 1708; or (f) the HVR-H3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 905-992, 1408, 1409, 1529, 1530, and 1583-1590. In some embodiments: (a) the HVR-L1 comprises the amino acid sequence of SEQ ID NO: 831, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 846, the HVR-L3 comprises the amino acid sequence of SEQ ID NO: 856, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 871, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 889, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 908; (b) the HVR-L1 comprises the amino acid sequence of SEQ ID NO: 834, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 848, the HVR-L3 comprises the amino acid sequence of SEQ ID NO: 859, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 873, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 891, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 910; (c) the HVR-L1 comprises the amino acid sequence of SEQ ID NO: 831, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 846, the HVR- L3 comprises the amino acid sequence of SEQ ID NO: 856, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 871, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 889, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 908; (d) the HVR-Ll comprises the amino acid sequence of SEQ ID NO: 836, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 849, the HVR-L3 comprises the amino acid sequence of SEQ ID NO: 855, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 875, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 893, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 912; (e) the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 978, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 896, and the HVR-H3 comprises

the amino acid sequence of SEQ ID NO: 915; (f) the HVR-Ll comprises the amino acid sequence of SEQ ID NO: 839, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 848, the HVR-L3 comprises the amino acid sequence of SEQ ID NO: 863, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 880, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 898, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 917; (g) the HVR-Ll comprises the amino acid sequence of SEQ ID NO: 840, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 848, the HVR- L3 comprises the amino acid sequence of SEQ ID NO: 868, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 881, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 899, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 918; (h) the HVR-Ll comprises the amino acid sequence of SEQ ID NO: 841, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 852, the HVR-L3 comprises the amino acid sequence of SEQ ID NO: 865, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 882, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 900, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 919; (i) the HVR-Ll comprises the amino acid sequence of SEQ ID NO: 842, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 849, the HVR-L3 comprises the amino acid sequence of SEQ ID NO: 866, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 883, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 902, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 920; or (j) the HVR-Ll comprises the amino acid sequence of SEQ ID NO: 936, the HVR-L2 comprises the amino acid sequence of SEQ ID NO: 849, the HVR-L3 comprises the amino acid sequence of SEQ ID NO: 855, the HVR-Hl comprises the amino acid sequence of SEQ ID NO: 885, the HVR-H2 comprises the amino acid sequence of SEQ ID NO: 904, and the HVR-H3 comprises the amino acid sequence of SEQ ID NO: 922. In some embodiments, the antibody comprises a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain comprises: (a) an HVR-Ll comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 829-843, 1401, 1510-1514, 1554-1558, and 1646-1648, or an amino acid sequence with at least about 90% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 829-843, 1401, 1510-1514, 1554-1558, and 1646-1648; (b) an HVR-L2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 844-853, 1515-1517, and 1559-1563, or an amino acid sequence with at least about 90% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 844-853, 1515-1517, and 1559-1563; and (c) an HVR-L3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 854-867, 1402, 1403, 1518-1522, and 1564-1566, or an amino acid sequence with at

least about 90% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 854-867, 1402, 1403, 1518-1522, and 1564-1566; and wherein the heavy chain variable domain comprises: (a) an HVR-H1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 868-885, 1404, 1523-1525, 1567-1574, and 1649-1655, or an amino acid sequence with at least about 90% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 868-885, 1404, 1523-1525, 1567-1574, and 1649-1655; (b) an HVR-H2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 886-904, 1405-1407, 1526-1528, 1575-1582, 1656-1662, and 1708, or an amino acid sequence with at least about 90% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 886-904, 1405-1407, 1526-1528, 1575-1582, 1656-1662, and 1708; and (c) an HVR-H3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 905-992, 1408, 1409, 1529, 1530, and 1583-1590, or an amino acid sequence with at least about 90% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 905-992, 1408, 1409, 1529, 1530, and 1583-1590. In some embodiments, the antibody comprises a light chain variable domain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1039-1218, 1422-1454, 1499-1509, 1544-1550, 1629-1636, 1641, 1643, 1664, 1669, and 1670; and/or a heavy chain variable domain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1219-1400, 1455-1498, 1551-1553, and 1637-1640, 1642-1645, and 1665-1667.

[00208] In some embodiments, the antibody comprises a light chain variable domain and a heavy chain variable domain, wherein: (a) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1153 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1341; (b) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1670 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1341; (c) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1154 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1342; (d) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1155 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1343; (e) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1156 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1344; (f) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1157 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1345; (g) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1158 and the heavy chain variable domain comprises the amino acid

sequence of SEQ ID NO:1346; (h) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1159 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1346; (i) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1160 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1347; (j) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1161 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1348; (k) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1162 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1349; (1) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1163 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1350; (m) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1663 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1665; (n) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1664 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1666; (o) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1664 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1667; (p) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1039 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1219; (q) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1050 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1229; (r) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1072 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1239; (s) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1061 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1249; (t) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1669 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1249; (u) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1083 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1259; (v) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1094 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1269; (w) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1105 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1279; (x) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1106 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1280; (y) the

light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1107 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1281; (z) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1118 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1249; (aa) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1119 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1291; (bb) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1130 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1281; (cc) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1499 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1301; (dd) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1131 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1311; (ee) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1142 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1331; (ff) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1164 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1351; (gg) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1175 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1455; (hh) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1185 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1361; (ii) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1216 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1371; (jj) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1217 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1381; (kk) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1218 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1391; (11) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1544 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1551; (mm) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1629 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1551; (nn) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1545 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1552; (oo) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1546 and the heavy chain variable domain

comprises the amino acid sequence of SEQ ID NO: 1551; (pp) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1546 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1637; (qq) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1547 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1551; (rr) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1548 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1553; (ss) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1630 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1638; (tt) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1631 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1553; (uu) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1549 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1551; (vv) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1632 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1639; (ww) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1549 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1640; (xx) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1550 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1551; (yy) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1633 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1551; (zz) the light chain variable domain comprises the amino acid sequence of SEQ ID NO: 1634 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1642; (aaa) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1635 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO: 1644; or (bbb) the light chain variable domain comprises the amino acid sequence of SEQ ID NO:1636 and the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:1645. In any of the above embodiments, the light chain variable domain and/or heavy chain variable domain comprises an amino acid sequence with at least about 90% homology to the amino acid sequence indicated.

[00209] In some embodiments, the antibody is an antibody disclosed in Tables 2A, 2B, 3A, 3B, 4A, 4B, 7A and 7B of PCT Patent Application Publication No. WO2017/062672A1, reproduced below as **Tables 7A-7H**.

Table 7A. EU or Kabat light chain HVR sequences

Ab	HVRL1	HVRL2	HVRL3
4D11	RASENIYSFLA (SEQ ID NO: 829)	NSKTFAE (SEQ ID NO: 844)	QHHYGTPPWT (SEQ ID NO: 854)
78C5	RASENIYSFLA (SEQ ID NO: 829)	NSKTFAE (SEQ ID NO: 844)	QHHYGTPPWT (SEQ ID NO: 854)
6G12	KSSQSLLYSSNQKNCLA (SEQ ID NO: 830)	WAFTRES (SEQ ID NO: 845)	QQYYSYPLT (SEQ ID NO: 855)
8F11	KSSQSLLYSSNQKNCLA (SEQ ID NO: 830)	LVSKLDS (SEQ ID NO: 846)	MQGTHFPLT (SEQ ID NO: 856)
8E10	KSSQSLLDSDGKTYLN (SEQ ID NO: 832)	LSVSKLDS (SEQ ID NO: 846)	WQGTHFPYT (SEQ ID NO: 857)
7E5	KSSQSLLYSNGKTFLS (SEQ ID NO:831)	LVSKLDS (SEQ ID NO:846)	MQGTHFPLT (SEQ ID NO:856)
7F8	SASSSVSYMY (SEQ ID NO:833)	LTSILAS (SEQ ID NO:847)	QQWSFNPYT (SEQ ID NO:858)
8F8	RSSQSLVHSNGNTYLH (SEQ ID NO:834)	KVSNRFS (SEQ ID NO:848)	SQSTHVPLT (SEQ ID NO:859)
H7	SASSSVSYMY (SEQ ID NO:833)	LTSILAS (SEQ ID NO:847)	QQWSFNPYT (SEQ ID NO:858)
2H8	SASSSVSYMY (SEQ ID NO:13)	LTSILAS (SEQ ID NO:847)	QQWSFNPYT (SEQ ID NO:858)
3A2	RSSQTIIHSNGNTYLE (SEQ ID NO:835)	KVSNRFS (SEQ ID NO: 848)	FQGSHVPYT (SEQ ID NO:860)
3A7	KSSQSLLYSNGKTFLS (SEQ ID NO:831)	LVSKLDS (SEQ ID NO:846)	MQGTHFPLT (SEQ ID NO:856)
3B10	KSSQSLLYSSDQKNYLA (SEQ ID NO:836)	WASTRES (SEQ ID NO: 849)	QQYYSYPLT (SEQ ID NO:855)
4F11	RSSQTIIHSNGNTYLE (SEQ ID NO:835)	KVSNRFS (SEQ ID NO:848)	FQGSHVPYT (SEQ ID NO:860)
6H6	KSSQSVFYSSNQKNYLA (SEQ ID NO:1401)	WASTRES (SEQ ID NO:849)	HQYLSSLT (SEQ ID NO:1402)
7A9	RASENIYSYLA (SEQ ID NO:837)	KAKTLAE (SEQ ID NO:850)	QHHYGTPFT (SEQ ID NO:861)
8A1	RTSENVYSNLA (SEQ ID NO:838)	AATNLAD (SEQ ID NO:851)	HHFWGTPYT (SEQ ID NO:862)
9F5	RSSQSLVHSNGYTYLH (SEQ ID NO:839)	KVSNRFS (SEQ ID NO:848)	SQSTRVPYT (SEQ ID NO:863)
9G1	RFSQSLVHSNGNTYLH (SEQ ID NO:840)	KVSNRFS (SEQ ID NO: 848)	SQSTRVPPT (SEQ ID NO:864)
9G3	KASSNVNYMS (SEQ ID NO:841)	FTSNLPS (SEQ ID NO:852)	SGEVTQFT (SEQ ID NO:865)
10A9	RSSQTIIHSNGNTYLE (SEQ ID NO:835)	KVSNRFC (SEQ ID NO:853)	FQGSHVPYT (SEQ ID NO:860)
11A8	KSSQSLLNSGNQKKYLT (SEQ ID NO:842)	WASTRES (SEQ ID NO: 849)	QNDYGFPLT (SEQ ID NO:866)
12D9	KSSQSLLYSGNQKNFLA (SEQ ID NO:843)	WASTRES (SEQ ID NO:849)	QQYYSYPFT (SEQ ID NO:867)
12F9	KSSQSLLYSSDQKNYLA (SEQ ID NO:846)	WASTRES (SEQ ID NO:849)	QQYYSYPLT (SEQ ID NO:855)
10C1	KSSQSVFYSSNQKNYLA (SEQ ID NO: 1401	WASTRES (SEQ ID NO:849)	HQYLSSLT (SEQ ID NO: 1402)

7E9	KSSQSLLYSSNQKNCLA (SEQ ID NO:830)	WASTRES (SEQ ID NO:849)	QQYYSYPLT (SEQ ID NO:855)
8C3	RSSQSLVHSNGNTYLH (SEQ ID NO:834)	KVSNRFS (SEQ ID NO:848)	SQSTHVPPT (SEQ ID NO:1403)
IB4v1	SQDVSTTVA (SEQ ID NO:1510)	SASYRYT (SEQ ID NO:1515)	QQHYSTPPT (SEQ ID NO:1518)
IB4v2	SQSLVHSNGNTYLH (SEQ ID NO:1554)	KVSNRVS (SEQ ID NO:1559)	SQSTHVPLT (SEQ ID NO:859)
6H2	SQSIVHSNGNTYLE (SEQ ID NO:1511)	KVSNRFS (SEQ ID NO:848)	FQGSHVPFT (SEQ ID NO:1519)
7B11	SQGVSTAVA (SEQ ID NO:1512)	WASTRHT (SEQ ID NO:1516)	HQHYSTYT (SEQ ID NO:1520)
18D8	SQDVRTAVA (SEQ ID NO:1513)	SASYRYT (SEQ ID NO:1515)	QQHYGTPPWT (SEQ ID NO:1521)
18E4v1	SENVVTYVS (SEQ ID NO:1514)	GASNRYT (SEQ ID NO:1517)	GQGYSYPYT (SEQ ID NO:1522)
18E4v2	SQSLVHSNGNTYLH (SEQ ID NO:1554)	KVSDRFS (SEQ ID NO:1560)	SQSTHVPLT (SEQ ID NO:859)
29F6v1	SQDVRTAVA (SEQ ID NO:1513)	SASYRYT (SEQ ID NO:1515)	QQHYGTPPWT (SEQ ID NO:1521)
29F6v2	SQSLVHSNGDTYLH (SEQ ID NO:1555)	KVSNRFS (SEQ ID NO:848)	SQSTHVPLT (SEQ ID NO:859)
40D5	SQDVRTAVA (SEQ ID NO:1513)	SASYRYT (SEQ ID NO:1515)	QQHYGTPPWT (SEQ ID NO:1521)
43B9	SQDVRTAVA (SEQ ID NO:1513)	SASYRYT (SEQ ID NO:1515)	QQHYGTPPWT (SEQ ID NO:1521)
44A8v1	SQDVSTTVA(SEQ ID NO:1510)	SASYRYT (SEQ ID NO:1515)	QQHYSTPPT (SEQ ID NO:1518)
44A8v2	SESVDYHGTSLMQ (SEQ ID NO:1556)	AASNVES (SEQ ID NO:1561)	QQNRKILWT (SEQ ID NO:1564)
44B4v1	SQDVRTAVA (SEQ ID NO:1513)	SASYRYT (SEQ ID NO:1515)	QQHYGTPPWT (SEQ ID NO:1521)
44B4v2	SENIZYSLA (SEQ ID NO:1557)	NANSLED (SEQ ID NO:1562)	KQAYDVPWT (SEQ ID NO:1565)
29F7	RASQSIGTSIH (SEQ ID NO:1558)	FASESIS (SEQ ID NO:1563)	QQTNTWPIT (SEQ ID NO:1566)
32G1	RSSQSLVHSNGNTYLH (SEQ ID NO:834)	KVSNRFS (SEQ ID NO:848)	SQSTHVPLT (SEQ ID NO:859)

Table 7B: EU or Kabat light chain HVR consensus sequences

	HVR 1,1
Consensus 1	RXSENXYSXLA (SEQ ID NO:1646)
Consensus 2	RSSQXXXHSNGXTYLX (SEQ ID NO:1647)
Consensus 3	KSSQSXXXSXXQKXXLX (SEQ ID NO:1648)

Table 7C: EU or Kabat heavy chain HVR sequences

Ab ID	**HVR H1**	**HVR H2**	**HVR H3**
4D11	FTLSSYAMS (SEQ ID NO:868)	VASISRGGSTYYP (SEQ ID NO:886)	TRGYGYYRTPFAN (SEQ ID NO:905)
78C5	FTLSSYAMS (SEQ ID NO:868)	VASISRGGSTYYP (SEQ ID NO:886)	TRGYGYYRTPFAN (SEQ ID NO:905)
6G12	YTFTEYTMH (SEQ ID NO:869)	IGGINPNNGGTSYS (SEQ ID NO:887)	ARGGSHYYAMDY (SEQ ID NO:906)
8E10	YTFTDYEMH (SEQ ID NO:870)	IGVIDPETGGTAYN (SEQ ID NO:888)	TSPDYYGSSYPLYYAMDY (SEQ ID NO:907)

7E5	FTFSDAWMG (SEQ ID NO:871)	VAEIRDKVKNHATYYA (SEQ ID NO:889)	RLGVFDY (SEQ ID NO:908)
7F8	FSFNTYAMN (SEQ ID NO:872)	IARIRSKSNNYATYYA (SEQ ID NO:890)	VRHGDGNLWYIDV (SEQ ID NO:909)
8F8	YTVSRYWMH (SEQ ID NO:873)	IGRIDPNSGGTKYN (SEQ ID NO:891)	VLTGTDFDY (SEQ ID NO:90)
1H7	FSFNTYAMN (SEQ ID NO:872)	IARIRSKSNNYATYYA (SEQ ID NO:890)	VRHGDGNLWYIDV (SEQ ID NO:909)
2H8	FSFNTYAMN (SEQ ID NO:872)	IARIRSKSNNYATYYA (SEQ ID NO:890)	VRHGDGNLWYIDV (SEQ ID NO:909)
3A2	YPFSNFWIT (SEQ ID NO:874)	IGDIYPGSDNSNYN (SEQ ID NO:892)	AREAYYTNPGFAY (SEQ ID NO:911)
3A7	FTFSDAWMG (SEQ ID NO:871)	VAEIRDKVKNHATYYA (SEQ ID NO:889)	RLGVFDY (SEQ ID NO:908)
3B10	LTSNTYTQT (SEQ ID NO:875)	ESVIRSKSNNFSTLYA (SEQ ID NO:893)	VRHKSNRYPGVY (SEQ ID NO:912)
4F11	YPFSNFWIT (SEQ ID NO:874)	IGDIYPGSDNSNYN (SEQ ID NO:892)	AREAYYTNPGFAY (SEQ ID NO:911)
6H6	FTFSDAWMD (SEQ ID NO:876)	VAEIRNKVNNHATYYA (SEQ ID NO:894)	TSLYDGYYLRFAY (SEQ ID NO:913)
7A9	FTFNTYSMN (SEQ ID NO:877)	VAHIKTKZNNFATFYA (SEQ ID NO:895)	VZHZSNNYPFAY (SEQ ID NO:914)
7B3	YTFTTYWIH (SEQ ID NO:878)	IGRNDPNSGGSNYN (SEQ ID NO:896)	VRTNWDGDF (SEQ ID NO:915)
8A1	YAFSNYWMS (SEQ ID NO:879)	IGQIYPGDGDTKYN (SEQ ID NO:897)	SREKGADYYGSTYSAWFSY (SEQ ID NO:916)
9F5	YAFSSSWMN (SEQ ID NO:880)	IGRIYPGDGDTNYN (SEQ ID NO:898)	ARLLRNQPGESYAMDY (SEQ ID NO:917)
9F5a	YAFSSSWMN (SEQ ID NO:880)	RIYPGDGDTNYNGEFRV (SEQ ID NO:888)	ARLLRNQPGESYAMDY (SEQ ID NO:917)
9G1	YIFTTYWIH (SEQ ID NO:881)	IGRIDPNNGDTNYN (SEQ ID NO:899)	VMTGTDFDY (SEQ ID NO:918)
9G3	FNFNTYAMK (SEQ ID NO:882)	IARIRSNSNDYATNYS (SEQ ID NO:900)	VGHKINNYPFAH (SEQ ID NO:919)
10A9	YPFSNFWIT (SEQ ID NO:874)	IGDIYPGSDNRNFN (SEQ ID NO:901)	AREAYYTNPGFAY (SEQ ID NO:911)
11A8	FNFNTYAMN (SEQ ID NO:883)	VARIRSKSNNYATYYA (SEQ ID NO:902)	VRHYSNYGWGFAY (SEQ ID NO:920)
12D9	YTFSDYYIH (SEQ ID NO:884)	IGYIYPNNGDNGYN (SEQ ID NO:903)	ARRGYYGGSYDY (SEQ ID NO:921)
12F9	FRFNTYAMT (SEQ ID NO:885)	EGVIRRKSSNFATLYA (SEQ ID NO:904)	VRHKSNKYPFVY (SEQ ID NO:922)
10C1	FTFSDAWMD (SEQ ID NO:876)	VAEIRNKINNHATYYA(SEQ ID NO:1405)	TSLYDGSYLRFAY (SEQ ID NO:1408)
7E9	YTFTEYTMH (SEQ ID NO:869)	IGGINPNNGGTSYK (SEQ ID NO:1406)	ARGGSHYYAMDY (SEQ ID NO:906)
8C3	YSFTGYYMH (SEQ ID NO:1404)	IGRVNPNNGGTSYN (SEQ ID NO:1407)	VLTGGYFDY (SEQ ID NO:1409)
1B4	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
6H2	SAFSLTNYAVH (SEQ ID NO:1524)	LGVIWSGGSTAFN (SEQ ID NO:1527)	ATHYYRSTYAFSY (SEQ ID NO:1530)
7B11v1	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
7B1lv2	SGYTFTDFYMN (SEQ ID NO:1567)	IGDINPNNGHTTYN (SEQ ID NO:1575)	AREPYSYGSSPWYFLV (SEQ ID NO:1583)

18D8	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
18E4v1	SRFTFSSYAVS (SEQ ID NO:1525)	VATISGGGRYTYYP (SEQ ID NO:1528)	ARHYDGYLDY (SEQ ID NO:1529)
18E4v2	SGYTFTAYWMH (SEQ ID NO:1568)	IGRTHPSDSDTNYN (SEQ ID NO:1576)	ATYSNYVTGAMDS (SEQ ID NO:1584)
29F6v1	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
29F6v2	SGFNIKNTYIH (SEQ ID NO:1569)	IGRIDPAIGNTNYA (SEQ ID NO:1577)	VSPGMDY (SEQ ID NO:1585)
40D5v1	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
40D5v2	SGYTFTNYWIH (SEQ ID NO:1570)	IGRIHPSDSDINYN (SEQ ID NO:1578)	VKTGTSFAS (SEQ ID NO:1586)
43B9	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
44A8	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
44B4v1	SRFTFSSYAMS (SEQ ID NO:1523)	VAAISGGGRYTYYP (SEQ ID NO:1526)	ARHYDGYLDY (SEQ ID NO:1529)
44B4v2	SGYTFTSATMH (SEQ ID NO:1571)	IGYINPNSGYSKYN (SEQ ID NO:1579)	ARWGIDGNYGGGFFDV (SEQ ID NO:1587)
45D6	YSFTDYNIH (SEQ ID NO:1572)	IGYINPNSDNTRYI (SEQ ID NO:1580)	TRGFSNLGAMDY (SEQ ID NO:1588)
29F7	FTLSNYWMN (SEQ ID NO:1573)	VAQIRLKSDNYATHYA (SEQ ID NO:1581	TGAGGNHENY (SEQ ID NO:1589)
32G1	YTFTDYNIH (SEQ ID NO:1574)	IGYINPNNGGTTYN (SEQ ID NO:1582	ATTYVSFSY (SEQ ID NO:1590)

Table 7D: EU or Kabat heavy chain HVR consensus sequences

	HVR H1	**HVR H2**
Consensus 1	$YX_1X_2X_3XYXXH$ X_1 is T or S X_2 is F or V X_3 is T or S (SEQ ID NO:1649)	$IGXXXPX_1X_2X_3X_4X_5XYX_6$ X_1 is N or E X_2 is N, S, or T $X_3$is G or D X_4 is G, D, or N X_5 is T, S, or N X_6 is N, S, K, or I (SEQ ID NO:1656)
Consensus 2	YTFTXYXXH (SEQ ID NO:1650)	IGXXXPNNGGTXYN (SEQ ID NO:1657)
Consensus 3	$FTFSDAWMX_1$ X_1 is D or G (SEQ ID NO:1651)	$VAEIRX_1KX_2X_3NHATYYA$ X_1 is N or D X_2 is V or I X_3 is N or K (SEQ ID NO:1658)

Consensus 4	$FXX_1X_2X_3YX_4MX_5$ X_1 is F or L X_2 is N or S X_3 is T or N X_4 is A, S, or W X_5 is N, K, or T (SEQ ID NO:1652)	$XX_1XIX_2X_3X_4X_5X_6X_7X_8ATXYX_9$ X_1 is A or G X_2 is R or K X_3 is S, T, R, or L X_4 is K or N X_5 is S, E, or Q X_6 is N, S, or D X_7 is N or D X_8 is Y or F X_9 is A or S (SEQ ID NO:1659)
Consensus 5	FXFNTYAMN (SEQ ID NO:1653)	XAXIRSKSNNYATXYA (SEQ ID NO:1660)
Consensus 6	$YXFX_1X_2XWX_3X$ X_i is S or T X_2 is N, S, or T X_3 is I or M (SEQ ID NO:1654)	$IGXIX_1PX_2XX_3X_4X_5X_6X_7N$ X_1 is Y or D X_2 is G or N X_3 is G or D X_4 is N or D X_5 is T, R, or S X_6 is N or K X_7 is Y or F (SEQ ID NO:1661)
Consensus 7	YXFSNXWIX (SEQ ID NO:1655)	IGXIYPGXGDTNYN (SEQ ID NO:1662)

Table 7E: EU or Kabat light chain Framework sequences

Ab ID	VL FR1	VL FR2	VL FR3	VL FR4
4D11	DIZVTQSPASLSA SVGETVTITC (SEQ ID NO:923)	WYQLKQGKSPQLL VY (SEQ ID NO:940)	GVPSRFSGSGSGTQFS LRINSLQPEDFGSYYC (SEQ ID NO:950)	FGGGTKLEIK (SEQ ID NO:968)
78C5	DIZVTQSPASLSA SVGETVTITC (SEQ ID NO:923)	WYQLKQGKSPQLL VY (SEQ ID NO:940)	GVPSRFSGSGSGTQFS LRINSLQPEDFGSYYC (SEQ ID NO:950)	FGGGTKLEIK (SEQ ID NO:968)
6G12	TMSQSPSSLAVS VGEKVTMSC (SEQ ID NO:924)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSGTDFT LTISSVKAEDLAVYYC (SEQ ID NO:951)	FGAGTKLELK (SEQ ID NO:969)
8F11	DVZMTQTPLTLS VTIGQPASISC (SEQ ID NO:925)	WLLQRPGQSPKRLI Y (SEQ ID NO:942)	GVPDRFAGSGSGTDFT LKISRLEADDLGIYYC (SEQ ID NO:952)	FGAGTKLELK (SEQ ID NO:969)
8E10	DVZMTQTPLTLS VTIGQPASISC (SEQ ID NO:925)	WLLQRPGQSPKRLI Y (SEQ ID NO:942)	GVPDRFTGSGSGTDFT LKISRVEAEDLGVYYC (SEQ ID NO:953)	FGGGTKLEIK (SEQ ID NO:968)
7E5	DVZMTQTPLTLS VTIGQPASISC (SEQ ID NO:925)	WLLQRPGQSPKRLI Y (SEQ ID NO:942)	GVPDRFAGSGSGTDFT LKISRLEADDLGIYYC (SEQ ID NO:952)	FGAGTKLELK (SEQ ID NO:969)
7E5v2	DVVMTQTPLTLS VTIGQPASISC (SEQ ID NO:931)	WLLQRPGQSPKRLI Y (SEQ ID NO:942)	GVPDRFAGSGSGTDFT LKISRLEADDLGIYYC (SEQ ID NO:952)	FGAGTKLELK (SEQ ID NO:969)
7F8	VLTQSPALMSAS PGEKVTMTC (SEQ ID NO:926)	WYQQKPRSSPKPW IY (SEQ ID NO:943)	GVPARFSGSGSGTSYS LTINNMEAEDAATYY C (SEQ ID NO:954)	FGGGTKLVIK (SEQ ID NO:970)
8F8	DVZMTQTPLSLP VSLGDQASISC (SEQ ID NO:927)	WYLQKPGQSPKLLI Y (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYFC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)
1H7	VLTQSPAIMZASP GEKVTMTC (SEQ ID NO:928)	WYQQKPRSSPKPW IY (SEQ ID NO:943)	GVPARFSGSGSGTSYS LTISSMEAEDAATYYC (SEQ ID NO:956)	FGGGTKLVIK (SEQ ID NO:970)

2H8	NVLTQSPALMSA SPGEKVTMTC (SEQ ID NO:929)	WYQQKPRSSPKPW IY (SEQ ID NO:943)	GVPARFSGSGSGTSYS LTISSMEAEDAATYYC (SEQ ID NO:956)	FGGGTKLVIK (SEQ ID NO:970)
3A2	DVVMTQTPLSLP VSLGDQASISC (SEQ ID NO:930)	WYLRKPGQSPKLLI Y (SEQ ID NO:945)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYYC (SEQ ID NO:957)	FGGGTELEIK (SEQ ID NO:971)
3A7	DVVMTQTPLTLS VTIGQPASISC (SEQ ID NO:931)	WLLQRPGQSPKRLI Y (SEQ ID NO:942)	GVPDRFAGSGSGTDFT ZKISRLEADDLGIYYC (SEQ ID NO:958)	FGGGTKLEMK (SEQ ID NO:972)
3B10	ITMSQSPSSLAVS VGEKVTMSC (SEQ ID NO:932)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSGTDFT LTISSVKAEDLAVYCC (SEQ ID NO:959)	FGAGTKLELK (SEQ ID NO:969)
4F11	DVZMTQTPLSLP VSLGDQASISC (SEQ ID NO:927)	WYLRKPGQSPKLLI Y (SEQ ID NO:945)	GVPDRFSGSGSGTDFT LKISRVEGEDLGVYYC (SEQ ID NO:960)	FGGGTELEIK (SEQ ID NO:971)
6H6	QTQSPSSLAVSA GEKVTLSC (SEQ ID NO:1410)	WYQQKPGQSPKLLI S (SEQ ID NO:1413)	GVPDRFTGSGFGTDFT LTISSVQGEDLAVYYC (SEQ ID NO:1414)	FGAGTKLELK (SEQ ID NO:969)
7A9	QMSQSPACLZAZ VGESVTITC (SEQ ID NO:933)	WYQQKQGKSPKLV VY (SEQ ID NO:946)	GVPSRFSGRGSGTQFF LKINSZQREDFGSYYC (SEQ ID NO:961)	FGSGTKLEIK (SEQ ID NO:973)
8A1	DIQMTQSPASLSV SVGETVTITC (SEQ ID NO:934)	WYQQKQGKSPQLL VY (SEQ ID NO:947)	GVPSRFSASGSATQFS LKINSLQSADFGSYYC (SEQ ID NO:962)	FGGGTKLEMN (SEQ ID NO:974)
9F5	DVZMTQNPLSLP VSLGDQASISC (SEQ ID NO:935)	WYLQKPGQSPKLLI Y (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LKISRVEADDLGVYLC (SEQ ID NO:963)	FGGGTKLEIK (SEQ ID NO:968)
9F5v2	DVVMTQTPLSLP VSLGDQASISC (SEQ ID NO:930)	WYLQKPGQSPKLLI Y (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LKISRVEADDLGVYFC (SEQ ID NO:848)	FGGGTKLEIK (SEQ ID NO:968)
9G1	DVLMTQTPLSLP VSLGDQASISC (SEQ ID NO:936)	WYLQKPGQSPKLLI Y (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LRISGVEAEDLGVYFC (SEQ ID NO:964)	FGGGTKLEIK (SEQ ID NO:968)
9G3	NVLTQSPALIWAZP GEKVTMTC (SEQ ID NO:937)	WXXXKPRSSPKPGI Y (SEQ ID NO:948)	GVPGRFSGSGSGTYXSFK ISSMEGKMGPLIIFC (SEQ ID NO:965)	FGGGTKLEMK (SEQ ID NO:975)
10A9	DVVMTQTPLSLP VSLGDQASISC (SEQ ID NO:930)	WYLRKPGQSPKLLI Y (SEQ ID NO:945)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYYC (SEQ ID NO:957)	FGGGTELEIK (SEQ ID NO:971)
11A8	DIZMTQSPSSLTV TAGEKVTMSC (SEQ ID NO:938)	WYQQKPGQPZKLL IY (SEQ ID NO:949)	GVRDRFTGSGZGTDFT LTISSVQGEDLAIYYC (SEQ ID NO:966)	FGGGTKLEMK (SEQ ID NO:972)
12D9	TQSPSSLAVSVGE KVTMTC (SEQ ID NO:939)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSGTDFT LTISTVKAEDLAVYYC (SEQ ID NO:967)	FGSGTKLEIK (SEQ ID NO:973)
12F9	TMSQSPSSLAVS VGEKVTMSC (SEQ ID NO:924)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSGTDFT LTISSVKAEDLAVYCC (SEQ ID NO:959)	FGAGTKLELK (SEQ ID NO:969)
10C1	QTQVFLSLLLWVS GTCGNIMLTQSPSS LAVSAGEKVTLSC (SEQ ID NO:1411)	WYQQKPGQSPKLLI S (SEQ ID NO:1413)	GVPDRFTGSGSGTDFT LTINSVQAEDLAVYYC (SEQ ID NO:1415)	FGAGTKLELK (SEQ ID NO:969)
7E9	DIVMSQSPSSLAV SVGEKVTMSC (SEQ ID NO:1412)	WYQQKPGQSPKLLI (SEQ ID NO:941)	GVPDRFTGSGSGTDFT LTISSVKAEDLAVYYC (SEQ ID NO:951)	FGAGTKLELK (SEQ ID NO:969)

8C3	DVVMTQTPLSLP VSLGDQASISC (SEQ ID NO:930)	WYLQKPGQSPKLLI Y (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYFC (SEQ ID NO:955)	FGSGTKLEIK (SEQ ID NO:973)
IB4v1	DIVMTQSHKFMS TSVGDRVSITCK A (SEQ ID NO:1531)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGFGTDFT FTISSVQAEDLAVYYC (SEQ ID NO:1535)	FGGGTKLEIK (SEQ ID NO:968)
IB4v2	ZVVZTQTPLSLPV SLGDQASFSCRS (SEQ ID NO:1591)	WFLQKPGQSPKLLI F (SEQ ID NO:1597)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYFC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)
6H2	DVLMTQTPLSLP VSLGDQASISCRS (SEQ ID NO:1532)	WYLQKPGQSPKLLI Y (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYYC (SEQ ID NO:957)	FGSGTKLEIK (SEQ ID NO:973)
7B11	DIVMTQSHKFMS TSVGDRVSITCK A (SEQ ID NO:1531)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSGTDYT LTISSVQAEDLALYYC (SEQ ID NO:1536)	FGGGTKLEIK (SEQ ID NO:968)
18D8	DIVMTQSHKFMS TSIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGFGTDFT FTISSVQAEDLAVYYC (SEQ ID NO:1535)	FGGGTKLEIK (SEQ ID NO:968)
18E4v1	DIVMTQSPKSMS MSVGERVTLTCKA (SEQ ID NO:1534)	WYQQKPEQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSATDFT LTISSVQAEDLADYHC (SEQ ID NO:1537)	FGGGTKLEIK (SEQ ID NO:968)
18E4v2	NIVMTQSPKSMS MSVGERVTLTCK A (SEQ ID NO:1592)	WYQQKPEQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSATDFT LTISSVQAEDLADYHC (SEQ ID NO:1537)	FGGGTKLEIK (SEQ ID NO:968)
18E4v3	DVVMTQTPLSLP VSLGDQASISCRS (SEQ ID NO:1593)	WYLQKPGQSPKLLI Y (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LRISRVEAEDLGVYFC (SEQ ID NO:1601)	FGAGTKLELK (SEQ ID NO:969)
29F6v1	DIVMTQSHKFMS TSIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPKLLI Y (SEQ ID NO:941)	GVPDRFTGSGSGTDFTFT ISSVQAEDLAVYYC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
29F6v2	DVVMTQTPLSLPV SLGDQASISCRS (SEQ ID NO:1593)	WYLQKPGQSPKLI JY (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYFC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)
40D5	DIVMTQSHKFMS TSIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPKLI JY (SEQ ID NO:941)	GVPDRFTGSGSGTDFTFT ISSVQAEDLAVYYC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
43B9	DIVMTQSHKFMS TSIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPKLI JY (SEQ ID NO:941)	GVPDRFTGSGSGTDFTFT ISSVQAEDLAVYYC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
44A8v1	DIVMTQSHKFM S TSVGDRVSITCK A (SEQ ID NO:1531)	WYQQKPGQSPKLI JY (SEQ ID NO:941)	GVPDRFTGSGSGTDFTFT ISSVQAEDLAVYYC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
44A8v2	DIVLTQSPASLA VSLGQRATISCRA (SEQ ID NO:1594)	WYQQKPGQPPKLI JY (SEQ ID NO:1598)	GVPARFSGSGSGTDFSLN IHPVEEDDIAMYFC (SEQ ID NO:1602)	FGGGTKLEIK (SEQ ID NO:968)
44B4v1	DIVMTQSHKFMS TSIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPKLI JY (SEQ ID NO:941)	GVPDRFTGSGSGTDFTFT ISSVQAEDLAVYYC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
44B4v2	DIQMTQFPASLAA XVGESVTITCRA (SEQ ID NO:1595)	WYQQKQGKSPQL LIY (SEQ ID NO:1599)	GVPSRFSGSGSGTQYSM KINSMQPEDTAIYFC (SEQ ID NO:1603)	FGGGTKLEIK (SEQ ID NO:968)
29F7	ILLTQSPAILSVSP GERVSFSC (SEQ ID NO:1596)	WYQQRTNGSPRLI J K (SEQ ID NO:1600)	GIPSRFSGSGSGTDFTLNI NSVESEDIADYYC (SEQ ID NO:1604)	FGAGTKLELK (SEQ ID NO:969)
32G1	DVVMTQTPLSLP VSLGDQASISC (SEQ ID NO:930)	WYLQKPGQSPKLI JY (SEQ ID NO:944)	GVPDRFSGSGSGTDFT LKISRVEAEDLGVYFC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)

Table 7F: EU or Kabat heavy chain Framework sequences

Ab ID	VH FR1	VH FR2	VH FR3	VH FR4
44D11	EVKLVESGGGLVK PGGSLKLSCAASG (SEQ ID NO:976)	WVRQTPEKRLEW (SEQ ID NO:995)	DSVQGRFTFSRDNARNIL YLQMSSLRSEDTAMYYC (SEQ ID NO:1008)	WGQGTLVTVSA (SEQ ID NO:1029)
78C5	EVKLVESGGGLVK PGGSLKLSCAASG (SEQ ID NO:976)	WVRQTPEKRLEW (SEQ ID NO:995)	DSVQGRFTFSRDNARNIL YLQMSSLRSEDTAMYYC (SEQ ID NO:1008)	WGQGTLVTVSA (SEQ ID NO:1029)
6G12	EVQLQQSGPELVKP GTSVKISCKTSG (SEQ ID NO:977)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGKASLTVDKSSST AYMELHSLASDDSAVY YC (SEQ ID NO:1009)	WGQGTSVTVSS (SEQ ID NO:1030)
8E10	QVQLQQSGAELVR PGASVTLSCKASG (SEQ ID NO:978)	WVKQTPVHGLEW (SEQ ID NO:997)	QKFKGKAILTADK SSS TAYMELRSLTSEDSAV YYC (SEQ ID NO:1010)	WGQGTSVTVSS (SEQ ID NO:1030)
7E5	EVKLEESGGGLVQPG GSMKLSCAASG (SEQ ID NO:979)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSKSTV YLQMNTLRADDTGIYC (SEQ ID NO:1011)	WGQGTTLTVSS (SEQ ID NO:1031)
7F8	EVQLVESGGGLVQ PKGSLKLSCAASG (SEQ ID NO:980)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRITCSRDDSENM FYLQLSSLKTEDTAMYY C (SEQ ID NO:1012)	WGTGTTVTVST (SEQ ID NO:1032)
8F8	QVQLQQSGAELVKPG ASVKLSCKASG (SEQ ID NO:981)	WVKQRPGRGLEW (SEQ ID NO:1000)	EKFKTKATLTVDK PSS TAYMQVSSLTSEDSAV YYC (SEQ ID NO:1013)	WGQGTTLTVSS (SEQ ID NO:1031)
IH7	ZVQLVESGGGLVQ PKGSLKLSCAASG (SEQ ID NO:982)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTCSRDDSENM FYLQLSSLKTEDTAIYYC (SEQ ID NO:1014)	WGTGTTVTVSS (SEQ ID NO:1033)
2HS	EVQLVESGGGLVQPK GSLKLSCAASG (SEQ ID NO:980)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTCSRDDSENM FYLQLSSLKTEDTAMYY C (SEQ ID NO:1015)	WGTGTTVTVSS (SEQ ID NO:1033)
3A2	QVQLQQSGAELVKPG ASVKMSCKTSG (SEQ ID NO:983)	WVKQRPGQGLVW (SEQ ID NO:1001)	EKFKTKATLT VDTS SS TAYMHLS SLTSEDSAV YFC (SEQ ID NO:1016)	WGQGTLVTVST (SEQ ID NO:1034)
3A7	EVKLEESGGGLVQPG GSMKLSCAASG (SEQ ID NO:979)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSKST VYLQMNTLRADDTGI YYC (SEQ ID NO:1011)	WGQGTTLTVSS (SEQ ID NO:1031)
3B10	EVQLVZZGRGZSQ GKGSXZZGRAZRC (SEQ ID NO:984)	GVPQGPGKGREW (SEQ ID NO:1002)	DSVKDRFTZSRDDSES LFYZQMSZZKZEDTA MYYZ (SEQ ID NO:1017)	WGQGTIVTVS (SEQ ID NO:1035)
4F11	QVQLQQSGAELVKPG ASVKMSCKTSG (SEQ ID NO:983)	WVKQRPGQGLVW (SEQ ID NO:1001)	EKFKTKATLT VDTS SS TAYMHLS SLTSEDSAV YFC (SEQ ID NO:1016)	WGQGTLVTVST (SEQ ID NO:1034)
6H6	EVKLEESGGGLVQPG GSMKLSCTASG (SEQ ID NO:985)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSKST VYLQMNSLRTEDTGIY YC (SEQ ID NO:1018)	WGQGTLVTVSA (SEQ ID NO:1029)
7A9	LSCAASG (SEQ ID NO:986)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTISRDDSES MLYLQMZNLKTEDTA MYYC (SEQ ID NO:1019)	WGQGTLVTVSA (SEQ ID NO:1029)
7B3	QVQLQQSGAVLV] PGASVKLSCKASG (SEQ ID NO:987)	WVKQRPGRGPEW (SEQ ID NO:1003)	EKFRNKAILTVDKPSSTA YMQLNSLTSEDZAVYYC (SEQ ID NO:1020)	WGQGTTLTVSS (SEQ ID NO:1031)

8A1	EVQLQQSGAELVK PGASVKISCKASG (SEQ ID NO:988)	WVKQRPGKGLEW (SEQ ID NO:1004)	GKFEGKATLT ADKS SS TAYMQLS SLTSEDSAV YFC (SEQ ID NO:1021)	WGQGTLVTVSA (SEQ ID NO:1029)
9F5	QVQLQQSGPELVK PGASLKISCKASG (SEQ ID NO:989)	WVKQRPGKGLEW (SEQ ID NO:1004)	GEFRVRATLTADTSST TAYMQLS SLTSEDSAV YFC (SEQ ID NO:1022)	WGQGASVTVSS (SEQ ID NO:1036)
9G1	QVQLQQSGAELVI C PGASVKLSCKASG (SEQ ID NO:981)	WVKQRPGRGPEW (SEQ ID NO:1003)	EKFKTKATLTVDKPSS TADMQLSSLTSEDSAV YYC (SEQ ID NO:1023)	WGQGTTLTVSS (SEQ ID NO:1031)
9G3	EVQLVESGGGLVC) PKGSLKLSCAAFG (SEQ ID NO:990)	WVRQTPGKGLEW (SEQ ID NO:1005)	DSVKDRFTISRDDSESI VYVQMNNLKTEDTG MYSC (SEQ ID NO:1024)	WGRGTLV (SEQ ID NO:1037)
10A9	QVQLQQSGAEVVKP GASVKMSCKTSG (SEQ ID NO:991)	WVKQRPGQGLVW (SEQ ID NO:1001)	ERFKTKATLT VDTS SS TAYMHLS SLTSEDSAV YFC (SEQ ID NO:1025)	WGQGTLVTVSA (SEQ ID NO:1029)
11A8	EVQLVESGGRLVQPK GSLKLSCAASG (SEQ ID NO:992)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTISRDDSES MLYLQMNNLKTEDTA MYYC (SEQ ID NO:1026)	WGQGTLVTVSA (SEQ ID NO:1029)
12D9	QVQLQQYGPELVKPG ASVKMSCKVSG (SEQ ID NO:993)	WMKQSHGKSLEW (SEQ ID NO:1006)	QEFKGKATLT VDKS SS TAYMELRS LTFED SAV YZC (SEQ ID NO:1027)	WGQGT (SEQ ID NO:1038)
12F9	WRIGQGKGSLKLARA ARG (SEQ ID NO:994)	RVRQGPGKGREW (SEQ ID NO:1007)	DSVKDRFRASRDDSES MLYVQMSNWKQEDT AMYYG (SEQ ID NO:1028)	WGQGTLVTVS (SEQ ID NO:1029)
iOCi	GVQSEVKFEESGG GLVQPGGSMKLSC TASG (SEQ ID NO:1416)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSKSS VSLQMNSLRTEDTGIY YC (SEQ ID NO:1419)	WGQGTLVTVS (SEQ ID NO:1029)
7E9	QVQLQQSGPELVK PGASVKISCKTSG (SEQ ID NO:1417)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGK ATLTVDRS SS TAYMELRS LTSEDSAV YYC (SEQ ID NO:1420)	WGQGTSVTVS (SEQ ID NO:1030)
SC3	QVQLQQSGPDLVI PGASVKISCKASG (SEQ ID NO:1418)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGK AILTVDKS SS TAYMELRS LTSEDSAV YYC (SEQ ID NO:1421)	WGQGTTLTVSS (SEQ ID NO:1031)
1B4	EVQLVESGGGLVKPG GSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNF LYLQMSSLRSEDTAMYY C (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
6H2	QVQLQESGPGLVC PSQSLSIICTV (SEC ID NO:1540)	WIRQSPGKGLEW (SEQ ID NO:1541)	AAFISRLNISKDNSK SQ VFFKMNSLQSDDTA IY YC (SEQ ID NO:1543)	WGQGTLVTVSA (SEQ ID NO:1029)
7B11v1	EVQLVESGGGLVKPG GSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNF LYLQMSSLRSEDTAMYY C (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
7B11v2	EVQZQQSGPELVK GASVKISCKA (SEQ ID NO:1605)	WVKQSLGKSLEW (SEQ ID NO:1613)	QKFKGKATLTVDKSSST AYMELRSLTXEESAVYY C (SEQ ID NO:1618)	RGTGTTVTV (SEQ ID NO:1626)
18D8	EVQLVESGGGLVKPG GSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNF LYLQMSSLRSEDTAMYY C (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)

18E4v1	EVQLVESGGGLVKPGGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNFLYLQMSSLRSEDTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
18E4v2	QVQLQQPGAELVICPGASVKVSCKA (SEQ ID NO:1606)	WVKEKPGQGLEW (SEQ ID NO:1614)	HNFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYC (SEQ ID NO:1619)	WGQGTSVTVSS (SEQ ID NO:1030)
29F6v1	EVQLVESGGGLVKPGGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNFLYLQMSSLRSEDTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
29F6v2	QVQLQQSVAELVIPGASVKLSCTA (SEQ ID NO:1607)	WVKQRPEQGLEW (SEQ ID NO:1615)	PKFQATATIT VATS SNSAYLQLSSLASEDTAIYYC (SEQ ID NO:1620)	WGHGTSVTVSS (SEQ ID NO:1627)
40D5v1	EVQLVESGGGLVKPGGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNFLYLQMSSLRSEDTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
40D5v2	QVQLQQSGAELVICPGASVKVSCKA (SEQ ID NO:1608)	WVKQRPGQGLEW (SEQ ID NO:1616)	QKFKGKATLTVDKSSSTAYMQILSSLTSEDSAVYYC (SEQ ID NO:1621)	WSQGTLVTVS (SEQ ID NO:1628)
43B9	EVQLVESGGGLVKPGGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNFLYLQMSSLRSEDTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
44A8	EVQLVESGGGLVKPGGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNFLYLQMSSLRSEDTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
44B4v1	EVQLVESGGGLVKPGGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNAKNFLYLQMSSLRSEDTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
44B4v2	XXXXXQSGTELAIPGASVKMPCKA (SEQ ID NO:1609)	WVKQRPGQGLEW (SEQ ID NO:1616)	QKFKDKATLTADKSSSTAYMQLSSLTSEESAVYYC (SEQ ID NO:1622)	WGTGTTVTVSS (SEQ ID NO:1033)
45D6	QVQLQQSGRELVICPGASVKMSCMSSG (SEQ ID NO:1610)	WVIQSHGESLEW (SEQ ID NO:1617)	QKFKGKATLTVNKS SSTAYMELRSLTSEDSAVYYC (SEQ ID NO:1623)	WGQGTSVTVSS (SEQ ID NO:1030)
29F7	QVKLEESGGGLVCPGGSMKLSCVASG (SEQ ID NO:1611)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSKSSVYLQMNNLRAVDTGIYYC (SEQ ID NO:1624)	WGQGTTLTVSS (SEQ ID NO:1031)
32G1	QVQLQQSGPELVGPGASVQMSCEASG (SEQ ID NO:1612)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGKATLTVNKS SSTAYIELRSLTSEDSAVYHC (SEQ ID NO:1625)	WGQGTLVTVSA (SEQ ID NO:1029)

Table 7G: Humanized light chain variable region sequences

Antibody variant	Humanized sequences
Antibody 4D11	Antibody 4D11
4D11V3-15	EIVMTQSPATLSCSPGLRATLSCRASENIYSFLAWYQQKPGQAPRLLIYNSKTFAEGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1040)

4D11V1-9	DIQLTQSPSFLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTFAEGVPS RFSGSGSGTEFTLTISSLQPEDFATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1041)
4D11V3-11	EIVLTQSPATLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIYNSKTFA EGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1042)
4D11V1-5	DIQMTQSPSTLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTF AEGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1043)
4D11V1-39	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTF AEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1044)
4D11V1-33	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTF AEGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1045)
4D11V3-20	EIVLTQSPGTLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIYNSKTFA EGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1046)
4D11V2-28	DIVMTQSPLSLPVTPGEPASISCRASENIYSFLAWYLQKPGQSPQLLIYNSKTFA EGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1047)
4D11V2-30	DVVMTQSPLSLPVTLGQPASISCRASENIYSFLAWFQQRPGQSPRRLIYNSKTF AEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1048)
4D11V4-1	DIVMTQSPDSLAVSLGERATINCRASENIYSFLAWYQQKPGQPPKLLIYNSKTF AEGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1049)
Antibody 7C5	Antibody 7C5
7C5V3-15	EIVMTQSPATLSVSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIYNSKTF AEGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1040)
7C5V1-9	DIQLTQSPSFLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTF AEGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1041)
7C5V3-11	EIVLTQSPATLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIYNSKTFA EGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1042)
7C5V1-5	DIQMTQSPSTLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTF AEGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1043)
7C5V1-39	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTF AEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1044)
7C5V1-33	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLIYNSKTF AEGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1045)
7C5V3-20	EIVLTQSPGTLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIYNSKTFA EGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1046)
7C5V2-28	DIVMTQSPLSLPVTPGEPASISCRASENIYSFLAWYLQKPGQSPQLLIYNSKTFA EGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1047)
7C5V2-30	DVVMTQSPLSLPVTLGQPASISCRASENIYSFLAWFQQRPGQSPRRLIYNSKTF AEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1048)

7C5V4-1	DIVMTQSPDSLAVSLGERATINCRASENIYSFLAWYQQKPGQPPKLLIYNSKTF AEGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHHYGTPPWTFGQGTKVEIK (SEQ ID NO: 1049)
Antibody 6G12	Antibody 6G12
6G12V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNCLAWYQQKPGQPPKLL IYWAFTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1051)
6G12V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSNQKNCLAWFQQRPGQSPRRLI YWAFTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1052)
6G12V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSNQKNCLAWYLQKPGQSPQLLI YWAFTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1053)
6G12V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLLI YWAFTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1054)
6G12V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLL IYWAFTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1055)
6G12V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPGQAPRLLI YWAFTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1056)
6G12V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLLI YWAFTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1057)
6G12V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLLI YWAFTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1058)
6G12V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPGQAPRLLI YWAFTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1059)
6G12V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPGQAPRLLI YWAFTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1060)
Antibody 8F11	Antibody 8F11
8F11V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTFLSWFQQRPGQSPRRLIY LVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1062)
8F11V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSNGKTFLSWYLQKPGQSPQLLIYL VSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1063)
8F11V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSNGKTFLSWYQQKPGQPPKLLIY LVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1064)
8F11V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1065)
8F11V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1066)
8F11V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1067)
8F11V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1068)

8F11V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIY LVSKLDSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1069)
8F11V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIY LVSKLDSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1070)
8F11V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIY LVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1071)
Antibody 8E10	Antibody 8E10
8E10V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNWFQQRPGQSPRRLIY LVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1073)
8E10V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLDSDGKTYLNWYLQKPGQSPQLLIY LVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1074)
8E10V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLDSDGKTYLNWYQQKPGQPPKLLI YLVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1075)
8E10V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1076)
8E10V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLI YLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1077)
8E10V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLI YLVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1078)
8E10V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLI YLVSKLDSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1079)
8E10V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSDGKTYLNWYQQKPGQAPRLLIY LVSKLDSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1080)
8E10V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLDSDGKTYLNWYQQKPGQAPRLLI YLVSKLDSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1081)
8E10V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLDSDGKTYLNWYQQKPGQAPRLLIY LVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO: 1082)
Antibody 7E5	Antibody 7E5
7E5V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTFLSWFQQRPGQSPRRLIY LVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1062)
7E5V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSNGKTFLSWYLQKPGQSPQLLIYL VSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1063)
7E5V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSNGKTFLSWYQQKPGQPPKLLIY LVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1064)
7E5V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1065)
7E5V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1066)

7E5V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1067)
7E5V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIYLVSKLD SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1068)
7E5V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIYLVSKLD SGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO : 1069)
7E5V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIYLVSKLD SGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCMQGTHFPLTFGQGTK EIK (SEQ ID NO : 1070)
7E5V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIY LVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1071)
Antibody 7F8	Antibody 7F8
7F8V3-11	EIVLTQSPATLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILAS GIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1084)
7F8V1-39	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILA SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1085)
7F8V1-5	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILA SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1086)
7F8V3-15	EIVMTQSPATLSVSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILA SGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1087)
7F8V1-9	DIQLTQSPSFLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILAS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1088)
7F8V1-33	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILA SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1089)
7F8V3-20	EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1090)
7F8V2-28	DIVMTQSPLSLPVTPGEPASISCSASSSVSYMYWYLQKPGQSPQLLIYLTSILAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1091)
7F8V2-30	DVVMTQSPLSLPVTLGQPASISCSASSSVSYMYWFQQRPGQSPRRLIYLTSILAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1092)
7F8V4-1	DIVMTQSPDSLAVSLGERATINCSASSSVSYMYWYQQKPGQPPKLLIYLTSILA SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO : 1093)
Antibody 8F8	Antibody 8F8
8F8V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGNTYLHWFQQRPGQSPRRLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO : 1095)
8F8V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO : 1096)
8F8V4-1	DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGNTYLHWYQQKPGQPPKLLIYKVSNRF SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO : 1097)

8F8V3-11	EIVLTQSPATLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQAPRLLIYKVSNRF SGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQSTHVPLTFGQGTKV EIK (SEQ ID NO : 1098)
8F8V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNR FSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO : 1099)
8F8V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO : 1100)
8F8V3-15	EIVMTQSPATLSVSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQAPRLLIYKVSNRFS GIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO: 1101)
8F8V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNR FSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO: 1102)
8F8V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO: 1103)
8F8V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQAPRLLIYKVSNRFS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQSTHVPLTFGQGTKVEIK (SEQ ID NO: 1104)
Antibody1H7	Antibody1H7
1H7V1-39	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILASGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1085)
1H7V3-11	EIVLTQSPATLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILASGIPARFSG SGSGTDFTLTISSLEPEDFAVYYCQQWSFNPYTFGQGTKVEIK(SEQ ID NO: 1084)
1H7V1-5	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILA SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1086)
1H7V1-9	DIQLTQSPSFLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILASGVPSRFS GSGSGTEFTLTISSLQPEDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1088)
1H7V3-15	EIVMTQSPATLSVSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILASGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1087)
1H7V1-33	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILASGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1089)
1H7V3-20	EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILASGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1090)
1H7V2-28	DIVMTQSPLSLPVTPGEPASISCSASSSVSYMYWYLQKPGQSPQLLIYLTSILASGVPDRF SGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1091)
1H7V2-30	DVVMTQSPLSLPVTLGQPASISCSASSSVSYMYWFQQRPGQSPRRLIYLTSILASGVPDRF SGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1092)
1H7V4-1	DIVMTQSPDSLAVSLGERATINCSASSSVSYMYWYQQKPGQPPKLLIYLTSILASGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1093)
Antibody 2H8	Antibody 2H8
2H8V3-11	EIVLTQSPATLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILASGIPARFSG SGSGTDFTLTISSLEPEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1084)
2H8V1-39	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILA SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1085)

2H8V1-5	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILA SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1086)
2H8V3-15	EIVMTQSPATLSVSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILA SGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1087)
2H8V1-9	DIQLTQSPSFLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILASGVPSRFS GSGSGTEFTLTISSLQPEDFATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1088)
2H8V1-33	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYLTSILA SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1089)
2H8V3-20	EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLTSILASGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1090)
2H8V2-28	DIVMTQSPLSLPVTPGEPASISCSASSSVSYMYWYLQKPGQSPQLLIYLTSILAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1091)
2H8V2-30	DVVMTQSPLSLPVTLGQPASISCSASSSVSYMYWFQQRPGQSPRRLIYLTSILAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1092)
2H8V4-1	DIVMTQSPDSLAVSLGERATINCSASSSVSYMYWYQQKPGQPPKLLIYLTSILA SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQWSFNPYTFGQGTKVEIK (SEQ ID NO: 1093)
Antibody 3A2	Antibody 3A2
3A2 V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQTIIHSNGNTYLEWFQQRPGQSPRRLIYKVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1108)
3A2 V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQTIIHSNGNTYLEWYLQKPGQSPQLLIYK VSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1109)
3A2 V4-1	DIVMTQSPDSLAVSLGERATINCRSSQTIIHSNGNTYLEWYQQKPGQPPKLLIYKVSNRF SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1110)
3A2 V3-11	EIVLTQSPATLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYK VSNRFSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1111)
3A2 I-9	DIQLTQSPSFLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRFS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1112)
3A2 I-33	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1113)
3A2 VI -39	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1114)
3A2 V3-15	EIVMTQSPATLSVSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYKVSNRF SGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1115)
3A2 VI -5	DIQMTQSPSTLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1116)
3A2 V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYK VSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCFQGSHVPYTFGQGTKV EIK (SEQ ID NO: 1117)
Antibody 3A7	Antibody 3A7

3A7 V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTFLSWFQQRPGQSPRRLIY LVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1062)
3A7 V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSNGKTFLSWYLQKPGQSPQLLIYL VSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1063)
3A7 V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSNGKTFLSWYQQKPGQPPKLLIY LVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1064)
3A7 VI -39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1067)
3A7 I-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1066)
3A7 I-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIY LVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1065)
3A7 VI -33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKAPKLLIYLVSKLD SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1068)
3A7 V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIYLVSKLD SGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1069)
3A7 V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIYLVSKLD SGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1070)
3A7 V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQAPRLLIY LVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCMQGTHFPLTFGQGTKVEIK (SEQ ID NO: 1071)
Antibody 3B10	Antibody 3B10
3B10V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSDQKNYLAWYQQKPGQPPKLLIYWAST RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1120)
3B10V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSDQKNYLAWYLQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1121)
3B10V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSDQKNYLAWFQQRPGQSPRRLIYWASTR ESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1122)
3B10V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1123)
3B10V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLIYWASTR ESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1124)
3B10V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPGQAPRLLI YWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1125)
3B10V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLIYWASTR ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1126)
3B10V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPGQAPRLLIYWAST RESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1127)

3B10V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1128)
3B10V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPGQAPRLLIYWAST RESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1129)
Antibody 4F11	Antibody 4F11
4F11V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQTIIHSNGNTYLEWFQQRPGQSPRRLIYKVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1108)
4F11V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQTIIHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1109)
4F11V4-1	DIVMTQSPDSLAVSLGERATINCRSSQTIIHSNGNTYLEWYQQKPGQPPKLLIYKVSNRFSG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1110)
4F11V3-11	EIVLTQSPATLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYKVSNRFS GIPARFSGSGSGTDFTLTISSLEPEDFAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1111)
4F11V3-15	EIVMTQSPATLSVSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYKVSNRF SGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1115)
4F11V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1113)
4F11V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1114)
4F11V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1112)
4F11V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1116)
4F11V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYK VSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCFQGSHVPYTFGQGTKV EIK (SEQ ID NO: 1117)
Antibody 6H6	Antibody 6H6
6H6V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSVFYSSNQKNYLAWYQQKPGQPPKLL IYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1500)
6H6V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSVFYSSNQKNYLAWYLQKPGQSPQLLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1501)
6H6V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSVFYSSNQKNYLAWFQQRPGQSPRRLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1502)
6H6V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLL IYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1503)
6H6V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1504)
6H6V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPGQAPRLLI YWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1505)

6H6V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1506)
6H6V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPGQAPRLLI YWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1507)
6H6V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1508)
6H6V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPGQAPRLLI YWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1509)
Antibody 7A9	Antibody 7A9
7A9V1-9	DIQLTQSPSFLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLIYKAKTL AEGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1132)
7A9V3-11	EIVLTQSPATLSLSPGERATLSCRASENIYSYLAWYQQKPGQAPRLLIYKAKTLAEGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1133)
7A9V1-5	DIQMTQSPSTLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLIYKAKT LAEGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1134)
7A9V3-15	EIVMTQSPATLSVSPGERATLSCRASENIYSYLAWYQQKPGQAPRLLIYKAKTLAEGIPA RFSGSGSGTEFTLTISSLQSEDFAVYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1135)
7A9V1-39	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLIYKAKTLAEGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1136)
7A9V1-33	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLIYKAKTLAEGVPS RFSGSGSGTDFTFTISSLQPEDIATYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1137)
7A9V3-20	EIVLTQSPGTLSLSPGERATLSCRASENIYSYLAWYQQKPGQAPRLLIYKAKTLAEGIPD RFSGSGSGTDFTLTISRLEPEDFAVYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1138)
7A9V2-28	DIVMTQSPLSLPVTPGEPASISCRASENIYSYLAWYLQKPGQSPQLLIYKAKTLAEGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1139)
7A9V4-1	DIVMTQSPDSLAVSLGERATINCRASENIYSYLAWYQQKPGQPPKLLIYKAKTLAEGVP DRFSGSGSGTDFTLTISSLQAEDVAVYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1140)
7A9V2-30	DVVMTQSPLSLPVTLGQPASISCRASENIYSYLAWFQQRPGQSPRRLIYKAKTL AEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPFTFGQGTKVEIK (SEQ ID NO: 1141)
Antibody 8A1	Antibody 8A1
8A1V3-15	EIVMTQSPATLSVSPGERATLSCRTSENVYSNLAWYQQKPGQAPRLLIYAATN LADGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1143)
8A1V3-11	EIVLTQSPATLSLSPGERATLSCRTSENVYSNLAWYQQKPGQAPRLLIYAATNL ADGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1144)
8A1V1-9	DIQLTQSPSFLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLLIYAATNL ADGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1145)
8A1V1-5	DIQMTQSPSTLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLLIYAATN LADGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1146)

8A1V1-39	DIQMTQSPSSLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLLIYAATN LADGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1147)
8A1V1-33	DIQMTQSPSSLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLLIYAATN LADGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1148)
8A1V3-20	EIVLTQSPGTLSLSPGERATLSCRTSENVYSNLAWYQQKPGQAPRLLIYAATNL ADGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1149)
8A1V2-28	DIVMTQSPLSLPVTPGEPASISCRTSENVYSNLAWYLQKPGQSPQLLIYAATNL ADGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1150)
8A1V2-30	DVVMTQSPLSLPVTLGQPASISCRTSENVYSNLAWFQQRPGQSPRRLIYAATNL ADGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1151)
8A1V4-1	DIVMTQSPDSLAVSLGERATINCRTSENVYSNLAWYQQKPGQPPKLLIYAATN LADGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHHFWGTPYTFGQGTKVEIK (SEQ ID NO: 1152)
Antibody 9F5	Antibody 9F5
9F5V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGYTYLHWFQQRPGQSPRRLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1154)
9F5V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGYTYLHWYLQKPGQSPQLLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1155)
9F5V4-1	DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGYTYLHWYQQKPGQPPKLLIYKVSNRF SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1156)
9F5V3-11	EIVLTQSPATLSLSPGERATLSCRSSQSLVHSNGYTYLHWYQQKPGQAPRLLIYKVSNRF SGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQSTRVPYTFGQGTKV EIK (SEQ ID NO: 1157)
9F5V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1158)
9F5V3-15	EIVMTQSPATLSVSPGERATLSCRSSQSLVHSNGYTYLHWYQQKPGQAPRLLIYKVSNRF SGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1159)
9F5V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPGKAPKLLIYKVSNR FSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1160)
9F5V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPGKAPKLLIYKVSNR FSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1161)
9F5V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1162)
9F5V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQSLVHSNGYTYLHWYQQKPGQAPRLLIYKVSNRF SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQSTRVPYTFGQGTKVEIK (SEQ ID NO: 1163)
9F5-L1	DIVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYLQKPGQSPQLLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO: 1663)
9F5-L2	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYLQKPGQSPQLLIYKVSNR FSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTRVPYTFGQG TKLEIK (SEQ ID NO: 1664)
Antibody 9G1	Antibody 9G1

9G1V2-30	DVVMTQSPLSLPVTLGQPASISCRFSQSLVHSNGNTYLHWFQQRPGQSPRRLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1165)
9G1V2-28	DIVMTQSPLSLPVTPGEPASISCRFSQSLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNRFSGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1166)
9G1V4-1	DIVMTQSPDSLAVSLGERATINCRFSQSLVHSNGNTYLHWYQQKPGQPPKLLI YKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1167)
9G1V3-11	EIVLTQSPATLSLSPGERATLSCRFSQSLVHSNGNTYLHWYQQKPGQAPRLLIYKVSNRF SGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQSTRVPPTFGQGTKV EIK (SEQ ID NO: 1168)
9G1V3-15	EIVMTQSPATLSVSPGERATLSCRFSQSLVHSNGNTYLHWYQQKPGQAPRLLI YKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1169)
9G1V1-9	DIQLTQSPSFLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1170)
9G1V1-5	DIQMTQSPSTLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1171)
9G1V1-39	DIQMTQSPSSLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGKAPKLLI YKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1172)
9G1V1-33	DIQMTQSPSSLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGKAPKLLI YKVSNRFSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQSTRVPPTFGQGTKVEIK (SEQ ID NO: 1173)
9G1V3-20	EIVLTQSPGTLSLSPGERATLSCRFSQSLVHSNGNTYLHWYQQKPGQAPRLLIYKVSNRF SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQSTRVPPTFGQGTKV EIK (SEQ ID NO: 1174)
Antibody 9G3	Antibody 9G3
9G3V1-33	DIQMTQSPSSLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIYFTSNLPSGVPSRF SGSGSGTDFTFTISSLQPEDIATYYCSGEVTQFTFGQGTKVEIK(SEQ ID NO: 1176)
9G3V1-9	DIQLTQSPSFLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIYFTSNLPSGVPSR FSGSGSGTEFTLTISSLQPEDFATYYCSGEVTQFTFGQGTKVEIK(SEQ ID NO: 1177)
9G3V1-39	DIQMTQSPSSLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIYFTSNL PSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 1178)
9G3V3-11	EIVLTQSPATLSLSPGERATLSCKASSNVNYMSWYQQKPGQAPRLLIYFTSNLPSGIPARFS GSGSGTDFTLTISSLEPEDFAVYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 821)
9G3V1-5	DIQMTQSPSTLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIYFTSNL PSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 1179)
9G3V3-15	EIVMTQSPATLSVSPGERATLSCKASSNVNYMSWYQQKPGQAPRLLIYFTSNLPSGIPARF SGSGSGTEFTLTISSLQSEDFAVYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 1180)
9G3V3-20	EIVLTQSPGTLSLSPGERATLSCKASSNVNYMSWYQQKPGQAPRLLIYFTSNLP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 1181)
9G3V2-28	DIVMTQSPLSLPVTPGEPASISCKASSNVNYMSWYLQKPGQSPQLLIYFTSNLPSGVPDRF SGSGSGTDFTLKISRVEAEDVGVYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 1182)
9G3V2-30	DVVMTQSPLSLPVTLGQPASISCKASSNVNYMSWFQQRPGQSPRRLIYFTSNLPSGVPDRFS GSGSGTDFTLKISRVEAEDVGVYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 1183)

9G3V4-1	DIVMTQSPDSLAVSLGERATINCKASSNVNYMSWYQQKPGQPPKLLIYFTSNLPSGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCSGEVTQFTFGQGTKVEIK (SEQ ID NO: 1184)
Antibody10A9	Antibody10A9
10A9V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQTIIHSNGNTYLEWFQQRPGQSPRRLIYKVSNRFCGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1186)
10A9V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQTIIHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFC GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1187)
10A9V4-1	DIVMTQSPDSLAVSLGERATINCRSSQTIIHSNGNTYLEWYQQKPGQPPKLLIYKVSNRF CGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1188)
10A9V3-11	EIVLTQSPATLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYK VSNRFCGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCFQGSHVPYTFGQGTKV EIK (SEQ ID NO: 1189)
10A9V3-15	EIVMTQSPATLSVSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYKVSNRF CGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1190)
10A9V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSN RFCGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1191)
10A9V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAPRLLIYK VSNRFCGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCFQGSHVPYTFGQGTKV EIK (SEQ ID NO: 1192)
10A9V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF CGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1193)
10A9V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRF CGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1194)
10A9V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKAPKLLIYKVSNRFC GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGSHVPYTFGQGTKVEIK (SEQ ID NO: 1195)
Antibody11A8	Antibody11A8
11A8V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKKYLTWYQQKPGQPPKLL IYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDYGFPLTFGQ GTKVEIK (SEQ ID NO: 1197)
11A8V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLNSGNQKKYLTWFQQRPGQSPRRLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1198)
11A8V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLNSGNQKKYLTWYLQKPGQSPQLLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQNDYGFPLTFGQ GTKVEIK (SEQ ID NO: 1199)
11A8V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPGKAPKLL IYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1200)
11A8V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLNSGNQKKYLTWYQQKPGQAPRLLI YWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1201)
11A8V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLNSGNQKKYLTWYQQKPGQAPRLL IYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1202)
11A8V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPGKAPKLL IYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1203)

11A8V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLNSGNQKKYLTWYQQKPGQAPRLLI YWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1204)
11A8V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1205)
11A8V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPGKAPKLL IYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQNDYGFPLTFGQGTKVEIK (SEQ ID NO: 1206)
Antibody12D9	Antibody12D9
12D9V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSGNQKNFLAWYQQKPGQPPKLL IYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPFTFGQ GTKVEIK (SEQ ID NO: 1208)
12D9V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSGNQKNFLAWYLQKPGQSPQLLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1209)
12D9V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSGNQKNFLAWFQQRPGQSPRRLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1210)
12D9V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1211)
12D9V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1212)
12D9V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSGNQKNFLAWYQQKPGQAPRLLIYWAST RESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1213)
12D9V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1214)
12D9V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSGNQKNFLAWYQQKPGQAPRLLIYWASTR ESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1215)
12D9V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1216)
12D9V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSGNQKNFLAWYQQKPGQAPRLLIYWASTR ESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYYSYPFTFGQGTKVEIK (SEQ ID NO: 1217)
Antibody12F9	Antibody12F9
12F9V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSDQKNYLAWYQQKPGQPPKLLIYWAST RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1120)
12F9V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSDQKNYLAWYLQKPGQSPQLLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1121)
12F9V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSDQKNYLAWFQQRPGQSPRRLI YWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1122)
12F9V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPGQAPRLLIYWASTR ESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1125)
12F9V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1123)

12F9V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1124)
12F9V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLIYWASTR ESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1128)
12F9V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPGQAPRLLIYWASTR ESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1127)
12F9V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPGKAPKLLIYWASTR ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1126)
12F9V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPGQAPRLLIYWASTR ESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1129)
Antibody10C1	Antibody10C1
10C1V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSVFYSSNQKNYLAWYQQKPGQPPKLLIYWAST RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1423)
10C1V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSVFYSSNQKNYLAWFQQRPGQSPRRLIYWASTR ESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1424)
10C1V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSVFYSSNQKNYLAWYLQKPGQSPQLLIYWASTR ESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1425)
lOC1V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1426)
10C1V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPGQAPRLLIYWASTR ESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1427)
lOC1V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLLIYWAST RESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1428)
10C1V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPGQAPRLLIYWASTR ESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1429)
lOC1V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLLIYWASTR ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1430)
lOC1V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPGKAPKLLIYWASTR ESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1431)
10C1V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPGQAPRLLIYWASTR ESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCHQYLSSLTFGQGTKVEIK (SEQ ID NO: 1432)
Antibody 7E9	Antibody 7E9
7E9V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNCLAWYQQKPGQPPKLLIYWAST RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1434)
7E9V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSNQKNCLAWYLQKPGQSPQLLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1435)
7E9V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSNQKNCLAWFQQRPGQSPRRLIYWAST RESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYYSYPLTFGQ GTKVEIK (SEQ ID NO: 1436)

7E9V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLLIYWASTR ESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1437)
7E9V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPGQAPRLLIYWASTR ESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1438)
7E9V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLL IYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1439)
7E9V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1440)
7E9V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPGKAPKLLI YWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1441)
7E9V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPGQAPRLLI YWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1442)
7E9V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPGQAPRLLI YWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYYSYPLTFGQGTKVEIK (SEQ ID NO: 1443)
Antibody 8C3	Antibody 8C3
8C3V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGNTYLHWFQQRPGQSPRRLIYKVSNRF SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1445)
8C3V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNRFSG VPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1446)
8C3V4-1	DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGNTYLHWYQQKPGQPPKLLIYKVSNR FSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1447)
8C3V3-11	EIVLTQSPATLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQAPRLLIYKVSNRF SGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1448)
8C3V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNR FSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1449)
8C3V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1450)
8C3V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNR FSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1451)
8C3V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKLLIYKVSNRF SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1452)
8C3V3-15	EIVMTQSPATLSVSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQAPRLLI YKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1453)
8C3V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQAPRLLIYKVSNRF SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQSTHVPPTFGQGTKVEIK (SEQ ID NO: 1454)

Table 7H: Humanized heavy chain variable region sequences

Antibody variant	Humanized sequences

Antibody 4D11	Antibody 4D11
4D11V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEWVASISR GGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1220)
4D11V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASIS RGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1221)
4D11V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASIS RGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1222)
4D11V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASIS RGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1222)
4D11V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASI SRGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGYGYY RTPFANWGQGTLVTVSS (SEQ ID NO:1223)
4D11V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTLSSYAMSWVRQAPGQGLEWVASI SRGGSTYYPQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1224)
4D11V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTLSSYAMSWVRQAPGQGLEWVASI SRGGSTYYPQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCTRGYGYY RTPFANWGQGTLVTVSS (SEQ ID NO:1225)
4D11V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTLSSYAMSWVRQMPGKGLEWVASIS RGGSTYYPPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1226)
4D11V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEWVASISR GGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1227)
4D11V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTLSSYAMSWIRQPPGKGLEWVASISR GGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1228)
Antibody 7C5	Antibody 7C5
7C5V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEWVASISR GGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1220)
7C5V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASIS RGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1221)
7C5V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASIS RGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1222)
7C5V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASIS RGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1222)
7C5V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTLSSYAMSWVRQAPGKGLEWVASI SRGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGYGYY RTPFANWGQGTLVTVSS (SEQ ID NO:1223)
7C5V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTLSSYAMSWVRQAPGQGLEWVASI SRGGSTYYPQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1224)
7C5V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTLSSYAMSWVRQAPGQGLEWVASI SRGGSTYYPQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCTRGYGYY RTPFANWGQGTLVTVSS (SEQ ID NO:1225)
7C5V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTLSSYAMSWVRQMPGKGLEWVASIS RGGSTYYPPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGYGYYR TPFANWGQGTLVTVSS (SEQ ID NO:1226)

7C5V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEWVASISR GGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1227)
7C5V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTLSSYAMSWIRQPPGKGLEWVASISR GGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1228)
Antibody 6G12	Antibody 6G12
6G12V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTMHWVRQAPGQGLEWIGG INPNNGGTSYSQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGS HYYAMDYWGQGTLVTVSS (SEQ ID NO:1230)
6G12V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTEYTMHWVRQMPGKGLEWIGGI NPNNGGTSYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGGSHY YAMDYWGQGTLVTVSS (SEQ ID NO:1231)
6G12V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTEYTMHWVRQAPGQGLEWIGG INPNNGGTSYSQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1232)
6G12V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1233)
6G12V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1234)
6G12V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1235)
6G12V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1235)
6G12V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEWIGGIN PNNGGTSYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGSHYYAMDYW GQGTLVTVSS (SEQ ID NO:1236)
6G12V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYSAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1237)
6G12V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEWIGGIN PNNGGTSYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGSHYY AMDYWGQGTLVTVSS (SEQ ID NO:1238)
Antibody 8E10	Antibody 8E10
8E10V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGLEWIGV IDPETGGTAYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1240)
8E10V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTDYEMHWVRQMPGKGLEWIGVI DPETGGTAYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTSPDYYG SSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1241)
8E10V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIGVI DPETGGTAYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1242)
8E10V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIGVI DPETGGTAYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1243)
8E10V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYEMHWVRQAPGQGLEWIGV IDPETGGTAYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1244)

8E10V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIGVI DPETGGTAYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1245)
8E10V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIGVI DPETGGTAYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1245)
8E10V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTDYEMHWIRQPPGKGLEWIGVID PETGGTAYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTSPDYYGSS YPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1246)
8E10V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIGVI DPETGGTAYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1247)
8E10V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYTFTDYEMHWIRQPPGKGLEWIGVID PETGGTAYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTSPDYYGSS YPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1248)
Antibody 7E5	Antibody 7E5
7E5V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1250)
7E5V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1251)
7E5V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1252)
7E5V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1251)
7E5V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1253)
7E5V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMGWVRQAPGQGLEWVA EIRDKVKNHATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1254)
7E5V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMGWVRQAPGQGLEWVAEIRDKVKNHA TYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCRL GVFDYWGQGTLVTVSS (SEQ ID NO:1255)
7E5V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMGWVRQMPGKGLEWVAE IRDKVKNHATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1256)
7E5V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAEIR DKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRLGVFD YWGQGTLVTVSS (SEQ ID NO:1257)
7E5V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAEIR DKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRLGVFD YWGQGTLVTVSS (SEQ ID NO:1258)
Antibody 7F8	Antibody 7F8
7F8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1260)
7F8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)

7F8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1262)
7F8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
7F8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1263)
7F8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFSFNTYAMNWVRQAPGQGLEWIARI RSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1264)
7F8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYAMNWVRQMPGKGLEWIARI RSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1265)
7F8V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFSFNTYAMNWVRQAPGQGLEWIAR IRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1266)
7F8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARIRS KSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHGDGN LWYIDVWGQGTLVTVSS (SEQ ID NO:1267)
7F8V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARIRS KSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHGDGN LWYIDVWGQGTLVTVSS (SEQ ID NO:1268)
Antibody 8F8	Antibody 8F8
8F8V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTVSRYWMHWVRQAPGQGLEWIG RIDPNSGGTKYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVLTG TDFDYWGQGTLVTVSS (SEQ ID NO:1270)
8F8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWIGR IDPNSGGTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1271)
8F8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTVSRYWMHWVRQAPGQGLEWIG RIDPNSGGTKYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1272)
8F8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTVSRYWMHWVRQMPGKGLEWIGR IDPNSGGTKYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVLTGTD FDYWGQGTLVTVSS (SEQ ID NO:1273)
8F8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWIGR IDPNSGGTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1274)
8F8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWIGR IDPNSGGTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1275)
8F8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWIGR IDPNSGGTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1274)
8F8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTVSRYWMHWIRQPPGKGLEWIGRID PNSGGTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVLTGTDFD YWGQGTLVTVSS (SEQ ID NO:1276)
8F8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWIGR IDPNSGGTKYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1277)
8F8V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYTVSRYWMHWIRQPPGKGLEWIGRID PNSGGTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVLTGTDFD YWGQGTLVTVSS (SEQ ID NO:1278)

Antibody 1H7	Antibody 1H7
1H7V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1260)
1H7V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1262)
1H7V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
1H7V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
1H7V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1263)
1H7V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYAMNWVRQMPGKGLEWIARI RSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1265)
1H7V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFSFNTYAMNWVRQAPGQGLEWIARI RSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1264)
1H7V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFSFNTYAMNWVRQAPGQGLEWIAR IRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1266)
1H7V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARIRS KSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHGDGN LWYIDVWGQGTLVTVSS (SEQ ID NO:1267)
1H7V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARIRS KSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHGDGN LWYIDVWGQGTLVTVSS (SEQ ID NO:1268)
Antibody 2H8	Antibody 2H8
2H8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1260)
2H8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
2H8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1262)
2H8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHGDGNLWYIDV WGQGTLVTVSS (SEQ ID NO:1261)
2H8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIARI RSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1263)
2H8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYAMNWVRQMPGKGLEWIARI RSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1265)
2H8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFSFNTYAMNWVRQAPGQGLEWIARI RSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRHG DGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1264)

2H8V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFSFNTYAMNWVRQAPGQGLEWIAR IRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1266)
2H8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARIRS KSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHGDGN LWYIDVWGQGTLVTVSS (SEQ ID NO:1267)
2H8V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARIRS KSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHGDGN LWYIDVWGQGTLVTVSS (SEQ ID NO:1268)
Antibody 3A2	Antibody 3A2
3A2V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYPFSNFWITWVRQMPGKGLEWIGDIY PGSDNSNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAREAYYTN PGFAYWGQGTLVTVSS (SEQ ID NO:1282)
3A2V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYPFSNFWITWVRQAPGQGLEWIGDI YPGSDNSNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1283)
3A2V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYPFSNFWITWVRQAPGQGLEWIGDI YPGSDNSNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1284)
3A2V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1285)
3A2V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDI YPGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1286)
3A2V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1285)
3A2V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1287)
3A2V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIYP GSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYYTNP GFAYWGQGTLVTVSS (SEQ ID NO:1288)
IGHV3-15	EVQLVESGGGLVKPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1289)
3A2V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIYP GSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYYTNP GFAYWGQGTLVTVSS (SEQ ID NO:1290)
Antibody 3A7	Antibody 3A7
3A7V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1250)
3A7V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1251)
3A7V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAEIRDKVKNHAT YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1252)

3A7V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1251)
3A7V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWVAE IRDKVKNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1253)
3A7V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMGWVRQAPGQGLEWVA EIRDKVKNHATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1254)
3A7V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMGWVRQAPGQGLEWVA EIRDKVKNHATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCRL GVFDYWGQGTLVTVSS (SEQ ID NO:1255)
3A7V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMGWVRQMPGKGLEWVAE IRDKVKNHATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCRLG VFDYWGQGTLVTVSS (SEQ ID NO:1256)
3A7V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAEIR DKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRLGVFD YWGQGTLVTVSS (SEQ ID NO:1257)
3A7V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAEIR DKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRLGVFD YWGQGTLVTVSS (SEQ ID NO:1258)
Antibody 3B10	Antibody 3B10
3B10V3-15	EVQLVESGGGLVKPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWESVI RSKSNNFSTLYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRHKS NRYPGVYWGQGTLVTVSS (SEQ ID NO:1292)
3B10V3-30	QVQLVESGGGVVQPGRSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWESVI RSKSNNFSTLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHKS NRYPGVYWGQGTLVTVSS (SEQ ID NO:1293)
3B10V3-23	EVQLLESGGGLVQPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWESVI RSKSNNFSTLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHKS NRYPGVYWGQGTLVTVSS (SEQ ID NO:1294)
3B10V1-46	QVQLVQSGAEVKKPGASVKVSCKASGLTSNTYTQTWVRQAPGQGLEWESVI RSKSNNFSTLYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVRHK SNRYPGVYWGQGTLVTVSS (SEQ ID NO:1295)
3B10V3-48	EVQLVESGGGLVQPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWESVI RSKSNNFSTLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHK SNRYPGVYWGQGTLVTVSS (SEQ ID NO:1296)
3B10V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGLTSNTYTQTWVRQAPGQGLEWESVI RSKSNNFSTLYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRHKS NRYPGVYWGQGTLVTVSS (SEQ ID NO:1297)
3B10V3-7	EVQLVESGGGLVQPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWESVI RSKSNNFSTLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHK SNRYPGVYWGQGTLVTVSS (SEQ ID NO:1296)
3B10V5-51	EVQLVQSGAEVKKPGESLKISCKGSGLTSNTYTQTWVRQMPGKGLEWESVI RSKSNNFSTLYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRHKS NRYPGVYWGQGTLVTVSS (SEQ ID NO:1298)
3B10V4-59	QVQLQESGPGLVKPSETLSLTCTVSGLTSNTYTQTWIRQPPGKGLEWESVIRS KSNNFSTLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHKSNR YPGVYWGQGTLVTVSS (SEQ ID NO:1299)

3B10V4-39	QLQLQESGPGLVKPSETLSLTCTVSGLTSNTYTQTWIRQPPGKGLEWESVIRS KSNNFSTLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHKSNR YPGVYWGQGTLVTVSS (SEQ ID NO:1300)
Antibody 4F11	Antibody 4F11
4F11V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYPFSNFWITWVRQMPGKGLEWIGDIY PGSDNSNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAREAYYTN PGFAYWGQGTLVTVSS (SEQ ID NO:1282)
4F11V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYPFSNFWITWVRQAPGQGLEWIGDI YPGSDNSNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1283)
4F11V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYPFSNFWITWVRQAPGQGLEWIGDI YPGSDNSNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1284)
4F11V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1285)
4F11V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDI YPGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1286)
4F11V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1285)
4F11V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1287)
4F11V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIYP GSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYYTNP GFAYWGQGTLVTVSS (SEQ ID NO:1288)
4F11V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNSNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1289)
4F11V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIYP GSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYYTNP GFAYWGQGTLVTVSS (SEQ ID NO:1290)
Antibody 6H6	Antibody 6H6
6H6V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWWV AEIRNKVNNHATYYAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCCT SLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1302)
6H6V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWWV AEIRNKVNNHATYYDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCCT SLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1303)
6H6V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWWVA EIRNKVNNHATYYDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCCTS LYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1304)
6H6V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWWV AEIRNKVNNHATYYDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCCT SLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1303)
6H6V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWWV AEIRNKVNNHATYYDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCCT SLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1305)

6H6V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMDWVRQAPGQGLEWWV AEIRNKVNNHATYYQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCCT SLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1306)
6H6V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMDWVRQAPGQGLEWWV AEIRNKVNNHATYYQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCCTS LYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1307)
6H6V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMDWVRQMPGKGLEWWVA EIRNKVNNHATYYPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCCTSL YDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1308)
6H6V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMDWIRQPPGKGLEWWVAE IRNKVNNHATYYPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCCTSLY DGYYLRFAWGQGTLVTVSS (SEQ ID NO:1309)
6H6V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMDWIRQPPGKGLEWWVAEI RNKVNNHATYYPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCCTSLYD GYYLRFAWGQGTLVTVSS (SEQ ID NO:1310)
Antibody7A9	Antibody 7A
7A9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVAHI KTKZNNFATFYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVZHZ SNNYPFAYWGQGTLVTVSS (SEQ ID NO:1312)
7A9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVAHI KTKZNNFATFYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVZHZ SNNYPFAYWGQGTLVTVSS (SEQ ID NO:1313)
7A9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVAHI KTKZNNFATFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVZHZ SNNYPFAYWGQGTLVTVSS (SEQ ID NO:1314)
7A9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVAHI KTKZNNFATFYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVZHZ SNNYPFAYWGQGTLVTVSS (SEQ ID NO:1313)
7A9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVAH IKTKZNNFATFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVZH ZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1315)
7A9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFNTYSMNWVRQAPGQGLEWVAH IKTKZNNFATFYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVZH ZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1316)
7A9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFNTYSMNWVRQAPGQGLEWVAH IKTKZNNFATFYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVZHZ SNNYPFAYWGQGTLVTVSS (SEQ ID NO:1317)
7A9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFNTYSMNWVRQMPGKGLEWVAHI KTKZNNFATFYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVZHZS NNYPFAYWGQGTLVTVSS (SEQ ID NO:1318)
7A9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFNTYSMNWIRQPPGKGLEWVAHIK TKZNNFATFYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVZHZSN NYPFAYWGQGTLVTVSS (SEQ ID NO:1319)
7A9V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTFNTYSMNWIRQPPGKGLEWVAHIK TKZNNFATFYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVZHZSN NYPFAYWGQGTLVTVSS (SEQ ID NO:1320)
Antibody 7B3	Antibody 7B3
7B3V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYWIHWVRQAPGQGLEWIGR NDPNSGGSNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVRTNW DGDFWGQGTLVTVSS (SEQ ID NO:1322)

7B3V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTTYWIHWVRQMPGKGLEWIGRN DPNSGGSNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRTNWD GDFWGQGTLVTVSS (SEQ ID NO:1323)
7B3V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTTYWIHWVRQAPGQGLEWIGR NDPNSGGSNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRTNW DGDFWGQGTLVTVSS (SEQ ID NO:1324)
7B3V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIGRN DPNSGGSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRTNWD GDFWGQGTLVTVSS (SEQ ID NO:1325)
7B3V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIGRN DPNSGGSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRTNWD GDFWGQGTLVTVSS (SEQ ID NO:1326)
7B3V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIGR NDPNSGGSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRTNW DGDFWGQGTLVTVSS (SEQ ID NO:1327)
7B3V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIGRN DPNSGGSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRTNWD GDFWGQGTLVTVSS (SEQ ID NO:1326)
7B3V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTTYWIHWIRQPPGKGLEWIGRND PNSGGSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRTNWDGD FWGQGTLVTVSS (SEQ ID NO:1328)
7B3V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIGRN DPNSGGSNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRTNWD GDFWGQGTLVTVSS (SEQ ID NO:1329)
7B3V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYTFTTYWIHWIRQPPGKGLEWIGRND PNSGGSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRTNWDGD FWGQGTLVTVSS (SEQ ID NO:1330)
Antibody 8A1	Antibody 8A1
8A1V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYAFSNYWMSWVRQMPGKGLEWIGQI YPGDGDTKYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCSREKGA DYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1332)
8A1V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYAFSNYWMSWVRQAPGQGLEWIG QIYPGDGDTKYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCSREK GADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1333)
8A1V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLEWIGQI YPGDGDTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCSREKGA DYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1334)
8A1V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSNYWMSWVRQAPGQGLEWIGQ IYPGDGDTKYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCSREKGA DYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1335)
8A1V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLEWIGQI YPGDGDTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCSREKGA DYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1336)
8A1V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLEWIGQI YPGDGDTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCSREKGA DYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1336)
8A1V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYAFSNYWMSWVRQAPGKGLEWIGQ IYPGDGDTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCSREKG ADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1337)
8A1V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYAFSNYWMSWIRQPPGKGLEWIGQIY PGDGDTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCSREKGADY YGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1338)
8A1V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLEWIGQI YPGDGDTKYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCSREKGA DYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO: 1339)

8A1V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYAFSNYWMSWIRQPPGKGLEWIGQIY PGDGDTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCSREKGADY YGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1340)
Antibody 9F5	Antibody 9F5
9F5V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYAFSSSWMNWVRQMPGKGLEWIGRI YPGDGDTNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLLRN QPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1342)
9F5V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGLEWIGR IYPGDGDTNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARLLR NQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1343)
9F5V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGLEWIGR IYPGDGDTNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1344)
9F5V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLEWIGRI YPGDGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1345)
9F5V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLEWIGRI YPGDGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1346)
9F5V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLEWIGRI YPGDGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1346)
9F5V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYAFSSSWMNWVRQAPGKGLEWIGRI YPGDGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS (SEQ ID NO:1347)
9F5V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYAFSSSWMNWIRQPPGKGLEWIGRIY PGDGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLLRNQP GESYAMDYWGQGTLVTVSS (SEQ ID NO:1348)
9F5V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLEWIGRI YPGDGDTNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1349)
9F5V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYAFSSSWMNWIRQPPGKGLEWIGRIY PGDGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLLRNQP GESYAMDYWGQGTLVTVSS (SEQ ID NO:1350)
9F5-H1	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGLEWMG RIYPGDGDTNYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO: 1665)
9F5-H2	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGLEWIGR IYPGDGDTNYAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCARLLR NQPGESYAMDYWGQGTLVTVSS (SEQ ID NO: 1666)
9F5-H3	QVQLVQSGAEVKKPGASLKISCKASGYAFSSSWMNWVRQAPGQGLEWIGRI YPGDGDTNYAQKFQGRATLTADTSTSTAYMELSSLRSEDTAVYYCARLLRN QPGESYAMDYWGQGALVTVSS (SEQ ID NO: 1667)
Antibody 9G1	Antibody 9G1
9G1V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYIFTTYWIHWVRQMPGKGLEWIGRID PNNGDTNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVMTGTDF DYWGQGTLVTVSS (SEQ ID NO:1352)
9G1V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYIFTTYWIHWVRQAPGQGLEWIGRI DPNNGDTNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVMTGT DFDYWGQGTLVTVSS (SEQ ID NO:1353)
9G1V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYIFTTYWIHWVRQAPGQGLEWIGRI DPNNGDTNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVMTGTD FDYWGQGTLVTVSS (SEQ ID NO:1354)
9G1V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLEWIGRID PNNGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVMTGTDF DYWGQGTLVTVSS (SEQ ID NO:1355)

9G1V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYIFTTYWIHWVRQAPGKGLEWIGRI DPNNGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVMTGT DFDYWGQGTLVTVSS (SEQ ID NO:1356)
9G1V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLEWIGRID PNNGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVMTGTD FDYWGQGTLVTVSS (SEQ ID NO:1357)
9G1V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLEWIGRID PNNGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVMTGTD FDYWGQGTLVTVSS (SEQ ID NO:1357)
9G1V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYIFTTYWIHWIRQPPGKGLEWIGRIDP NNGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVMTGTDFD YWGQGTLVTVSS (SEQ ID NO:1358)
9G1V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLEWIGRID PNNGDTNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVMTGTDF DYWGQGTLVTVSS (SEQ ID NO:1359)
9G1V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYIFTTYWIHWIRQPPGKGLEWIGRIDP NNGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVMTGTDFD YWGQGTLVTVSS (SEQ ID NO:1360)
Antibody 9G3	Antibody 9G3
9G3V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLEWIARI RSNSNDYATNYSAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVGHKI NNYPFAHWGQGTLVTVSS (SEQ ID NO:1456)
9G3V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLEWIARI RSNSNDYATNYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVGHKI NNYPFAHWGQGTLVTVSS (SEQ ID NO:1457)
9G3V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFNFNTYAMKWVRQAPGKGLEWIARIRSNSNDY ATNYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVGHKI NNYPFAHWGQGTLVTVSS (SEQ ID NO:1458)
9G3V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLEWIARI RSNSNDYATNYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVGHK INNYPFAHWGQGTLVTVSS (SEQ ID NO:1459)
9G3V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLEWIARI RSNSNDYATNYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVGHK INNYPFAHWGQGTLVTVSS (SEQ ID NO:1460)
9G3V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFNFNTYAMKWVRQAPGQGLEWIAR IRSNSNDYATNYSQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVGHKI NNYPFAHWGQGTLVTVSS (SEQ ID NO:1461)
9G3V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFNFNTYAMKWVRQAPGQGLEWIAR IRSNSNDYATNYSQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVGH KINNYPFAHWGQGTLVTVSS (SEQ ID NO:1462)
9G3V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFNFNTYAMKWVRQMPGKGLEWIARI RSNSNDYATNYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVGHKI NNYPFAHWGQGTLVTVSS (SEQ ID NO:1463)
9G3V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFNFNTYAMKWIRQPPGKGLEWIARIR SNSNDYATNYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVGHKINN YPFAHWGQGTLVTVSS (SEQ ID NO:1464)
9G3V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFNFNTYAMKWIRQPPGKGLEWIARIR SNSNDYATNYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVGHKINN YPFAHWGQGTLVTVSS (SEQ ID NO:1465)
Antibody10A9	Antibody10A9
10A9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYPFSNFWITWVRQMPGKGLEWIGDIY PGSDNRNFNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAREAYYTN PGFAYWGQGTLVTVSS (SEQ ID NO:1362)
10A9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYPFSNFWITWVRQAPGQGLEWIGDI YPGSDNRNFNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1363)

10A9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYPFSNFWITWVRQAPGQGLEWIGDI YPGSDNRNFNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1364)
10A9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNRNFNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1365)
10A9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNRNFNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1365)
10A9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDI YPGSDNRNFNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1366)
10A9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNRNFNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1367)
10A9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIYP GSDNRNFNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYYTNP GFAYWGQGTLVTVSS (SEQ ID NO:1368)
10A9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGDIY PGSDNRNFNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCAREAYYT NPGFAYWGQGTLVTVSS (SEQ ID NO:1369)
10A9V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIYP GSDNRNFNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYYTNP GFAYWGQGTLVTVSS (SEQ ID NO:1370)
Antibody11A8	Antibody11A8
11A8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLEWVAR IRSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRH YSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1372)
11A8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLEWVAR IRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRH YSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1373)
11A8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLEWVARI RSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHY SNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1374)
11A8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFNFNTYAMNWVRQAPGKGLEWVAR IRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRH YSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1375)
11A8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLEWVAR IRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRH YSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1373)
11A8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFNFNTYAMNWVRQAPGQGLEWVAR IRSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRHY SNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1376)
11A8V1 -46	QVQLVQSGAEVKKPGASVKVSCKASGFNFNTYAMNWVRQAPGQGLEWVA RIRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVR HYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1377)
11A8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFNFNTYAMNWVRQMPGKGLEWVARI RSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRHYS NYGWGFAYWGQGTLVTVSS (SEQ ID NO:1378)
11A8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFNFNTYAMNWIRQPPGKGLEWVARIR SKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHYSN YGWGFAYWGQGTLVTVSS (SEQ ID NO:1379)
11A8V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFNFNTYAMNWIRQPPGKGLEWVARIR SKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHYSN YGWGFAYWGQGTLVTVSS (SEQ ID NO:1380)
Antibody12D9	Antibody12D9

12D9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFSDYYIHWVRQAPGQGLEWIGYI YPNNGDNGYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARRGY YGGSYDYWGQGTLVTVSS (SEQ ID NO:1382)
12D9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFSDYYIHWVRQMPGKGLEWIGYIY PNNGDNGYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARRGYYG GSYDYWGQGTLVTVSS (SEQ ID NO:1383)
12D9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSDYYIHWVRQAPGQGLEWIGYI YPNNGDNGYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARRGYY GGSYDYWGQGTLVTVSS (SEQ ID NO:1384)
12D9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLEWIGYIY PNNGDNGYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARRGYY GGSYDYWGQGTLVTVSS (SEQ ID NO:1385)
12D9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFSDYYIHWVRQAPGKGLEWIGYI YPNNGDNGYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRGY YGGSYDYWGQGTLVTVSS (SEQ ID NO:1386)
12D9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLEWIGYIY PNNGDNGYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRGYY GGSYDYWGQGTLVTVSS (SEQ ID NO:1387)
12D9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLEWIGYIY PNNGDNGYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARRGYY GGSYDYWGQGTLVTVSS (SEQ ID NO:1385)
12D9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFSDYYIHWIRQPPGKGLEWIGYIYP NNGDNGYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARRGYYGG SYDYWGQGTLVTVSS (SEQ ID NO:1388)
12D9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLEWIGYIY PNNGDNGYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCARRGYY GGSYDYWGQGTLVTVSS (SEQ ID NO:1389)
12D9V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYTFSDYYIHWIRQPPGKGLEWIGYIYP NNGDNGYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARRGYYGG SYDYWGQGTLVTVSS (SEQ ID NO:1390)
Antibody12F9	Antibody12F9
12F9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLEWEGVI RRKSSNFATLYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRHK SNKYPFVYWGQGTLVTVSS (SEQ ID NO:1392)
12F9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLEWEGVI RRKSSNFATLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHK SNKYPFVYWGQGTLVTVSS (SEQ ID NO:1393)
12F9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLEWEGVI RRKSSNFATLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHK SNKYPFVYWGQGTLVTVSS (SEQ ID NO:1394)
12F9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFRFNTYAMTWVRQAPGKGLEWEGV IRRKSSNFATLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHK SNKYPFVYWGQGTLVTVSS (SEQ ID NO:1395)
12F9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLEWEGVI RRKSSNFATLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRHK SNKYPFVYWGQGTLVTVSS (SEQ ID NO:1394)
12F9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFRFNTYAMTWVRQAPGQGLEWEGV IRRKSSNFATLYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRHK SNKYPFVYWGQGTLVTVSS (SEQ ID NO:1396)
12F9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFRFNTYAMTWVRQAPGQGLEWEG VIRRKSSNFATLYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVRH KSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1397)
12F9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFRFNTYAMTWVRQMPGKGLEWEGVI RRKSSNFATLYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRHKS NKYPFVYWGQGTLVTVSS (SEQ ID NO:1398)

12F9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFRFNTYAMTWIRQPPGKGLEWEGVIR RKSSNFATLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHKSN KYPFVYWGQGTLVTVSS (SEQ ID NO:1399)
12F9V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFRFNTYAMTWIRQPPGKGLEWEGVIR RKSSNFATLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHKSN KYPFVYWGQGTLVTVSS (SEQ ID NO:1400)
Antibody10C1	Antibody10C1
10C1V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWVAE IRNKINNHATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSLY DGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1467)
10C1V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWVAE IRNKINNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTSLY DGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1468)
10C1V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWVAEI RNKINNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTSLY DGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1469)
10C1V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWVAE IRNKINNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTSLY DGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1470)
10C1V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWVAE IRNKINNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTSLY DGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1471)
lOClVl-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMDWVRQAPGQGLEWVA EIRNKINNHATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCTSL YDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1472)
lOClVl-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMDWVRQAPGQGLEWVA EIRNKINNHATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCTSL YDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1473)
10C1V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMDWVRQMPGKGLEWVAE IRNKINNHATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTSLY DGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1474)
10C1V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMDWIRQPPGKGLEWVAEIR NKINNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTSLYDGSYLRFA YWGQGTLVTVSS (SEQ ID NO:1475)
10C1V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTFSDAWMDWIRQPPGKGLEWVAEIR NKINNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTSLYDG SYLRFAYWGQGTLVTVSS (SEQ ID NO:1476)
Antibody 7E9	Antibody 7E9
7E9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTMHWVRQAPGQGLEWIGG INPNNGGTSYKQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGS HYYAMDYWGQGTLVTVSS (SEQ ID NO:1478)
7E9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTEYTMHWVRQAPGQGLEWIGG INPNNGGTSYKQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1479)
7E9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTEYTMHWVRQMPGKGLEWIGGI NPNNGGTSYKPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1480)
7E9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYKDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1481)
7E9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYKDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1482)
7E9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYKDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1483)

7E9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYKDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1484)
7E9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEWIGGIN PNNGGTSYKPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGSHYY AMDYWGQGTLVTVSS (SEQ ID NO:1485)
7E9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWIGGI NPNNGGTSYKAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCARGGSH YYAMDYWGQGTLVTVSS (SEQ ID NO:1486)
7E9V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEWIGGIN PNNGGTSYKPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGSHYY AMDYWGQGTLVTVSS (SEQ ID NO:1487)
Antibody 8C3	Antibody 8C3
8C3V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYSFTGYYMHWVRQAPGQGLEWIGR VNPNNGGTSYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC VLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1489)
8C3V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYSFTGYYMHWVRQMPGKGLEWIGR VNPNNGGTSYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVLTGG YFDYWGQGTLVTVSS (SEQ ID NO:1490)
8C3V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLEWIGR VNPNNGGTSYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLTGG YFDYWGQGTLVTVSS (SEQ ID NO:1491)
8C3V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYSFTGYYMHWVRQAPGQGLEWIGR VNPNNGGTSYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVLTGG YFDYWGQGTLVTVSS (SEQ ID NO:1492)
8C3V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYSFTGYYMHWVRQAPGKGLEWIGR VNPNNGGTSYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLTGG YFDYWGQGTLVTVSS (SEQ ID NO:1493)
8C3V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLEWIGR VNPNNGGTSYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVLTGG YFDYWGQGTLVTVSS (SEQ ID NO:1494)
8C3V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLEWIGR VNPNNGGTSYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVLTGG YFDYWGQGTLVTVSS (SEQ ID NO:1495)
8C3V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYSFTGYYMHWIRQPPGKGLEWIGRVNPNNGGT SYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVLTGGYFD YWGQGTLVTVSS (SEQ ID NO:1496)
8C3V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLEWIGR VNPNNGGTSYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVLTGG YFDYWGQGTLVTVSS (SEQ ID NO:1497)
8C3V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYSFTGYYMHWIRQPPGKGLEWIGRVN PNNGGTSYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVLTGGYFD YWGQGTLVTVSS (SEQ ID NO:1498)

[00210] In some embodiments, anti-TREM2 antibodies of the present disclosure comprise a light chain variable region of any one of the antibodies listed in Tables **7A-7H**, or selected from 1A7, 3A2, 3B 10, 6G12, 6H6, 7A9, 7B3, 8A1 , 8E10, 8F11 , 8F8, 9F5, 9F5v2, 9G1 , 9G3, 10A9, 10C1 , 11A8, 12E2, 12F9, 12G6, 2C7, 2F5, 3C1 , 4D7, 4D11 , 6C11 , 6G12, 7A3, 7C5, 7E9, 7F6, 7G1 , 7H1 , 8C3, 8F10, 12A1 , 1E9, 2C5, 3C5, 4C12, 4F2, 5A2, 6B3, 7D1 , 7D9, 11D8, 8A12, 10E7, 10B 11 , 10D2, 7D5, 2A7, 3G12, 6H9, 8G9, 9B4, 10A1 , 11A8, 12F3, 2F8, 10E3, 1H7, 2F6, 2H8, 3A7, 7E5, 7E5v2, 7F8, 11H5, 7C5, 4F11 , 12D9, lB4vl , 1B4V2, 6H2, 7B l lvl , 7B l lv2, 18D8, 18E4vl , 18E4v2, 29F6vl , 29F6v2, 40D5vl , 40D5v2, 43B9, 44A8vl , 44A8v2, 44B4vl , and 44B4v2; and/or a heavy chain variable region of any one of the antibodies listed in Tables **7A-7H**, or selected from 1A7, 3A2, 3B 10, 6G12, 6H6, 7A9, 7B3, 8A1 , 8E10, 8F11 , 8F8, 9F5, 9G1 , 9G3, 10A9, 10C1 , 11A8, 12E2, 12F9, 12G6, 2C7, 2F5, 3C1 , 4D7, 4D11 , 6C11 , 6G12, 7A3, 7C5, 7E9, 7F6, 7G1, 7H1 , 8C3, 8F10, 12A1 , 1E9, 2C5, 3C5, 4C12, 4F2, 5A2, 6B3, 7D1 , 7D9, 11D8, 8A12, 10E7, 10B 11, 10D2, 7D5, 2A7, 3G12, 6H9, 8G9, 9B4, 10A1 , 11A8, 12F3, 2F8, 10E3, 1H7, 2F6, 2H8, 3A7, 7E5, 7F8, 11H5, 7C5, 4F11 , 12D9, lB4vl , 1B4V2, 6H2, 7B l lvl , 7B l lv2, 18D8, 18E4vl, 18E4v2, 29F6vl, 29F6v2, 40D5vl , 40D5v2, 43B9, 44A8vl , 44A8v2, 44B4vl , and 44B4v2.

[00211] In some embodiments, the anti-TREM2 antibody is an anti-TREM2 monoclonal antibody selected from 1A7, 3A2, 3B 10, 6G12, 6H6, 7A9, 7B3, 8A1, 8E10, 8F11, 8F8, 9F5, 9G1, 9G3, 10A9, 10C1, 11A8, 12E2, 12F9, 12G6, 2C7, 2F5, 3C1 , 4D7, 4D11 , 6C11 , 6G12, 7A3, 7C5, 7E9, 7F6, 7G1 , 7H1 , 8C3, 8F10, 12A1 , 1E9, 2C5, 3C5, 4C12, 4F2, 5A2, 6B3, 7D1 , 7D9, 11D8, 8A12, 10E7, 10B 11 , 10D2, 7D5, 2A7, 3G12, 6H9, 8G9, 9B4, 10A1 , 11A8, 12F3, 2F8, 10E3, 1H7, 2F6, 2H8, 3A7, 7E5, 7F8, 11H5, 7C5, 4F11 , 12D9, lB4vl , 1B4V2, 6H2, 7B l lvl , 7B l lv2, 18D8, 18E4vl , 18E4v2, 29F6vl , 29F6v2, 40D5vl , 40D5v2, 43B9, 44A8vl , 44A8v2, 44B4vl, and 44B4v2, and humanized variants thereof.

[00212] In some embodiments, each of the light chain variable regions disclosed in listed in Tables **7A-7H**, or selected from 1A7, 3A2, 3B 10, 6G12, 6H6, 7A9, 7B3, 8A1 , 8E10, 8F11 , 8F8, 9F5, 9F5v2, 9G1 , 9G3, 10A9, 10C1 , 11A8, 12E2, 12F9, 12G6, 2C7, 2F5, 3C1 , 4D7, 4D11 , 6C11 , 6G12, 7A3, 7C5, 7E9, 7F6, 7G1 , 7H1 , 8C3, 8F10, 12A1 , 1E9, 2C5, 3C5, 4C12, 4F2, 5A2, 6B3, 7D1 , 7D9, 11D8, 8A12, 10E7, 10B 11 , 10D2, 7D5, 2A7, 3G12, 6H9, 8G9, 9B4, 10A1

, 11A8, 12F3, 2F8, 10E3, 1H7, 2F6, 2H8, 3A7, 7E5, 7E5v2, 7F8, 11H5, 7C5, 4F11 , 12D9, lB4vl , 1B4V2, 6H2, 7B l lvl , 7B l lv2, 18D8, 18E4vl , 18E4v2, 29F6vl , 29F6v2, 40D5vl , 40D5v2, 43B9, 44A8vl , 44A8v2, 44B4vl , and 44B4v2; and/or each of the heavy chain variable region of any one of the antibodies listed in Tables **7A-7H**, or selected from 1A7, 3A2, 3B 10, 6G12, 6H6, 7A9, 7B3, 8A1 , 8E10, 8F11 , 8F8, 9F5, 9G1 , 9G3, 10A9, 10C1 , 11A8, 12E2, 12F9, 12G6, 2C7, 2F5, 3C1 , 4D7, 4D11 , 6C11 , 6G12, 7A3, 7C5, 7E9, 7F6, 7G1 , 7H1 , 8C3, 8F10, 12A1 , 1E9, 2C5, 3C5, 4C12, 4F2, 5A2, 6B3, 7D1 , 7D9, 11D8, 8A12, 10E7, 10B 11 , 10D2, 7D5, 2A7, 3G12, 6H9, 8G9, 9B4, 10A1 , 11A8, 12F3, 2F8, 10E3, 1H7, 2F6, 2H8, 3A7, 7E5, 7F8, 11H5, 7C5, 4F11 , 12D9, lB4vl , 1B4V2, 6H2, 7B l lvl , 7B l lv2, 18D8, 18E4vl , 18E4v2, 29F6vl , 29F6v2, 40D5vl , 40D5v2, 43B9, 44A8vl , 44A8v2, 44B4vl , and 44B4v2 may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

E. PCT Patent Application Publication No. WO2019/028292A1

[00213] In some embodiments, the TREM2 agonist is an antibody, or antigen binding fragment thereof, as described in PCT Patent Application Publication No. WO2019/028292A1 ("the '292 application"), which is incorporated by reference herein, in its entirety.

[00214] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3 (also referred to as HVR-L1, HVR-L2, and HVR-L3, respectively), and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 (also referred to as HVR-H1, HVR-H2, and HVR-H3, respectively) disclosed in the '573 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '573 application specification.

[00215] In some embodiments, anti-TREM2 antibodies of the present disclosure bind both human and cynomolgus monkey TREM2 with an affinity that is at least about 1-fold higher than an anti-TREM2 antibody selected from anti-TREM2 antibody comprising a heavy chain variable

region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763 *(e.g.,* antibody AL2p-h50); an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1810 *(e.g.,* antibody AL2p-h77); and an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1826 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1827 *(e.g.,* antibody AL2). In some embodiments, anti-TREM2 antibodies of the present disclosure bind to primary human immune cells with an affinity that is at least about 10 times higher than that of an anti-TREM2 antibody selected from an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763; an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1810; and an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1826 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1827. In some embodiments, anti-TREM2 antibodies of the present disclosure cluster and activate TREM2 signaling in an amount that is at least about 1-fold greater than that of an anti-TREM2 antibody selected from an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763; an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1810; and an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1826 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1827. In some embodiments, anti-TREM2 antibodies of the present disclosure increase immune cell survival *in vitro* that to an extent that is greater than an anti-TREM2 antibody selected from an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763; an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region

comprising the amino acid sequence of SEQ ID NO: 1810; and an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1826 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1827. In some embodiments, anti-TREM2 antibodies of the present disclosure may also have improved *in vivo* half-lives. In some embodiments, anti-TREM2 antibodies of the present disclosure may also decreases plasma levels of soluble TREM2 *in vivo*. In some embodiments, anti-TREM2 antibodies of the present disclosure may also decrease soluble TREM2. In some embodiments, the soluble TREM2 is decreased about any of 10, 20, 30, 40, 50 or 60%.

[00216] In some embodiments, the antibody binds to a TREM2 protein, wherein the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises: an HVR-H1 comprising the sequence according to Formula I: $YAFX_1X_2X_3WMN$, wherein X_1 is S or W, X_2 is S, L, or R. and X_3 is S, D, H, Q, or E (SEQ ID NO: 1828); an HVR-H2 comprising the sequence according to Formula II: $RIYPGX_1GX_2TNYAX_3KX_4X_5G$, wherein X_1 is D, G, E, Q, or V, X_2 is D or Q, X_3 is Q, R, H, W, Y, or G, X_4 is F, R, or W, and X_5 is Q, R, K, or H (SEQ ID NO: 1829); and an HVR-H3 comprising the sequence according to Formula III: $ARLLRNX_1PGX_2SYAX_3DY$, wherein X, is Q or K, X_2 is E, S, or A, and X_3 is M or H (SEQ ID NO: 1830), and wherein the antibody is not an antibody comprising a heavy chain variable region comprising an HVR-H1 comprising the sequence of YAFSSSWMN (SEQ ID NO: 1831), an HVR-H2 comprising the sequence of RIYPGDGDTNYAQKFQG (SEQ ID NO: 1832), and an HVR-H3 comprising the sequence of ARLLRNQPGESYAMDY (SEQ ID NO: 1833). In some embodiments, the TREM2 agonist is an antibody that binds to a TREM2 protein, wherein the antibody comprises a heavy chain variable region and a light chain variable region, wherein the light chain variable region comprises: an HVR-L1 comprising the sequence according to Formula IV: $RX_1SX_2SLX_3HSNX_4YTYLH$, wherein X_1 is S or T, X_2 is Q, R, or S, X_3 is V or I, and. X_4 is G, R, W, Q, or A (SEQ ID NO: 1834); an HVR-L2 comprising the sequence according to Formula V: $KVSNRX_1S$, wherein $X_)$ is F, R, V, or K (SEQ ID NO: 1835); and an HVR-L3 comprising the sequence according to Formula V: SQSTRVPYT (SEQ ID NO: 1836), and wherein the antibody is not an antibody comprising a light chain variable region comprising an HVR-L1 comprising the sequence of RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), an HVR-L2 comprising the sequence of KVSNRFS (SEQ ID NO: 1838), and an HVR-L3 comprising the sequence of SQSTRVPYT (SEQ

ID NO: 1836). In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises: an HVR-H1 comprising the sequence according to Formula I: $YAFX_1X_2X_3WMN$, wherein X_1 is S or W, X_2 is S, L, or R, and X_3 is S, D, H, Q, or E (SEQ ID NO: 1828); an HVR-H2 comprising the sequence according to Formula II: $RIYPGX_1GX_2TNYAX_3KX_4X_5G$, wherein X_1 is D, G, E, Q, or V, X_2 is D or Q, X_3 is Q, R, H, W, Y, or G, X_4 is F, R, or W, and X_5 is Q, R, K, or H (SEQ ID NO: 1829); and an HVR-H3 comprising the sequence according to Formula III: $ARLLRNX_1PGX_2SYAX_3DY$, wherein X_1 is Q or K, X_2 is E, S, or A, and X_3 is M or H (SEQ ID NO: 1830), and the light chain variable region comprises: an HVR-L1 comprising the sequence according to Formula IV: $RX_15X_2SLX_3HSNX_4YTYLH$, wherein X, is S or T, X_2 is Q, R, or S, X_3 is V or I, and X_4 is G, R, W, Q, or A (SEQ ID NO: 1834); an HVR-L2 comprising the sequence according to Formula V: $KVSNRX_1S$, wherein X_1 is F, R, V, or K (SEQ ID NO: 1835); and an HVR-L3 comprising the sequence: SQSTRVPYT (SEQ ID NO: 1836), and wherein the antibody is not an antibody comprising a heavy chain variable region comprising an HVR-Hl comprising the sequence of YAFSSSWMN (SEQ ID NO: 1831), an HVR-H2 comprising the sequence of RIYPGDGDTNYAQKFQG (SEQ ID NO: 1832), and an HVR-H3 comprising the sequence of ARLLRNQPGESYAMDY (SEQ ID NO: 1833), and comprising a light chain variable region comprising an HVR-L1 comprising the sequence of RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), an HVR-L2 comprising the sequence of KVSNRFS (SEQ ID NO: 1838), and an HVR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836).

[00217] In some embodiments, the antibody binds to a TREM2 protein, wherein the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises: an HVR-H1 comprising a sequence selected from the group consisting of SEQ ID Nos: 1839 and 1843; an HVR-H2 comprising a sequence selected from the group consisting of SEQ ID Nos: 1840, 1842, 1844, and 1848; and an HVR-H3 comprising a sequence selected from the group consisting of SEQ ID Nos: 1833 and 1845; and/or the light the light chain variable region comprises: an HVR-L1 comprising a sequence selected from the group consisting of 1837, 1846, 1849, and 1851; an HVR-L2 comprising a sequence selected from the group consisting of SEQ ID Nos: 1838, 1841, and 1847; and an HVR-L3 comprising the sequence of SEQ ID NO: 1836. In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises: an HVR-H1

comprising the sequence of SEQ ID No: 1839; an HVR-H2 comprising a sequence selected from the group consisting of SEQ ID Nos: 1840, 1842, and 1848; and an HVR-H3 comprising the sequence of SEQ ID No: 1833; and/or the light the light chain variable region comprises: an HVR-L1 comprising a sequence selected from the group consisting of 1837, 1849, and 1851; an HVR-L2 comprising a sequence selected from the group consisting of SEQ ID Nos: 1838 and 1841; and an HVR-L3 comprising the sequence of SEQ ID NO: 1836.

[00218] In some embodiments, the antibody binds to a TREM2 protein, wherein the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the HVR-H1, HVR-H2, and HVR-H3 of antibody AL2p-2, AL2p-3, AL2p-4, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56. AL2p-57, AL2p-58. AL2p-59, AL2p-60. AL2p-61, or AL2p-62 (as shown in **Tables 8A to 8C**). In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the light chain variable region comprises the HVR-L1, HVR-L2, and HVR-L3 of antibody AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Tables 9A to 9C**). In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the HVR-H I, HVR-H2, and HVR-H3 of antibody AL2p-2, AL2p-3, AL2p-4, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52,

AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Tables 8A to 8C**); and the light chain variable region comprises the HVR-Ll. HVR-L2, and HVR-L3 of antibody AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22. AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45 AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-5I, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Tables 9A to 9C**). In some embodiments, the antibody comprises a heavy chain variable region comprising an HVR-H1, HVR-H2, and HVR-H3 and a light chain variable region comprising an HVR-L1, HVR-L2, and HVR-L3, wherein the antibody comprises the HVR-H1, HVR-H2, HVR-H3, HVR-L1, HVR-L2. and HVR-L3 of antibody AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43. AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Tables 8A to 8C** and **9A to 9C**).

[00219] In some embodiments, the heavy chain variable region comprises one, two, three or four frame work regions selected from VH FRI, VH FR2, VH FR3, and VH FR4, wherein: the VH FRI comprises a sequence selected from the group consisting of SEQ ID NOs: 1716-1718, the VH FR2 comprises a sequence selected from the group consisting of SEQ ID NOs: 1719 and 1720, the VH FR3 comprises a sequence selected from the group consisting of SEQ ID NOs: 1721 and 1722, and the VH FR4 comprises the sequence of SEQ ID NO: 1723; and/or the light chain variable region comprises one, two, three or four frame work regions selected from VL FRI. VL FR2, VL FR3, and VL FR4, wherein: the VL FRI comprises a sequence selected from the group consisting of SEQ ID NOs: 1724-1727, the VL FR2 comprises a sequence selected from the group consisting of SEQ ID NOs: 1728 and 1729, the VL FR3 comprises a sequence selected from the group consisting of SEQ ID NOs: 1730 and 1731, and the VL FR4 comprises a sequence selected from

the group consisting of SEQ ID NOs: 1732 and 1733. In some embodiments, the antibody comprises a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1734-1777 and 1798; and/or a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1799-1820 and 1825. In some embodiments, the antibody comprises the heavy chain variable region of antibody AL2p-h50, AL2p-2. AL2p-3, AL2p-4, AL2p-5, AL2p-6. AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Table 12A**); and/or the antibody comprises the light chain variable region of antibody AL2p-h50, AL2p-2, AL2p-3. AL2p-4, AL2p-5, AL2p-6, AL2p-7. AL2p-8. AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-5I, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Table 13A**). In some embodiments: (a) the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYARKFQG (SEQ ID NO: 1840), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), the HVR-L2 comprises the amino acid sequence KVSNRRS (SEQ ID NO: 1841), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836); (b) the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), the HVR-L2 comprises the amino acid sequence KVSNRFS (SEQ ID NO: 1838), and the HVR-L3 comprises

the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836); (c) the HVR-H1 comprises the amino acid sequence YAFSSDWMN (SEQ ID NO: 1843), the HVR-H2 comprises the amino acid sequence RIYPGEGDTNYARKFHG (SEQ ID NO: 1844) the HVR-H3 comprises the amino acid sequence ARLLRNKPGESYAMDY (SEQ ID NO: 1845) the HVR-L1 comprises the amino acid sequence RTSQSLVHSNAYTYLH (SEQ ID NO: 1846), the HVR-L2 comprises the amino acid sequence KVSNRVS (SEQ ID NO: 1847). and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836); (d) the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGEGDTNYARKFQG (SEQ ID NO: 1848), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNQYTYLH (SEQ ID NO: 1849), the HVR-L2 comprises the amino acid sequence KVSNRRS (SEQ ID NO: 1841), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836); (e) the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839). the HVR-H2 comprises the amino acid sequence RIYPGEGDTNYAGKFQG (SEQ ID NO: 1850). the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNQYTYLH (SEQ ID NO: 1849), the HVR-L2 comprises the amino acid sequence KVSNRFS (SEQ ID NO: 1838), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836); (f) the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842). the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), the HVR-L2 comprises the amino acid sequence KVSNRFS (SEQ ID NO: 1838), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836); or (g) the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYARKFQG (SEQ ID NO: 1840), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNRYTYLH (SEQ ID NO: 1851). the HVR-L2 comprises the amino acid sequence KVSNRRS (SEQ ID NO: 1841), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-H1 comprises the amino acid

sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYARKFQG (SEQ ID NO: 1840), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), the HVR-L2 comprises the amino acid sequence KVSNRRS (SEQ ID NO: 1841), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), the HVR-L2 comprises the amino acid sequence KVSNRFS (SEQ ID NO: 1838), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-HI comprises the amino acid sequence YAFSSDWMN (SEQ ID NO: 1843), the HVR-H2 comprises the amino acid sequence RIYPGEGDTNYARKFHG (SEQ ID NO: 1844), the HVR-H3 comprises the amino acid sequence ARLLRNKPGESYAMDY (SEQ ID NO: 1845), the HVR-L1 comprises the amino acid sequence RTSQSLVHSNAYTYLH (SEQ ID NO: 1846), the HVR-L2 comprises the amino acid sequence KVSNRVS (SEQ ID NO: 1847), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839). the HVR-H2 comprises the amino acid sequence RIYPGEGDTNYARKFQG (SEQ ID NO: 1848), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNQYTYLH (SEQ ID NO: 1849), the HVR-L2 comprises the amino acid sequence KVSNRRS (SEQ ID NO: 1841), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGEGDTNYAGKFQG (SEQ ID NO: 1850), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNQYTYLH (SEQ ID NO: 1849), the HVR-L2 comprises the amino acid sequence KVSNRFS (SEQ ID NO: 1838), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence

RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), the HVR-L2 comprises the amino acid sequence KVSNRFS (SEQ ID NO: 1838), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-HI comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYARKFQG (SEQ ID NO: 1840), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), the HVR-L2 comprises the amino acid sequence KVSNRRS (SEQ ID NO: 1841), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the HVR-H1 comprises the amino acid sequence YAFSSQWMN (SEQ ID NO: 1839), the HVR-H2 comprises the amino acid sequence RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842), the HVR-H3 comprises the amino acid sequence ARLLRNQPGESYAMDY (SEQ ID NO: 1833), the HVR-L1 comprises the amino acid sequence RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), the HVR-L2 comprises the amino acid sequence KVSNRFS (SEQ ID NO: 1838), and the HVR-L3 comprises the amino acid sequence SQSTRVPYT (SEQ ID NO: 1836).

[00220] In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises Kabat CDRs; and/or the light chain variable region comprises Kabat CDRs. In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842); and a CDR-H3 comprising the sequence of LLRNQPGESYAMDY (SEQ ID NO: 1902). In some embodiments, the light chain variable region comprises a CDR-L1 comprising the sequence of RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), a CDR-L2 comprising the sequence of KVSNRFS (SEQ ID NO: 1838); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the heavy chain variable region comprises a CDR-HI comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842); and a CDR-H3 comprising the sequence of LLRNQPGESYAMDY (SEQ ID NO: 1902); and the light chain variable region comprises a CDR-L1 comprising the sequence of RSSQSLVHSNGYTYLH (SEQ ID NO: 1837), a CDR-L2

comprising the sequence of KVSNRFS (SEQ ID NO: 1838); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836).

[00221] In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises Kabat CDRs; and/or the light chain variable region comprises Kabat CDRs. In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SDWMN (SEQ ID NO: 1903), a CDR-H2 comprising the sequence of RIYPGEGDTNYARKFHG (SEQ ID NO: 1844); and a CDR-H3 comprising the sequence of LLRNKPGESYAMDY (SEQ ID NO: 1904). In some embodiments, the light chain variable region comprises a CDR-L1 comprising the sequence of RTSQSLVHSNAYTYLH (SEQ ID NO: 1846), a CDR-L2 comprising the sequence of KVSNRVS (SEQ ID NO: 1847); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the heavy chain variable region comprises a CDR-HI comprising the sequence of SDWMN (SEQ ID NO: 1903), a CDR-H2 comprising the sequence of RIYPGEGDTNYARKFHG (SEQ ID NO: 1844); and a CDR-H3 comprising the sequence of LLRNKPGESYAMDY (SEQ ID NO: 1904); and the light chain variable region comprises a CDR-LI comprising the sequence of RTSQSLVHSNAYTYLH (SEQ ID NO: 1846), a CDR-L2 comprising the sequence of KVSNRVS (SEQ ID NO: 1847); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836).

[00222] In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises Kabat CDRs; and/or the light chain variable region comprises Kabat CDRs. In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842); and a CDR-H3 comprising the sequence of LLRNQPGESYAMDY (SEQ ID NO: 1902). In some embodiments, the light chain variable region comprises a CDR-Ll comprising the sequence of RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), a CDR-L2 comprising the sequence of KVSNRFS (SEQ ID NO: 1838)1 and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGGGDTNYAGKFQG (SEQ ID NO: 1842); and a Kabat CDR-H3 comprising the sequence of LLRNQPGESYAMDY (SEQ ID NO: 1902); and the light chain variable region comprises a

CDR-L1 comprising the sequence of RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), a CDR-L2 comprising the sequence of KVSNRFS (SEQ ID NO: 1838); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836).

[00223] In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises Kabat CDRs; and/or the light chain variable region comprises Kabat CDRs. In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGGGDTNYARKFQG (SEQ ID NO: 1840); and a CDR-H3 comprising the sequence of LLRNQPGESYAMDY (SEQ ID NO: 1902). In some embodiments, the light chain variable region comprises a CDR-L1 comprising the sequence of RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), a CDR-L2 comprising the sequence of KVSNRRS (SEQ ID NO: 1841); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGGGDTNYARKFQG(SEQ ID NO: 1840); and a CDR-H3 comprising the sequence of LLRNQPGESYAMDY (SEQ ID NO: 1902); and the light chain variable region comprises a CDR-L1 comprising the sequence of RSSQSLVHSNRYTYLH (SEQ ID NO: 1851), a CDR-L2 comprising the sequence of KVSNRRS (SEQ ID NO: 1841); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836).

[00224] In some embodiments, the antibody comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises Kabat CDRs; and/or the light chain variable region comprises Kabat CDRs. In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGEGDTNYARKFQG (SEQ ID NO: 1848); and a CDR-H3 comprising the sequence of LLRNQPGESYAMDY (SEQ ID NO: 1902). In some embodiments, the light chain variable region comprises a CDR-L1 comprising the sequence of RSSQSLVHSNQYTYLH (SEQ ID NO: 1849), a CDR-L2 comprising the sequence of KVSNRRS (SEQ ID NO: 1841); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836). In some embodiments, the heavy chain variable region comprises a CDR-H1 comprising the sequence of SQWMN (SEQ ID NO: 1901), a CDR-H2 comprising the sequence of RIYPGEGDTNYARKFQG (SEQ ID NO: 1848); and a CDR-H3 comprising the sequence of

LLRNQPGESYAMDY (SEQ ID NO: 1902); and the light chain variable region comprises a CDR-L1 comprising the sequence of RSSQSLVHSNQYTYLH (SEQ ID NO: 1849), a CDR-L2 comprising the sequence of KVSNRRS (SEQ ID NO: 1841); and a CDR-L3 comprising the sequence of SQSTRVPYT (SEQ ID NO: 1836).

[00225] In some embodiments, the antibody comprises a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1734-1778 and 1798; and/or a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1799-1820 and 1825. In some embodiments, the antibody comprises the heavy chain variable region of antibody AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-I0, AL2p-11, AL2p-I2, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Table 12A**); and/or the antibody comprises the light chain variable region of antibody AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, or AL2p-62 (as shown in **Table 13A**). In some embodiments: (a) the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1760, and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1804; (b) the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1766; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1811; (c) the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1771; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1815; (d) the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1777; and/or the light chain

variable region comprises the amino acid sequence of SEQ ID NO: 1817; (e) the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1778; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1818; (f) the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1766; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1819; or (g) the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1760; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1820. In some embodiments, the antibody comprises an Fc region comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 1853-1863. In some embodiments, the antibody comprises an Fe region comprising the amino acid sequence of SEQ ID NO: 1853. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1854. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1855. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1856. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1857. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1858. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1859. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1860. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1861. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1862. In some embodiments, the antibody comprises an Fc region comprising the amino acid sequence of SEQ ID NO: 1863. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1905-1920; and/or a light chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1921-1925. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1905 and 1906; and a light chain comprising the amino acid sequence of SEQ ID NO: 1921. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1907 and 1908; and a light chain comprising the amino acid sequence of SEQ ID NO: 1921. In some embodiments, the antibody comprises a heavy chain comprising an amino

acid sequence selected from the group consisting of SEQ ID NOs: 1909 and 1910; and a light chain comprising the amino acid sequence of SEQ ID NO: 1922. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1911 and 1912; and a light chain comprising the amino acid sequence of SEQ ID NO: 1922. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1913 and 1914; and a light chain comprising the amino acid sequence of SEQ ID NO: 1923. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1915 and 1916; and a light chain comprising the amino acid sequence of SEQ ID NO: 1925. in some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1917 and 1918; and a light chain comprising the amino acid sequence of SEQ ID NO: 1925. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1919 and 1920; and a light chain comprising the amino acid sequence of SEQ ID NO: 1924.

[00226] In some embodiments, the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1760, and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1804. In some embodiments, the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1766; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1811. In some embodiments, the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1771; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1815. In some embodiments, the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1777; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1817. In some embodiments, the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1778; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1718. In some embodiments, the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1766; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1819. In some embodiments, the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1760; and/or the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1820.

[00227] In some embodiments, the antibody comprises a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1734, 1763 and 1779-1797; and/or a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1799, 1811, and 1821-1824. In some embodiments, the antibody comprises the heavy chain variable region of antibody AL2p-h19, AL2p-h21, AL2p-h22, AL2p-h23, AL2p-h24, AL2p-h25, AL2p-h26, AL2p-h27, AL2p-h28, AL2p-h29, AL2p-h30, AL2p-h31, AL2p-h32, AL2p-h33, AL2p-h34, AL2p-1135, AL2p-h36, AL2p-h42, AL2p-h43, AL2p-h44, AL2p-h47, AL2p-h59, AL2p-h76, or AL2p-h90 (as shown in **Table 12A**); and/or the antibody comprises the light chain variable region of antibody AL2p-h19, AL2p-h21, AL2p-h22, AL2p-h23, AL2p-h24, AL2p-h25, AL2p-h26, AL2p-h27, AL2p-h28, AL2p-h29, AL2p-h30, AL2p-h31, AL2p-h32, AL2p-h33, AL2p-h34, AL2p-h35, AL2p-h36, AL2p-h42, AL2p-h43, AL2p-h44, AL2p-h47, AL2p-h59, AL2p-h76, or AL2p-h90 (as shown in **Table 13A**).

[00228] In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1905-1920; and/or a light chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1921-1925. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1905 and 1906; and a light chain comprising the amino acid sequence of SEQ ID NO: 1921. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1907 and 1908; and a light chain comprising the amino acid sequence of SEQ ID NO: 1921. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1909 and 1910; and a light chain comprising the amino acid sequence of SEQ ID NO: 1922. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1911 and 1912; and a light chain comprising the amino acid sequence of SEQ ID NO: 1922. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1913 and 1914; and a light chain comprising the amino acid sequence of SEQ ID NO: 1923. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1915 and 1916; and a light chain comprising the amino acid sequence of SEQ ID

NO: 1925. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1917 and 1918; and a light chain comprising the amino acid sequence of SEQ ID NO: 1925. In some embodiments, the antibody comprises a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1919 and 1920; and a light chain comprising the amino acid sequence of SEQ ID NO: 1924.

[00229] In some embodiments that may be combined with any of the preceding embodiments. the antibody is a bispecific antibody recognizing a first antigen and a second antigen, wherein the first antigen is human TREM2 or a naturally occurring variant thereof, and the second antigen is: (a) an antigen facilitating transport across the blood-brain-barrier; (b) an antigen facilitating transport across the blood-brain-barrier selected from the group consisting of transferrin receptor (TR), insulin receptor (HIR), insulin-like growth factor receptor (IGFR), low-density lipoprotein receptor related proteins 1 and 2 (LPR-1 and 2), diphtheria toxin receptor, CRM197, a llama single domain antibody, TMEM 30(A), a protein transduction domain, TAT, Syn-B, penetratin, a poly-arginine peptide, an angiopeptide, and ANG1005; (c) a disease-causing agent selected from the group consisting of disease-causing peptides or proteins or, disease-causing nucleic acids, wherein the disease-causing nucleic acids are antisense GGCCCC (G2C4) repeat-expansion RNA, the disease-causing proteins are selected from the group consisting of amyloid beta, oligomeric amyloid beta, amyloid beta plaques, amyloid precursor protein or fragments thereof, Tau, TAPP, alpha-synuclein, TDP-43, FUS protein, C9orf72 (chromosome 9 open reading frame 72), c9RAN protein, prion protein, PrPSc, huntingtin, calcitonin, superoxide dismutase, ataxin, ataxin 1, ataxin 2, ataxin 3, ataxin 7, ataxin 8, ataxin 10, Lewy body, atrial natriuretic factor, islet amyloid polypeptide, insulin, apolipoprotein AI, serum amyloid A, medin, prolactin, transthyretin, lysozyme, beta 2 microglobulin, gelsolin, keratoepithelin, cystatin, immunoglobulin light chain AL, S-IBM protein, Repeat-associated non-ATG (RAN) translation products, DiPeptide repeat (DPR) peptides, glycine-alanine (GA) repeat peptides, glycine-proline (GP) repeat peptides, glycine-arginine (GR) repeat peptides, proline-alanine (PA) repeat peptides, ubiquitin, and proline-arginine (PR) repeat peptides; (d) ligands and/or proteins expressed on immune cells, wherein the ligands and/or proteins selected from the group consisting of CD40, OX40, ICOS, CD28, CD137/4-1BB, CD27 , GITR, PD-L1, CTLA-4, PD-L2, PD-1, B7-H3, B7-H4, HVEM, BTLA, KIR, GAL9, TIM3, A2AR, LAG-3, and phosphatidylserine; and (e) a protein, lipid,

polysaccharide, or glycolipid expressed on one or more tumor cells. In some embodiments, the antibody binds specifically to both human TREM2 and cynomolgus monkey TREM2. In some embodiments, the antibody has a dissociation constant (K_D) for human TREM2 and/or cynomolgus monkey TREM2 that is at least 1-fold lower than an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763; or at least **1-fold** lower than an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1810. In some embodiments, the antibody has a dissociation constant (K_D) for human TREM2 that ranges from about 9μM to about 100 pM, or less than 100 pM, wherein the K_D is determined at a temperature of approximately 25°C. In some embodiments, the antibody has a dissociation constant (K_D) for cynomolgus monkey TREM2 that ranges from about 50 nM to about100 pM, or less than 100 pM, wherein the K_D is determined at a temperature of approximately 25°C. In some embodiments, the antibody binds to primary human immune cells with an affinity that is at least 10 times higher than that of an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763; or at least 10 times higher than an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1810. In some embodiments, the antibody clusters and activates TREM2 signaling in an amount that is at least 1-fold greater than that of an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763; or at least 1-fold greater than an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1810. In some embodiments, the antibody increases immune cell survival *in vitro* that to an extent that is greater than *an* anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1734 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 1763; or that is greater than an anti-TREM2 antibody comprising a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 1798 and a light chain variable region

comprising the amino acid sequence of SEQ ID NO: 1810. In some embodiments, the antibody has an *in vivo* half-life that is lower than *a* human control IgG1 antibody. In some embodiments, the antibody decreases plasma levels of soluble TREM2 *in vivo* by an amount that is at least 25% greater than that of a human control IgG1 antibody. In some embodiments, the antibody decreases plasma levels of soluble TREM2 *in vivo* by blocking cleavage, by inhibiting one or more metalloproteases, and/or by inducing internalization. In some embodiments, soluble TREM2 is decreased by about any of 10, 20, 30, 40, or 50%. In some embodiments, the antibody competes with one or more antibodies selected from the group consisting of AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, AL2p-62, AL2p-h19, AL2p-h21, AL2p-h22, AL2p-h23, AL2p-h24, AL2p-h25, AL2p-h26, AL2p-h27, AL2p-h28, AL2p-h29, AL2p-h30, AL2p-h31, AL2p-h32, AL2p-h33, AL2p-h34, AL2p-h35, AL2p-h36, AL2p-h42, AL2p-h43, AL2p-h44, AL2p-h47, AL2p-1159, AL2p-h76, AL2p-h90, and any combination thereof for binding to TREM2. In some embodiments, the antibody binds essentially the same TREM2 epitope as an antibody selected from the group consisting of: AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, AL2p-62, AL2p-h19, AL2p-h21, AL2p-h22, AL2p-h23, AL2p-h24, AL2p-h25, AL2p-h26, AL2p-h27, AL2p-h28, AL2p-h29, AL2p-h30, AL2p-h31, AL2p-h32, AL2p-h33, AL2p-h34, AL2p-h35, AL2p-h36, AL2p-h42, AL2p-h43, AL2p-h44, AL2p-h47, AL2p-h59, AL2p-h76, and AL2p-h90. In some embodiments, the antibody binds to one or more amino acids within amino acid residues

149-157 of SEQ ID NO: 1. In some embodiments, the antibody binds to one or more amino acid residues selected from the group consisting of E151, D152, and E156 of SEQ ID NO: 1.

[00230] In some embodiments, the antibody is an antibody disclosed in Tables 2A, 2B, 2C, 3A, 3B, 3C, 4A-4D, 5A-5D, 6A, 6B, 7A or 7B of PCT Patent Application Publication No. WO2019/028292A1, reproduced below as **Tables 8A-8C, 9A-9C, 10A-10D, 11A-11D, 12A, 12B, 13A and 13B**.

Table 8A: Heavy chain HVR H1 sequences of anti-TREM2 antibodies

Ab	HVR H1	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p- 6, AL2p-33, AL2p-h77, and AL2p-36	YAFSSSWMN	1831
AL2p-29, AL2p-30, AL2p-31, AL2p-37, AL2p-58, AL2p-60, AL2p-61, and AL2p-62	YAFSSQWMN	1839
AL2p-10, AL2p-11, AL2p-45, AL2p-46, AL2p-47, AL2p-48, and AL2p-49	YAFSSDWMN	1843
AL2p-7 and AL2p-8	YAFSLSWMN	1864
AL2p-9	YAFSRSWMN	1865
AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16,AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21,AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26AL2p-27, AL2p-28, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-50,AL2p-51, AL2p-52, AL2p-53, AL2p-54. AL2p-55,AL2p-56, AL2p-57, and AL2p-59	YAFSSHWMN	1866
AL2p-32	YAFSSEWMN	1867
AL2P-35	YAYAFWSSWMN	1868
Formula I	$YAFX_1X_2X_3WMN$ X_1 is S or W X_2 is S, L, or R	1828

	X_3 is S, D, H, Q, or E	

Table 8B: Heavy chain HVR 112 sequences of anti-TREM2 antibodies

Ab	HVR H2	SEQ ID NO:
AL2p-h50, AL2p-5, AL2p-6, AL2p-9, AL2p- 10, AL2p-14, AL2p-15, AL2p-29, AL2p-32, AL2p-33, AL2p-h77, and AL2p-35	RIYPGDGDTNYAQKFQG	1832
AL2p-31 and AL2p-60	RIYPGGGDTNYARKFQG	1840
AL2p-37 and AL2p-58	RIYPGGGDINYAGKFQG	1842
AL2p47, AL2p-48, AL2p-49	RIYPGQGDTNYAQKFQG	1844
AL2p-45, AL2p46, and AL2p-61	RIYPGEGDTNYARKFQG	1848
AL2p-62	RIYPGQGDTNYAQKFQG	1850
AL2p-2 and AL2p-24	RIYPGGGDTNYAQKFQG	1869
AL2p-3	RIYPGQGDTNYAQKFQG	1870
AL2p-4 and AL2p-27	RIYPGQGDTNYAQKFQG	1871
AL2p-7 and AL2p-16	RIYPGDGDTNYAQK FRG	1872
AL2p-8, AL2p-11, AL2p-19, AL2p-20, and AL2p-36	RIYPGDGDTNYARKFQG	1873
AL2p-12	RIYPGDGDTNYARK.FQG	1874
AL2p-13	RIYPGDGDTNYAQKFKG	1875
AL2p-17	RIYPGDGDTNYAQKRQG	1876
AL2p-18	RIYPGDGDTNYAQKWQG	1877
AL2p-21 and AL2p-30	RIYPGDGDTNYAWKFQG	1878
AL2p-22	RIYPGDGDTNYAWKFQG	1879
AL2p-23	RIYPGDGQTNYAQKRQG	1880
AL2p-25, AL2p-38, AL2p-39, and AL2p-40	RIYPGGGDTNYAQKFRG	1881
AL2p-26	RIYPGGGDTNYAQKRQG	1882
AL2p-28	RIYPGVGDTNYAQKFQG	1883

AL2p-41 and AL2p-42	RIYPGEGDTNYAQKFRG	1884
AL2p-43 and AL2p44	RIYPGGGDTNYAQKFRG	1885
AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, and AL2p-57	RIYPGQGDTNYAQKFQG	1886
AL2p-59	RIYPGEGQINYAQKRQG	1887
Formula II	RTYPGX1GX2TNYAX$_3$KX$_4$X$_5$G X$_1$ is D, G, F, Q, or V X$_2$ is D or Q X$_3$ is Q, R, it W, Y, or G X$_4$ is F, R, or W X$_5$ is Q, R, K, or H	1829

Table 8C: Heavy chain HVR H3 sequences of anti-TREM2 antibodies

Ab	HVR 113	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14. A L2p-15„Al2p-17, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30. AL2p-3 **1**, AL2p-32, AL2p-33, AL2p-h77, AL2p-37,	ARLLRNQPGSSYAMDY	1833
AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-54, AL2p-55, AL2p-56, and AL2p-57	ARLLRNKPGESYAMDY	1845
AL2p-8 and AL2p-18	ARLLRNQPGSSYAMDY	1888
AL2p-9, AL2p-16, AL2p-36, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, and AL2p-44	ARLLRNQPGASYAMDY	1889

AL2p-35	ARLIANQPGESYAHDY	1890
Formula III	ARLLRNX$_1$FGX$_2$SYAX$_3$DY X$_1$ is Q or K X$_2$ is E, S, or A X$_3$ is M or H	1830

Table 9A: Light chain HVR Ll sequences of anti-TREM2 antibodies

Ab	HVR L1	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-10, AL2p-12, AL2p-31, AL2p-32, AL2p-h77, AL2p-35, AL2p-36. and AL2p-37	RSSQSLVHSNGYTYLH	1837
AL2p-45, AL2p-47, AL2p-50. AL2p-52, AL2p-55, and AL2p-56	RTSQSLVHSNAYTYLH	1846
AL2p-61 and AL2p-62	RSSQSLVHSNQYTYLH	1849
AL2p-5, AL2p-58, and AL2p-	RSSQSLVHSNRYTYLH	1851
AL2p-6	RSSQSLVHSNWYTYLH	1891
AL2p-7, AL2p-8, AL2p-13, and	RSSQSLIHSNOYTYLH	1892
AL2p-9, AL2p-16, AL2p-18. AL2p-20, AL2p-23, AL2p-25, AL2p-28, and AL2p-33	RTSQSLVHSNGYTYLH	1893
AL2p-11, AL2p-14, AL2p-17, AL2p-19, AL2p-22, AL2p-24, AL2p-27. and AL2p-29	RSSRSLVHSNGYTYLH	1894
AL2p-15, AL2p-21, and	RSSSSLVHSNGYTYLH	1895
AL2p-38 and AL2p-43	RSSRSLVHSNRYTYLH	1896
AL2p-39 and AL2p-41	RSSRSLVHSNQYTYLH	1897
AL2p-40, AL2p-42, and AL2p-44	RTSRSLVHSNRYTYLH	1898
AL2p-46, AL2p-48, AL2p-49, AL2p-51, AL2p-53, AL2p-54, AL2p-57, and AL2p-59	RTSQSLVHSNQYTYLH	1899
Formula IV	RX$_1$SX$_2$SLX$_3$HSNX$_4$YTYLH X$_1$ is S or T X$_2$ is Q, R, or S X$_3$ is V or I X$_4$ is G, R, W, Q or A	1834

Table 9B: Light chain HVR L2 sequences of anti-TREM2 antibodies

Ab	HVR L2	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-14, AL2p-24, AL2p-29, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-58, and AL2p-62	KVSNRFS	1838

AL2p-7, AL2p-8, AL2p-10, AL2p-12, AL2p-13, AL2p-22, AL2p-26, AL2p-31, AL2p-32, AL2p-38, AL2p-39. AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-60, and AL2p-61	KVSNRRS	1841
AL2p-9, AL2p-11, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-23, AL2p-25, AL2p-27, AL2p-28, AL2p-33, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p- 49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, and AL2p-59	KVSNRVS	1847
AL2p-15, AL2p-21, and AL2p-30	KVSNRKS	1900
Formula V	KVSNRX_1S X_1 is F, R, V, or K	1835

Table 9C: Light chain HVR L3 sequences of anti-TR FM2 antibodies

Ab	HVR L3	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AI 2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, AL2p-61, and AL2p-62	SQSTRVPYT	1836

Table 10A: Heavy chain framework I sequences of anti-TREM2 antibodies

Ab	VH FR1	SEQ ID NO:

AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30,	QVQLVQSGAEVKKPGSSVKVSCKASG	1716
AL2p-33. AL2p-49, AL2p-52. AL2p-53, AL2p-55, AL2p-56, and	EVQLVQSGAEVKKPGSSVKVSCKASG	1717
AL2p-h77, AL2p-35, AL2p-36, AL2p-37. AL2p-58. and AL2p-62	QVQLVQSGAEVKKPGASVKVSCKASG	1718

Table 10B: Heavy chain framework 2 sequences of anti-TREM2 antibodies

Ab	VH FR2	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5,AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p48, AL2p-49, AL2p- 50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-59, AL2p-60, and AL2p-61	WVRQAPGQGLEWMG	1719
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-58, and AL2 -62	WVRQAPGQRLEWIG	1720

Table 10C: Heavy chain framework 3 sequences of anti-TREM2 antibodies

Ab	VH FR3	SEQ ID NO:

AL2p-h50, AL2p-2, AL2p-3. AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42,	RVTITADESTSTAYMELSSLRSEDTAVYYC	1721
AL2p-h77, AL2p-35, AL2p-36, AL2p-37- AL2p-58, and AL2p-	RVTITADTSASTAYMELSSLRSEDTAVYYC	1722

Table 10D: Heavy chain framework 4 sequences of anti-TREM2 antibodies

Ab	VH FR4	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-38, AL2p-39, AL2p- 40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60. AL2p-61, and AL2p-62	WGQGTLVTVSS	1723

Table 11A: Light chain framework 1 sequences of anti-TREM2 antibodies

Ab	VL FR1	SEQ ID NO:

AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-11, AL2p-17, AL2p-19, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, and AL2p-57	DVVMTQTPLSLSVTPGQPASISC	1724
AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-18, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-59, AL2p-60, and AL2p-61	GVVMTQTPLSLSVTPGQPASISC	1725
AL2p-33	GVVMAQTPLSLSVTPGQPASISC	1726
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-58, and AL2p-62	DVVMTQSPDSLAVSLGERATINC	1727

Table 11B: Light chain framework 2 sequences of anti-TREM2 antibodies

Ab	VL FR2	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-11, AL2p-12, AL2p-13, AL2p-AI 2p-16, AL2p-17, AL2p-18, AL2p-AL2p-21, AL2p-22, AL2p-23, AL2p-AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-40, AL2p-41, AL2p-42, AL2p-AL2p-45, AL2p-46, AL2p-47, AL2p-AL2p-50, AL2p-51, AL2p-52, AL2p-AL2p-55, AL2p-56, AL2p-57, AL2p-59, AL2p-60. and AL2p-61	WY LQKPGQSPQLLIY	1728
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-58, and AL2p-62	WYQQKPGQSPKLLIY	1729

Table 11C: Light chain framework 3 sequences of anti-TREM2 antibodies

Ab	VL FR3	SEQ ID NO:

AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p-6, AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11. AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p-33, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51. AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, and AL2p-61	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	1730
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, and AL2-67	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	1731

Table 11D: Light chain framework 4 sequences of anti-TREM2 antibodies

Ab	VL FR4	SEQ ID NO:

AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5. AI 2p-6. AL2p-7, AL2p-8, AL2p-9, AL2p-10, AL2p-11, AL2p-12, AL2p-13, AL2p-14, AL2p-15, AL2p-16, AL2p-17, AL2p-18, AL2p-19, AL2p-20, AL2p-21, AL2p-22, AL2p-23, AL2p-24, AL2p-25, AL2p-26, AL2p-27, AL2p-28, AL2p-29, AL2p-30, AL2p-31, AL2p-32, AL2p- 33, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, AL2p-57, AL2p-58, AL2p-59, AL2p-60, and AL2p-61	FGQGTKLEIK	1732
AL2p-h77. AL2p-35, AL2p-36, AL2p-37, and AL2p-62	FGGGTKVEIK	1733

Table 12A: Heavy chain variable region sequences of anti-TREM2 antibodies

Ab	HCVR	SEQ ID NO:
AL2p-h50. AL2p-5, and AL2p-6	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNW VRQAPGQGLEWMGRIYPGDGDTNYAQKFQGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1734
AL2p-2	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNW VRQAPGQGLEWMGRIYPCrGGDTNYAQKFQGRVTIT ADESTSTAYMELSSLRSEDTAVYYCARLLRNQPGES YAMDYWGQGTLVTVSS	1735
AL2p-3	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWM NWVRQAPGQGLEWMGRIYPGEGDTNYAQKFQGR VTITADESTSTAYMELSSLRSEDTAVYYCARLLRNQP GESYAMDYWGQGTLVTVSS	1736
AL2p-4	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWV RQAPGQGLEWMGRIYPGQGDTNYAQKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSS	1737
AL2p-7	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSLSWMNWV RQAPGQGLEWMGRIYPGDGDTNYAQKFRGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSS	1738
AL2p-8	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSLSWMNWV RQAPGQGLEWMGRIYPGDGDTNYARKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGSSYAMD YWGQGTLVTVSS	1739

AL2p-9	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSRSWMNWV RQAPGQGLEWMGRIYPGDGDTNYAQKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGASYAMD YWGQGTLVTVSS	1740
AL2p-10	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWV RQAPGQGLEWMGRIYPGDGDTNYAQKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSS	1741
AL2p-11	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWV RQAPGQGLEWMGRIYPGDGDTNYARKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSS	1742
AL2p-12	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGDGDTNYAH1CFQGRVTITAD ESTSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAM DYWGQGTLVTVSS	1743
AL2p-13	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGDGDTNYAQKFKGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSS	1744
AL2p-14 and AL2p-15	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGDGDTNYAQKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLL	1745
AL2p-I6	RNQPGESYAMDYWGQGTLVTVSSQVQLVQSGAEVKKP GSSVKVSCKASGYARSSIMMNWVRQAPGQGLEWMGRI YPGDGDTNYAQKFRGRVTITADESTSTAYMELSSLRS EDTAVYYCARLLRNQPGASYAMDYWGQGTLVTVSS	1746
AL2p-1 7	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGDGDTNYAQKRQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSS	1747
AL2p-18	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGDGDTNYAQKWQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGSSYAMD YWGQGTLVTVSS	1748
AL2p-19 and AL2p-20	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGDGDTNYARKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSS	1749
AL2p-21	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWVRQAPGQGLEWMGRIYPGDGDTNYAWKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1750
AL2p-22	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWVRQAPGQGLEWMGRIYPGDGDTNYAYKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1751

AL2p-23	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWRQAPGQGLEWMGRIYPGDGQTNYAQKRQGRVTIT ADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1752
AL2p-24	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWVRQAPGQGLEWMGRIYPGGGDTNYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1753
AL2p-25	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWVRQAPGQGLEWMGRIYPGGGDTNYAQKFR GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1754
AL2p-26	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWVRQAPGQGLEWMGRIYPGGGDTNYAQKRQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1755
AL2p-27	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWVRQAPGQGLEWMGRIYPGQGDTNYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS	1756
AL2p-28	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW' MNWVRQAPGQGLEWMGRIYPGVGDTNYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS	1757
AL2p-29	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQW MNWVRQAPGQGLEWMGRIYPGDGDTNYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1758
AL2p-30	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQW MNWVRQAPGQGLEWMGRIYPGDGDTNYAWKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1759
AL2p-31, AL2p-60, and AL2p-h31	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWV RQAPGQGLEWMGRIYPGGGDTNYARKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1760
AL2p-32	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSEWM NWVRQAPGQGLEWMGRIYPGDGDTNYAQKFQGR VTITADESTSTAYMELSSLRSEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS	1761
AL2p-33	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWM NWVRQAPGQGLEWMGRIYPGDGDTNYAQKFQGR VTITADESTSTAYMELSSLRSEDTAVYYCARLLRN QPGESYAMDYWGQGTLVTVSS	1762
AL2p-h77, AL2p-h26, and AL2p-h90	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQRLEWIGRIYPGDGDTNYAQKFQGRVTITA DTSASTAYMELSSLRSEDTAVYYCARLLR	1763

AL2p-35	QVQLVQSGAEVKKPGASVKVSCKASGYAFWSSW MNWVRQAPGQRLEWIGRIYPGDGDTNYAQKFQG RVTITADTSASTAYMELSSLRSEDTAVYYCARLLRN QPGESYAHDYWGQGTLVTVSS	1764
AL2p-36	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQRLEWIGRIYPGDGDTNYARKFQGRVTITA DTSASTAYMELSSLRSEDTAVYYCARLLRNQPGASY AMDYWGQGTLVTVSS	1765
AL2p-37 and AL2p-58	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNW VRQAPGQRLEWIGRIYPGGGDTNYAGKFQGRVTITA DTSASTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1766
AL2p-38, AL2p-39, and AL2p-40	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNW VRQAPGQGLEWMGRIYPGGGDTNYAQKFRGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNQPGASY AMDYWGQGTLVTVSS	1767
AL2p-41 and AL2p-42	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNW VRQAPGQGLEWMGRIYPGEGDTNYAQKFRGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNQPGASY AMDYWGQGTLVTVSS	1768
AL2p-43 and AL2p-44	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNW VRQAPGrQGLEWMGRIYPGGGDTNYARKFRGRVTIT ADESTSTAYMELSSLRSEDTAVYYCARLLRNQPGAS YAMDYWGQGTLVTVSS	1769
AL2p-45 and AL2p-46	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNW VRQAPGQGLEWMGRIYPGEGDTNYARKFQGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNKPGESY AMDYWGQGTLVTVSS	1770
AL2p-47 and AL2p-48	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNW VRQAPGQGLEWMGRIYPGEGDTNYARKFUGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNKPGESY AMDYWGQGTLVTVSS	1771
AL2p-49	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNW VRQAPGQGLEWMGRTYPGEGDTNYARKFHGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNKPGESY AMDYWGQGTLVTVSS	1772
AL2p-50 and AL2p-51	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNW VRQAPGQGLEWMGRIYPGEGDTNYAQKFHGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYVv'GQGTLVIVSS	1773
AL2p-52 and AL2p-53	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNW VRQAPGQGLEWMGRIYPGEGDTNYAQKFHGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1774
AL2p-54	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNW VRQAPGQGLEWMGRIYPGEGDTNYAQKFHGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNKPGESY AMDYWGQGTLVTVSS	1775

AL2p-55, AL2p-56, and AL2p-57	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNW VRQAPGQGLEWMGRIYPGEGDTNYAQKFHGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNKPGESY AMDYWGQGTLVTVSS	1776
AL2p-61	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNW VRQAPGQGLEWMGRIYPGEGDTNYARKFQGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1777
AL2p-62	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNW VRQAPGQRLEWIGRIYPGEGDTNYAGKFQGRVTITA DTSASTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1778
AL2p-h19 and AL2p-h35	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNW VRQAPGQGLEWMGRIYPGDGDTNYAQKFQGRATITA DTSTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1779
AL2p-h21	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQGLE'WMGRIYPGDGDTNYAQKFQGRVTMT RDTSTSTVYMELSSLRSEDTAVYYCARLLRNQPGES YAMDYWGQGTLVTVSS	1780
AL2p-h22	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYAQKFQGRVTMTA DTSTSTVYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1781
AL2p-h23	QVQLVQSGAEVKKPGASLKISCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYAQKFQGRATLTA DTSTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGGALVTVSS	1782
AL2p-h24	QVQLVQSGAEVVKPGASLKISCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYNQKFQGRATLTA DTSTSTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGALVTVSS	1783
AL2p-h25	QVQLVQSGAEVKKPGASLKISCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYNGEFRVRATLTA DTSTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGALVTVSS	1784
AL2p-h27	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYNGEFRVRATLTA DTSTSTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1785
AL2p-h28	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYAQKFQGRATLTA DTSTSTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1786
AL2p-h29	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYAQKFQGRATMTA DTSTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1787

AL2p-h30	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQGLEWMGRIYPGDGDTNYAQKFQGRVTMTA DTSTSTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1788
AL2p-h32	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYNGEFRVRATLTA DTSTTTAYMELSSIRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1789
A L2p-h33	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYAQKFQGRATLTA DTSTTTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1790
A L2p-h34	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNW VRQAPGQGLEWIGRIYPGDGDTNYAQKFQGRATITA DTSTSTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1791
A L2p-b36	EVQLLESGGGLVQPGGSLRLSCAASGYAFSSSWMNW VRQAPGKGLEWIGRIYPGDGDINYAQKFQGRATISA DTSKNTAYLQMNSLRAEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1792
AL2p-h42 and AL2p-h59	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQRLEWMGRIYPGDGDTNYAQKFQGRVT1TR DTSASTAYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1793
AL2p-h43	QVQLVQSGAEVKKPGASLKVSCKASGYAFSSSWMNW VRQAPGQRLEWIGRIYPGDGDTNYNGEFRVRATLTA DTSASTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1794
AL2p-h44	QVQLVQSGAEVKKPGASLKVSCKASGYAFSSSWMNW VRQAPGQRLEWIGRIYPGDGDTNYAQKFQGRATLTA DTSASTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1795
AL2p-h47	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQGLEWMGR1YPGDGDTNYNGEFRVRVTMTR DTSTSTVYMELSSLRSEDTAVYYCARLLRNQPGESY AMDYWGQGTLVTVSS	1796
AL2p-h76	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNW VRQAPGQRLEWIGRTYPGDGDTNYAQKFQGRATITA DTSASTAYMELSSLRSEDTAVYFCARLLRNQPGESY AMDYWGQGTLVTVSS	1797
AL2p-59	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHW MNWVRQAPGQGLEWMGR1YPGEGQTNY AQKRQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS	1798

Table 12B: Heavy chain sequences of anti-TREM2 antibodies

Ab	HC	SEQ ID NO:

AL2p-58 huIgG1	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWV RQAPGQRLEWIGRIYPGGGDTNYAGKFQGRVTITADT SASTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	1905
AL2p-58 huIgG1	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWV RQAPGQRLEWIGRIYPGGGDTNYAGKFQGRVTITADT SASTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM1 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPG	1906
AL2p-58 huIgG1 PSEG	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWV RQAPGQRLEWIGRIYPGGGDTNYAGKFQGRVTITADT SASTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM1 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHYTQ KSLSLSPGK	1907

AL2p-58 huIgG1 PSEG	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWV RQAPGQRLEWIGRIYPGGGDTNYAGKFQGRVTITADT SASTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM1 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHYTQ KSLSLSPG	1908
AL2p-47 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWV RQAPGQGLEWMGRIYPGEGDTNYARKFHGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNKPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM1 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	1909
AL2p-47 hulgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWV RQAPGQGLEWMGRIYPGEGDTNYARKFHGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNKPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPG	1910

AL2p-47 huIgG1 PSEG	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWV RQAPGQGLEWMGRIYPGEGDTNYARKFHGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNKPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHYTQ KSLSLSPGK	1911
AL2p-47 huIgG1 PSEG	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDVv'MN WVRQAPGQGLEWMGRIYPGEGDTNYARKFHGRVTITA DESTSTAYMELSSLRSEDTAVYYCARLLRNKPGESYA MDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHY TQKSLSLSPG	1912
AL2p-61 hulgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWV RQAPGQGLEWMGRIYPGEGDTNYARKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1913

AL2p-61 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWV RQAPGQGLEWMGRIYPGEGDTNYARKFQGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGESYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSI,SPG	1914
AL2p-40 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGGGDTNYAQKFRGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGASYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1915
AL2p-40 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGGGDTNYAQKFRGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGASYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPEI,LGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPG	1916

AL2p-44 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGGGDTNYARKFRGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGASYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1917
AL2p-44 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGGGDTNYARKFRGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGASYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPG	1918
AL2p-41 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGEGDTNYAQKFRGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGASYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1919

AL2p-41 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWV RQAPGQGLEWMGRIYPGEGDTNYAQKFRGRVTITADE STSTAYMELSSLRSEDTAVYYCARLLRNQPGASYAMD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPG	1920

Table 13A: Light chain variable region sequences of anti-TREM2 antibodies

Ab	LCVR	SEQ ID NO:
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-h42, AL2p-h43, AL2p-h44, and AL2p-h47	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1799
AL2p-5	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNRYTYL HWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1800
AL2p-6	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNWYTY LHWYLQKPGQSPQLLTYKVSNRFSGVPDRFSGSGSGT DFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTK	1801
AL2p-7, AL2p-8, AL2p-13, and AL2p-26	GVVMIQTPLSLSVTPOQPASISCRSSQSLIHSNGYTYLH WYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCSQSTRVPYTFGQGTKLE1K	1802
AL2p-9, AL2p-16, AL2p-18, AL2p-20, AL2p-23, AL2p-25, and AL2p-28	GVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNGYTYLH WYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCSQSTRVPYTFGQGTKLE1K	1803
AL2p-10, AL2p-12, AL2p-31, and AL2p-32	GVVMTQTPLSLSVTPGQPASISCRSSQSLVH.SNGYTY LHWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTD FTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1804
AL2p-11, AL2p-17, and AL2p-19	DVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1805

AL2p-14, AL2p-24, and AL2p-29	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1806
AL2p-15, AL2p-21, and AL2p-30	GVVMTQTPLSLSVTPGQPASISCRSSSSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRKSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1807
AL2p-22	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1808
AL2p-27	GVVMTQTPISLSVTPGQTASISCRSSRSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1809
AL2p-33	GVVMAQTPLSLSVTPGQPASISCRTSQSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1810
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, and AL2p-h76	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNGYTYL HWYQQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDF TLTISSLQAEDVAVYYCSQSTRVPYTFGGGTKVEIK	1811
AL2p-38 and AL2p-43	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNRYTYL HWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1812
AL2p-39 and AL2p-41	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNQYTYL HWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1813
AL2p-40, AL2p-42, and AL2p-44	GVVMTQTPLSLSVTPGQPASISCRTSRSLVHSNRYTYL HWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1814
AL2p-45, AL2p-47, AL2p-50, AL2p-52, AL2p-55, and AL2p-56	DVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNAYTYL HWYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1815
AL2p-46, AL2p-48, AL2p-49, AL2p-51, AL2p-53, AL2p-54, and AL2p-57	DVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNQYTYL HWYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1816
AL2p-61	GVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNQYTYL HWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1817
AL2p-62	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNQYTYL HWYQQKPGQSPKWYKVSNRFSGVPDRFSGSGSGTDFTL TISSLQAEDVAVYYCSQSTRVPYTFGQGTKVEIK	1818

AL2p-58	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNRYTYL HWYQQKPGQSPKLLTYKVSNRFSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1819
AL2p-60	GVVMIQTPLSLSVTPGQPASISCRSSQSLVHSNRYTYL HWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1820
AL2p-h19	DIVMTQTPLSLSVTPGQPAS1SCRSSQSLVHSNGYTYL HWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1821
A L2p-h21, AL2p-h22, AL2p-h23, AL2p-h24, AL2p-h25, AL2p-h26, AL2p-h27, AL2p-h28, AL2p-h29, AL2p-h30, AL2p-h31, AL2p-h32, AL2p-h33, AL2p-h34, AL2p-h35, AL2p-h36	DVVIVETQTPLSLSVTPGQPASISCRSSQSLVHSNGYT YLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGT DFTLKISRVEAEDLGVYFCSQSTRVPYTFGQGTKLEIK	1822
AL2p-h59	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGYTYL HWYLQKPGQSPQLLTYKVSNRFSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGGGTKVEIK	1823
AL2p-h90	DVQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGYTYL HWYQQKPGKSPKLLIYKVSNRFSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCSQSTRVPYTFGGGTKVE1K	1824
AL2p-59	GVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNQYTYL HWYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIK	1825

Table 13B: Light chain sequences of anti-TREM2 antibodies

Ab	LC	SEQ ID NO:
AL2p-58 huIgG1, and AL2p-58 huIgG1 PSEG	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNRYTY LHWYQQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGT DFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1921

AL2p-47 huIgG1, and AL2p-47 huIgG1 PSEG	DVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNAYTY LHWYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGT DFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1922
AL2p-61 huIgG1	GVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNQYTY LHWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGT DFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1923
AL2p-41 huIgG1	GVVMTQFPLSLSVTPGQPASISCRSSRSLVHSNQYTY LHWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGT DFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1924
AL2p-40 huIgG1, and AL2p-44 huIgG1	GVVMTQTPLSLSVTPGQPASISCRTSRSLVHSNRYTY LHWYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGT DFTLKISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1925

[00231] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in **Tables 8A-8C, 9A-9C, 10A-10D, 11A-11D, 12A, 12B, 13A and 13B** as well as specific combinations thereof and other embodiments of the anti-TREM2 antibody described in the '573 application and herein may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

F. PCT Patent Application Publication No. WO2018/015573A1

[00232] In some embodiments, the TREM2 agonist is an antibody, or antigen binding fragment thereof, that prevents the cleavage of TREM2 as described in PCT Patent Application Publication No. WO2018/015573A1 ("the '573 application"), which is incorporated by reference herein, in its entirety.

[00233] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3, and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 disclosed in the '573 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '573 application specification.

[00234] In some embodiments, the antibody is a binding molecule that inhibits (preferably prevents) TREM2 cleavage. More specifically, in the context of the present invention cleavage (i.e. shedding) of the TREM2 ectodomain is inhibited by the binding molecule of the present invention. In some embodiments, the antibody is a binding molecule that inhibits (preferably prevents) TREM2 cleavage and activates TREM2 activity. In some embodiments, the herein provided binding molecule has a binding site within the ectodomain of TREM2, preferably the stalk region of the TREM2 ectodomain.

[00235] In some embodiments, the antibody is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1955 and the light chain variable region comprises the sequence of SEQ ID NO: 1965; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1955, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1965; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1975; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1985; the CDR3 of the heavy chain variable region comprises

the amino acid sequence of SEQ ID NO: 1995; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2005; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2015; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2025; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1975; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1985; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1995; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 2005; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2015; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 2025; and wherein the antibody inhibits TREM2 cleavage.

[00236] In some embodiments, the antibody is antibody clone 14D3, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1946 and the light chain variable region comprises the sequence of SEQ ID NO: 1956; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85% identity to SEQ ID NO: 1946, and the light chain variable region comprises a sequence having at least 85% identity to SEQ ID NO: 1956; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1966; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1976; the CDR3 of the heavy chain variable

region comprises the amino acid sequence of SEQ ID NO: 1986; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1996; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2006; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2016; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1966; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1976; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1986; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1996; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60% identity to SEQ ID NO: 2006; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 2016; and wherein the antibody inhibits TREM2 cleavage.

[00237] In some embodiments, the antibody is antibody clone 14D8, which is:
(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1947 and the light chain variable region comprises the sequence of SEQ ID NO: 1957; and wherein the antibody inhibits TREM2 cleavage;
(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85% identity to SEQ ID NO: 1947, and the light chain variable region comprises a sequence having at least 85% identity to SEQ ID NO: 1957; and wherein the antibody inhibits TREM2 cleavage;
(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1967; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1977; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1987; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1997; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2007; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2017; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1967; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1977; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1987; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 1997; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60% identity to SEQ ID NO: 2007; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 2017; and wherein the antibody inhibits TREM2 cleavage.

[00238] In some embodiments, the antibody is antibody clone 7A12, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1948 and the light chain variable region comprises the sequence of SEQ ID NO: 1958; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1948, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1958; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1968; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1978; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1988; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1998; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2008; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2018; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1968; the CDR2 of the heavy chain

variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1978; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1988; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1998; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2008; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 2018; and wherein the antibody inhibits TREM2 cleavage.

[00239] In some embodiments, the antibody is antibody clone 8A11, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1949 and the light chain variable region comprises the sequence of SEQ ID NO: 1959; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1949, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1959; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1969; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1979; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1989; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1999; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2009; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2019; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1969; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1979; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1989; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1999; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2009; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 2019; and wherein the antibody inhibits TREM2 cleavage.

[00240] In some embodiments, the antibody is antibody clone 21A3, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1950 and the light chain variable region comprises the sequence of SEQ ID NO: 1960; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1950, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1960; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1970; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1980; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1990; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2000; the CDR2 of the light

chain variable region comprises the amino acid sequence of SEQ ID NO: 2010; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2020; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1970; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1980; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1990; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 2000; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2010; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 2020; and wherein the antibody inhibits TREM2 cleavage.

[00241] In some embodiments, the antibody is antibody clone 10C3, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1951 and the light chain variable region comprises the sequence of SEQ ID NO: 1961; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1951, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1961; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1971; the CDR2 of the heavy chain variable region

comprises the amino acid sequence of SEQ ID NO: 1981; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1991; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2001; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2011; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2021; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1971; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1981; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1991; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 2001; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2011; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 2021; and wherein the antibody inhibits TREM2 cleavage.

[00242] In some embodiments, the antibody is antibody clone 18F9, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1952 and the light chain variable region comprises the sequence of SEQ ID NO: 1962; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferred at least 99% identity to SEQ ID NO: 1952, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at

least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1962; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1972; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1982; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1992; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2002; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2012; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2022; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1972; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1982; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1992; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 2002; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2012; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 2022; and wherein the antibody inhibits TREM2 cleavage.

[00243] In some embodiments, the antibody is antibody clone 15C5, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1953 and the light chain variable region comprises the sequence of SEQ ID NO: 1963; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1953, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1963; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1973; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1983; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1993; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2003; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2013; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2023; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1973; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1983; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1993; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 2003; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2013; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 2023; and wherein the antibody inhibits TREM2 cleavage.

[00244] In some embodiments, the antibody is antibody clone 1G6, which is:

(1) an antibody, wherein the heavy chain variable region comprises the sequence of SEQ ID NO: 1954 and the light chain variable region comprises the sequence of SEQ ID NO: 1964; and wherein the antibody inhibits TREM2 cleavage;

(2) an antibody, wherein the heavy chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1954, and the light chain variable region comprises a sequence having at least 85%, preferably at least 90%, more preferably at least 95%, even more preferably at least 98%, and most preferably at least 99% identity to SEQ ID NO: 1964; and wherein the antibody inhibits TREM2 cleavage;

(3) an antibody, wherein the CDR1 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1974; the CDR2 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1984; the CDR3 of the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 1994; the CDR1 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2004; the CDR2 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2014; and the CDR3 of the light chain variable region comprises the amino acid sequence of SEQ ID NO: 2024; and wherein the antibody inhibits TREM2 cleavage; or

(4) an antibody, wherein the CDR1 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, and most preferably at least 85% identity to SEQ ID NO: 1974; the CDR2 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1984; the CDR3 of the heavy chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 1994; the CDR1 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%, even more preferably at least 85%, and most preferably at least 90% identity to SEQ ID NO: 2004; the CDR2 of the light chain variable region comprises an amino acid sequence having at least 60%, preferably 100% identity to SEQ ID NO: 2014; and the CDR3 of the light chain variable region comprises an amino acid sequence having at least 70%, preferably at least 75%, more preferably at least 80%,

and most preferably at least 85% identity to SEQ ID NO: 2024; and wherein the antibody inhibits TREM2 cleavage.

[00245] In some embodiments, the antibody is an antibody disclosed in Figure 9 of PCT Patent Application Publication No. WO2018/015573A1, reproduced below as **Tables 14A-14D**.

Table 14A

Clone name	Variable region of the heavy chain	SEQ ID NO
14D3	EVKLLEFGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGRAP EWLGLIRNKTKGYTTEYNRSVKGRFTISRDNTQNMLYLQMNSLRP EDTATYYCARIGVNNGGSLDYWGQGVMVTVSS	1946
14D8	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAP EWLGLIRNKANGYTTVYNPSVKGRFTISRDNTQNMLYLQMNTLRG EDTATYYCARIGINNGGSLDYWGQGVMVTVSS	1947
7AI2	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAP EWLGLIRNKANGYTTQYNPSVKGRFTISRDNTQNMLYLQMNTLRG EDTATYYCARIGINNGGSLDYWGQGVMVTVSS	1948
8A11	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAP EWLGLIRNKTKGYTTEYNTSVKGRFTISRDNTQNMLYLQMNSLRP EDTATYYCARIGVNNGGSLDYWGQGVMVTVSS	1949
21A3	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAP EWLGLIRNKANGYTTQYNPSVKGRFTISRDNTQNMLYLQMNTLRG EDTATYYCARIGINNGGSLDYWGQGVMVTVSS	1950
10C3	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGETP EWLGLIRNKTKGYTTEYNPSVKGRFTISRDNTQNMLYLQMNSLRP EDTATYYCARIGTNNGGSLDYWGQGVMVTVSS	1951
18F9	EVKLLESGGGLVQPGGSMRLSCVVSGFTFTDFYMNWIRQAAGKAP EWLGLIRNKVNGYRTEYNPSVKGRFTISRDNIQNMLYLQMNTLRA EDTATYYCARIGINNGGSLDYWGQGVMVTVSS	1952
15C5	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAP EWLGLIRNKAYGYTTEYNPSVKGRFTISRDNTQDMLYLQMNTLRA EDTATYYCARIGINYGGSLDYWGQGVMVTVSS	1953
1G6	EVKLLESGGGLVQPGGSLRLSCVASGFTFTDFYMNWIRQPAGKAP EWLGLIRNKANGFTTEYNPSVKGRFTISRDNTQHMLYLQMNTLRA EDTATYYCARIGINNGGSLDYWGQGVMVTVSS	1954
Consensus sequence	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAP EWLGLIRNKANGYTTEYNPSVKGRFTISRDNTQNMLYLQMNTLRE DTATYYCARIGINNGGSLDYWGQGVMVTVSS	1955

Table 14B

Clone name	Variable region of the light chain	SEQ ID NO
14D3	DILIIQSPASLTVSAGARVTMSCKSSQSLLYSENNQDYLAWYQQKP GQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1956
14D8	DILINQSPASLTVSTGEKVTMSCRSSQSLLYSEKNQDYLAWYQQKP GQFPKLLIYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1957
7AI2	DILINQSPASLTVSAGEKVTMSCKSSQSLLYSEKNQDYLAWYQQKP GQSPKLLMYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1958
8A11	DILIIQSPASLTVSAGARVTMSCKSSQSLLYSENNQDYLAWYQQKP GQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1959
21A3	DILINQSPASLTVSAGEKVTMSCKSSQSLLYSEKNQDYLAWYQQKP GQSPKLLMYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1960

10C3	DILIIQSPASLTVSAGARVTMSCKSSQSLLYSENNQDYLAWYQQKP GQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1961
18F9	DILINQSPASLTVSAGEKVTMSCKSSQSLLYSENNQDYLAWYQQKP GQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1962
15C5	DILINQSPASLTVSAGEKVTVSCKSSQSLLYSESNQDYLAWYQQKP GQFPKLLIYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLAHY YCEQTYSYPYTFGAGTKLELK	1963
1G6	DILINQSPASLTVSTGEKVTMSCKSSQSLLYSENKQDYLAWYQQKP GQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTINIVQAEDLADY YCEQTYSYPYTFGAGTKLELK	1964
Consensus sequence	**DILINQSPASLTVSAGEKVTMSCKSSQSLLYSENNQDYLAWYQQKP GQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADY YCEQTYSYPYTFGAGTKLELK**	1965

Table 14C

Clone name	Complementarity determining regions in the variable region of the heavy chain					
	CDR1	**SEQ**	**CDR2**	**SEQ**	**CDR3**	**SEQ**
14D3	GFTFTDFY	1966	IRNKTKGYTT	1976	ARIGVNNGGSLDYWG	1986
14D8	GFTFTDFY	1967	IRNKANGYTT	1977	ARIGINNGGSLDYWG	1987
7AI2	GFTFTDFY	1968	IRNKANGYTT	1978	ARIGINNGGSLDYWG	1988
8A11	GFTFTDFY	1969	IRNKTKGYTT	1979	ARIGVNNGGSLDYWG	1989
21A3	GFTFTDFY	1970	IRNKANGYTT	1980	ARIGINNGGSLDYWG	1990
10C3	GFTFTDFY	1971	IRNKTKGYTT	1981	ARIGTNNGGSLDYWG	1991
18F9	GFTFTDFY	1972	IRNKVNGYRT	1982	ARIGINNGGSLDYWG	1992
15C5	GFTFTDFY	1973	IRNKAYGYTT	1983	ARIGINYGGSLDYWG	1993
1G6	GFTFTDFY	1974	IRNKANGFTT	1984	ARIGINNGGSLDYWG	1994
Cons-ensus seq	**GFTFTDFY**	1975	**IRNKANGYTT**	1985	**ARIGINNGGSLDYWG**	1995

Table 14D

Clone name	Complementarity determining regions in the variable region of the light chain					
	CDR1	**SEQ**	**CDR2**	**SEQ**	**CDR3**	**SEQ**
14D3	QSLLYSENNQDY	1996	GAS	2006	EQTYSYPYT	2016
14D8	QSLLYSEKNQDY	1997	GAS	2007	EQTYSYPYT	2017
7AI2	QSLLYSEKNQDY	1998	GAS	2008	EQTYSYPYT	2018
8A11	QSLLYSENNQDY	1999	GAS	2009	EQTYSYPYT	2019
21A3	QSLLYSEKNQDY	2000	GAS	2010	EQTYSYPYT	2020
10C3	QSLLYSENNQDY	2001	GAS	2011	EQTYSYPYT	2021
18F9	QSLLYSENNQDY	2002	GAS	2012	EQTYSYPYT	2022
15C5	QSLLYSESNQDY	2003	GAS	2013	EQTYSYPYT	2023
1G6	QSLLYSENKQDY	2004	GAS	2014	EQTYSYPYT	2024

Cons-ensus seq	**QSLLYSENNQDY**	2005	**GAS**	2015	**EQTYSYPYT**	2025

[00246] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in in the above tables as well as specific combinations thereof and other embodiments of the anti-TREM2 antibody described in the '573 application and herein may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

G. PCT Patent Application Publication No. WO2019/055841A1

[00247] In some embodiments, the TREM2 agonist is an antibody or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. WO2019/055841A1 ("the '841 application"), which is incorporated by reference herein, in its entirety.

[00248] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3, and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 disclosed in the '841 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '841 application specification.

[00249] In some embodiments, the antibody comprises one or more (e.g., one, two, three, four, five, or all six) CDRs selected from the group consisting of:

(a) a heavy chain CDR1 sequence having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 2049, 2077, 2080, 2086, 2092, 2098, 2103, 2109, 2115, 2122, 2126, 2347, and 2355 or having up to two amino acid substitutions relative to the amino acid sequence of any one of SEQ ID NOs: 2049, 2077, 2080, 2086, 2092, 2098, 2103, 2109, 2115, 2122, 2126, 2347, and 2355;

(b) a heavy chain CDR2 sequence having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 2050, 2078, 2081, 2087, 2093, 2099, 2104, 2110, 2116, 2120, 2123, 2127, 2348, and 2356 or having up to two amino acid substitutions relative to the amino acid sequence of any one of SEQ ID NOs: 2050, 2078, 2081, 2087, 2093, 2099, 2104, 2110, 2116, 2120, 2123, 2127, 2348, and 2356;

(c) a heavy chain CDR3 sequence having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 2051, 2082, 2088, 2094, 2100, 2105, 2111, 2117, 2124, 2128, 2349, and 2357 or having up to two amino acid substitutions relative to the amino acid sequence of any one of SEQ ID NOs: 2051, 2082, 2088, 2094, 2100, 2105, 2111, 2117, 2124, 2128, 2349, and 2357;

(d) a light chain CDR1 sequence having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 2052, 2083, 2089, 2095, 2101, 2106, 2112, 2118, 2129, and 2351 or having up to two amino acid substitutions relative to the amino acid sequence of any one of SEQ ID NOs: 2052, 2083, 2089, 2095, 2101, 2106, 2112, 2118, 2129, and 2351;

(e) a light chain CDR2 sequence having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 2053, 2079, 2084, 2090, 2096, 2107, 2113, 2352, and 2359 or having up to two amino acid substitutions relative to the amino acid sequence of any one of SEQ ID NOs: 2053, 2079, 2084, 2090, 2096, 2107, 2113, 2352, and 2359; and

(f) a light chain CDR3 sequence having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 2054, 2085, 2091, 2097, 2102, 2108, 2114, 2119, 2121, 2125, 2130, and 2353 or having up to two amino acid substitutions relative to the amino acid sequence of any one of SEQ ID NOs: 2054, 2085, 2091, 2097, 2102, 2108, 2114, 2119, 2121, 2125, 2130, and 2353.

[00250] In some embodiments, the antibody comprises:

(a) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2049, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2050, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2051, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2052, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2052, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2053; or

(b) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2077, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2078, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2051, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2052, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2079, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2054; or

(c) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2080, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2081, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2082, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2083, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2084, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2085; or

(d) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2086, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2087, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2088, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2089, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2090, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2091; or

(e) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2092, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2093, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2094, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2095, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2096, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2097; or (f) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2098, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2099, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2100, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2101, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2079, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2102; or

(g) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2103, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2104, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2105, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2106, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2107, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2108; or

(h) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2109, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2110, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2111, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2112, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2113, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2114; or

(i) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2115, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2116, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2117, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2118, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2119, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2119; or

(j) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2115, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2120, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2117, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2118, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2079, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2121; or

(k) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2123, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2132, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2133, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2102, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2079, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2125; or

(1) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2126, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2127, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2128, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2129, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2079, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2130; or

(m) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2347, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2348, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2349, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2351, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2352, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2353; or

(n) a heavy chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2355, a heavy chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2356, a heavy chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2357, a light chain CDR1 sequence comprising the amino acid sequence of SEQ ID NO:2089, a light chain CDR2 sequence comprising the amino acid sequence of SEQ ID NO:2359, and a light chain CDR3 sequence comprising the amino acid sequence of SEQ ID NO:2091.

[00251] In some embodiments, the antibody or antigen-binding portion thereof comprises:

(a) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2047; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2048; or

(b) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2055; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2066; or

(c) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2056; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2067; or

(d) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2057; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2068; or

(e) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2058; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2069; or

(f) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2059; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2070; or

(g) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2060; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2071; or

(h) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2061; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2072; or

(i) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2062; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2073; or

(j) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2063; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2074; or

(k) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2064; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2075; or

(1) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2065; and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2076; or

(m) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2346, and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2350; or

(n) a heavy chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2354, and a light chain variable region comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:2358.

[00252] In some embodiments, the antibody is an antibody disclosed in Table 15 of PCT Patent Application Publication No. WO2019/055841A1, reproduced as **Table 15** below. In some embodiments, the antibody is an antibody comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3, and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 disclosed in Table 15.

Table 15

SEQ ID NO	Sequence	Description
2042	GGACAGGGATCCAGAGTTC	muIgG1 3' primer
2043	AGCTGGGAAGGTGTGCACAC	muIgG2 3' primer
2044	CAGGGGCCAGTGGATAGAC	muIgG3 3' primer
2045	GACATTGATGTCTTTGGGGT	muCkappa.1 3' primer
2046	TTCACTGCCATCAATCTTCC	muCkappa.2 3' primer
2047	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLEWIG RSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAVYYCVRTS GTGDYWGQGTSLTVSSAKTTAPSVYPLAPVCGGTTGSSVT	RS9.F6 VH amino acid sequence
2048	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHNNGNTFLHWYLQKPGQSPKL LIYkVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPPTFG GGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCF	RS9.F6 VL amino acid sequence
2049	GYTFTSY	RS9.F6 CDR-H1 amino acid sequence
2050	IGRSDPTTGGTNYNE	RS9.F6 CDR-H2 amino acid sequence
2051	VRTSGTGDY	RS9.F6 and RS.F10 CDR-H3 amino acid sequence
2052	RSSQSLVHNNGNTFLH	RS9.F6 and RS.F10 CDR-L1 amino acid sequence
2053	VSNRFS	RS9.F6 CDR-L2 amino acid sequence
2054	SQTTHVPPT	RS9.F6 and RS.F10 CDR-L3 amino acid sequence
2055	QVQLQQSGAELARPGASVKLSCKASGYTFTSYWIQWVKQRPGQGLEWIG TIYPGDGDARYTQKFKGKATLTADKSSSTTYMQLNSLASEDSAVYYCARN GITTAGYYAMDYWGQGTSVTVSS	21D11 VH amino acid sequence
2056	QVQLQQSGADLLRPGVSVKISCKGSGYTFTDHAMHWVKQSHAESLEWIG VISTYSGDTGYNQKFKGKATMTVDKSSSTAYLELARLTSEDSAIYYCARE GHYDDAMDYWGQGTSVTVSS	21D4.D1 VH amino acid sequence
2057	EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIG YINPYTDGTKYNEKFKGKATLTSDKSSSTAYMDLSSLTSEDSAVYYCARGE VRRYALDYWGQGTSVTVSS	26D2 VH amino acid sequence
2058	QVHLQQSGSELRSPGSSVKLSCKDFDSEVFPISYMSWIRQKPGHGFEWIG DILPSIGGRIYGVKFEDRATLDADTVSNTAYLELNSLTSEDSAIYYCARKD YGSLAYWGQGTLVTVSA	26E2.A3 VH amino acid sequence; 24B4.A1 VH amino acid sequence

2059	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWIGGVI PNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYCARGDDSY RRGYALDYWGQGTSVTVSS	3D3.A1 VH amino acid sequence
2060	EVQLQQSGAEVVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWI GRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAT LFAYWGQGTLVTVSA	40H3.A4 VH amino acid sequence
2061	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWM GYINYSGRTIYNPSLKSRISITRDTSKNHFFLQLISVTTEDTATYYCARWNG NYGFAYWGQGTLVTVSA	42E8.H1 VH amino acid sequence
2062	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNRLEWM GYISFSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARWNG NYGFAYWGQGTLVTVSA	49H1 LB 1 VH amino acid sequence
2063	QVHLQQSGSELRSPGSSVKLSCKDFDSEVFPIAYMSWVRQKPGHGFEWIG DILPSIGRRIYGVKFEDKATLDADTVSNTAYLELNSLTSEDSAIYYCTRKDY GSLAYWGQGTLVTVSA	54C2.A1 VH amino acid sequence
2064	QVQLKESGPGLVAPSQSLSITCTVSGFSLSRYSVYWVRQPPGKGLEWLGMI WGGGNTDYNSALKSRLSISKDNSKSQVFLKMNSLQTDDSAMYYCVQYG GMDYWGQGTSVTVSS	57D7.A1 VH amino acid sequence
2065	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLEWI GRSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAVYYCV RTSGTGDYWGQGTSLTVSS	RS9.F6 VH amino acid sequence; RS.F10 VH amino acid sequence
2066	DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQGRSPQLLVYA ATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGYYYCQHFWGTPYTFGG GTKVEIK	2 ID 11 VL amino acid sequence
2067	DWMTQTPLTLSVTIGQPASFSCKSSQSLLDSDGKTYLNWLLRRPGQSPK RLIYVVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHF PYTFGGGTKLEIK	2 1D4.D 1 VL amino acid sequence
2068	DIQMTQSSSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLISGA TSLETGVPSRFSGSGSGKDYTLSITSLQTEDVATYYCQQYWSTPWTFGGG TKLEIK	26D2 VL amino acid sequence
2069	DWMTQTPLSLPVSLGDQASISCRSSQSLVHINGNTYLQWFLQKPGQSPKL LIYKVSNRFSGVPDRFSGSGSGTAFTLKISRVEAEDLGVYFCSQSTHVPYT FGGGTKLEIK	26E2.A3 VL amino acid sequence; 24B4.A1 VL amino acid sequence
2070	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKSYLAWYQQKPGQSP KLLIYWASTRESGVPDRFRGSGSGTDFTLTISSVKAEDLAVYYCQQYFSYP PTFGGGTKLEIK	3D3.A1 VL amino acid sequence
2071	DIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQL LIYQMSNLASGVPDRFSSSGSGIDFTLRINRVEAEDVGVYYCAQNLELPTF GSGTKLEIK	40H3.A4 VL amino acid sequence
2072	DWMTQNPLSLPVSLGDQASISCRSSQSLVHINGNTYLHWYLQKPGQSPKL LIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHALFT FGSGTKLEIK	42E8.H1 VL amino acid sequence
2073	DWMTQTPLSLPVSLGDQASISCRSSQSLVHINGNTYLHWYLQKPGQSPKL LIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVTFTF GSGTKLEIK	49H1 LB 1 VL amino acid sequence
2074	DWMTQTPLSLPVSLGDQASISCRSSQSLVHINGNTYLQWYLQKPGQSPKL LIYKVSNRFSGVPDRFSGSGSGTDFTLRISRVEAEDLGVYFCSQSTHL PYTFGGGTKLEIK	54C2.A1 VL amino acid
2075	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKL LIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTF GGGTKLEIK	57D7.A1 VL amino acid sequence
2076	DWMTQTPLSLPVSLGDQASISCRSSQSLVHNNGNTFLHWYLQKPGQSPKL LIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPPTF GGGTKLEIK	RS9.F6 VL amino acid sequence; RS.F10 VL amino acid sequence

2077	GYTFTSYWMH	RS9.F6 and RS.F10 CDR-H1
2078	RSDPTTGGTNYNEKFKT	RS9.F6 and RS.F10 CDR-H2
2079	KVSNRFS	RS9.F6, RS.F10, 26E2.A3, 24B4.A1, 42E8.H1, 49H11.B1, 54C2.A1, and 57D7.A1 CDR-L2
2080	GYTFTSYWIQ	2ID11 CDR-H1
2081	TIYPGDGDARYTQKFKG	2 ID 11 CDR-H2
2082	ARNGITTAGYYAMDY	2 ID 11 CDR-H3
2083	RASENIYSNLA	2ID11 CDR-L1
2084	AATNLAD	2 ID 11 CDR-L2
2085	QHFWGTPYT	2 ID 11 CDR-L3
2086	GYTFTDHAMH	21D4.D1 CDR-H1
2087	VISTYSGDTGYNQKFKG	21D4.D1 CDR-H2
2088	AREGHYDDAMDY	21D4.D1 CDR-H3
2089	KSSQSLLDSDGKTYLN	21D4.D1 and 51D4 CDR-L1
2090	VVSKLDS	21D4.D1 CDR-L2
2091	WQGTHFPYT	21D4.D1 and 51D4 CDR-L3
2092	GYTFTSYVMH	26D2 CDR-H1

2093	YINPYTDGTKYNEKFKG	26D2 CDR-H2
2094	ARGEVRRYALDY	26D2 CDR-H3
2095	KASEDIYNRLA	26D2 CDR-L1
2096	GATSLET	26D2 CDR-L2
2097	QQYWSTPWT	26D2 CDR-L3
2098	DSEVFPISYMS	26E2.A3 and 24B4.A1 CDR-H1
2099	DILPSIGGRIYGVKF	26E2.A3 and 24B4.A1 CDR-H2
2100	ARKDYGSLAY	26E2.A3 and 24B4.A1 CDR-H3
2101	RSSQSLVHINGNTYLQ	26E2.A3, 24B4.A1, and 54C2.A1 CDR-L1
2102	SQSTHVPYT	26E2.A3 and 24B4.A1 CDR-L3
2103	GYTLSEYTMH	3D3.A1 CDR-H1
2104	GVIPNSGGTSYNQKFRD	3D3.A1 CDR-H2
2105	ARGDDSYRRGYALDY	3D3.A1 CDR-H3
2106	KSSQSLLYSSNQKSYLA	3D3.A1 CDR-L1
2107	WASTRES	3D3.A1 CDR-L2
2108	QQYFSYPPT	3D3.A1 CDR-L3

2109	GFNIKDTYMH	40H3.A4 CDR-H1
2110	RIDPANGNTKYDPKFQG	40H3.A4 CDR-H2
2111	ATLFAY	40H3.A4 CDR-H3
2112	RSSKSLLHSNGITYLY	40H3.A4 CDR-L1
2113	QMSNLAS	40H3.A4 CDR-L2
2114	AQNLELPT	40H3.A4 CDR-L3
2115	GYSITSDYAWN	42E8.H1 and 49Hll.Bl CDR-H1
2116	YINYSGRTIYNPSLKS	42E8.H1 CDR-H2
2117	ARWNGNYGFAY	42E8.H1 and 49Hll.Bl CDR-H3
2118	RSSQSLVHINGNTYLH	42E8.H1 and 49Hll.Bl CDR-L1
2119	SQTTHALFT	42E8.H1 CDR-L3
2120	YISFSGSTSYNPSLKS	49H11.B1 CDR-H2
2121	SQSTHVTFT	49H11.B1 CDR-L3
2122	DSEVFPIAYMS	54C2.A1 CDR-H1
2123	DILPSIGRRIYGVKFED	54C2.A1 CDR-H2
2124	KDYGSLAY	54C2.A1 CDR-H3

2125	SQSTHLPYT	54C2.A1 CDR-L3
2126	GFSLSRYSVY	57D7.A1 CDR-H1
2127	MIWGGGNTDYNSALKS	57D7.A1 CDR-H2
2128	YGGMDY	57D7.A1 CDR-H3
2129	RSSQSIVHSNGNTYLE	57D7.A1 CDR-L1
2130	FQGSHVPYT	57D7.A1 CDR-L3
2131	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLEWIG RSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAVYYCVRT SGTGDYWGQGTSLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTH	RS9.F6-Fd
2132	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLEWIG RSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAVYYCVRT SGTGDYWGQGTSLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWVDGVEVHNAKTKPREEQYNSTYRWSV LTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLWCLVKGFYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFF LYSKLTVTKEEWQQGFVFSCSVMHEALHNHYTQKSLSLSPGK	RS9.F6-Fd fused to Fc with LALAPG, TfR binding, and knob mutations
2133	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLEWIG RSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAVYYCVRT SGTGDYWGQGTSLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWVDGVEVHNAKTKPREEQYNSTYRWSV LTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL VSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	RS9.F6-Fd fused to Fc with LALAPG and hole mutations
2134	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWIGG VIPNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYCARGDD SYRRGYALDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTH	3D3.A1-Fd

2135	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWIGG VIPNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYCARGDD SYRRGYALDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRWSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQV YTLPPSRDELTKNQVSLWCLVKGFYPSDIAVLWESYGTEWASYKTTPPVL DSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEALHNHYTQKSLSLSPGK	3D3.A1-Fd fused to Fc with LALAPG, TfR binding, and knob mutations
2136	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWIGG VIPNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYCARGDD SYRRGYALDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRWSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQV YTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	3D3.A1-Fd fused to Fc with LALAPG and hole mutations
1	MEPLRLLTLLFVTELSGAHNTTWQGVAGQSLQVSCPYDSMKHWGRRKA WCRQLGEKGPCQRWSTHNLWLLSFLRRWNGSTAITDDTLGGTLTITLRNL QPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLDHRDAGDLWFPGESESF EDAHVEHSISRSLLEGEIPFPPTSILLLLACIFLIKTLAASALWAAAWGQKPG TPPSELDCGHDPGYQLQTLPGLRDT	Human TREM2 protein
2137	MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENAD NNTKANVTKPKRCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECEPX AGTESPVREEPGEDFPAARRLYWDDLKRKLSEKLDSTDFTGTIKLLNENSY VPREAGSQKDENLALYVENQFREFKLSKVWRDQHFVKIQVKDSAQNSVII VDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKKDFEDLYTPV NGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAH LGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCP SDWKTDSTCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVWG AQRDAWGPGAAKSGVGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSA GDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLI EKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAAFPFLAYSGIPAVSFC FCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKLTHDVEL NLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLT TDFGNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGS HTLPALLENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALSGDVWDI DNEF	Human transferrin receptor protein 1 (TFR1)
2138	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Wild-type human Fc sequence positions 231-447 EU index numbering
2139	EPKSCDKTHTCPPCP	Human IgG1 hinge sequence

2140	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20
2141	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21
2142	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.22
2143	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSC SVMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.23
2144	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.24
2145	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17
2146	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1
2147	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.2
2148	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.3

2149	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.4
2150	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.5
2151	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.6
2152	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.a.1
2153	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21.a.2
2154	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21.a.3
2155	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCS VMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.21.a.4
2156	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESFGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21.a.5
2157	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESFGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21.a.6

2158	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.1
2159	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.2
2160	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.3
2161	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.4
2162	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.5
2163	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.6
2164	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.24.1
2165	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.24.2
2166	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.24.3

2167	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVW WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSV MHEALHNHYTQKSLSLSPGK	Clone CH3C.35.24.4
2168	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESFGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.24.5
2169	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESFGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.24.6
2170	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.1
2171	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2
2172	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.3
2173	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.4
2174	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SFGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.5
2175	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SFGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.6

2176	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clones CH3C.35.N390 and CH3C.35.N163
2177	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGLVWVGYKTTPPVLDSDGSFFLYSKLTVAKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.1
2178	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTVWSHYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGYVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.2
2179	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESYGTEWSQYKTTPPVLDSDGSFFLYSKLTVEKSDWQQGHVFSCS VMHEALHNHYTQKSLSLSPGK	Clone CH3C.3
2180	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SVGTPWALYKTTPPVLDSDGSFFLYSKLTVLKSEWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.4
2181	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTVWSKYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C. 17
2182	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C. 18
2183	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGLVWVGYKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.21
2184	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SMGHVWVGYKTTPPVLDSDGSFFLYSKLTVDKSTWQQGWVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.25
2185	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGLVWVFSKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.34

2186	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35
2187	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.44
2188	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVGYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.51
2189	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVATKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.3. 1-3
2190	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGPVWVHTKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.3. 1-9
2191	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESLGHVWVDQKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCS VMHEALHNHYTQKSLSLSPGK	Clone CH3C.3.2-5
2192	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVNQKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.3.2-19
2193	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVNFKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.3.2-1
2194	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C. 18 variant

2195	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C. 18 variant
2196	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVYWE SLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C. 18 variant
2197	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWAVYQTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C. 18 variant
2198	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWAVYFTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C. 18 variant
2199	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWAVYHTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C. 18 variant
2200	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35. 13
2201	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWAVYQTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35. 14
2202	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESLGHVWAVYQTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35. 15
2203	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVW WESLGHVWVNQKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFS CSVMHEALHNHYTQKSLSLSPGK	Clone CH3C.35. 16
2204	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVNQQTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35. 17

2205	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESLGHVWVNQQTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35. 18
2206	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35. 19
2207	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSSYQTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.K165Q
2208	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSNYQTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.N163. K165Q
2209	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.1
2210	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.2
2211	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.3
2212	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTGEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.4
2213	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFSCWVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.5

2214	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCWVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.6
2215	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVL WESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFTC WVMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.21.7
2216	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFTCGVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.8
2217	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFECWVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.9
2218	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFKCWVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 10
2219	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTPEEWQQGFVFKCWVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21.il
2220	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 12
2221	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTGEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 13
2222	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFTCWVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 14

2223	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTGEEWQQGFVFTCWVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 15
2224	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQGFVFTCGVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 16
2225	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 18
2226	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPRFDYVTTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYGFHDLSLSPGK	Clone CH3B.1
2227	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPRFDMVTTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYGFHDLSLSPGK	Clone CH3B.2
2228	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPRFEYVTTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYGFHDLSLSPGK	Clone CH3B.3
2229	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPRFEMVTTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYGFHDLSLSPGK	Clone CH3B.4
2230	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPRFELVTTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYGFHDLSLSPGK	Clone CH3B.5
2231	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVEFIWYVDG VDVRYEWQLPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2A2.1

2232	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVGFVWYVDG VPVSWEWYWPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2A2.2
2233	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFDWYVDG VMVRREWHRPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2A2.3
2234	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVSFEWYVDG VPVRWEWQWPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH2A2.4
2235	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVAFTWYVDG VPVRWEWQNPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2A2.5
2236	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVWDPQTPPWEVKFNWYVDG VEVHNAKTKPREEEYYTYYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2C.1
2237	APELLGGPSVFLFPPKPKDTLMISRTPEVTCWVDPPSPPWEVKFNWYVDG VEVHNAKTKPREEEYYSNYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2C.2
2238	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVWDPQTPPWEVKFNWYVDG VEVHNAKTKPREEEYYSNYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2C.3
2239	APELLGGPSWLFPPKPKDTLMISRTPEVTCVVVDFRGPPWEVKFNWYVDG VEVHNAKTKPREEEYYHDYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	Clone CH2C.4
2240	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVWDPQTVPWEVKFNWVDGV EVHNAKTKPREEEYYSNYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2C.5

2241	APELLGGPSWLFPPKPKDTLMISRTPEVTCVVVDVSVPPRMVKFNWYVDG VEVHNAKTKSLTSQHNSTVRWSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2D.1
2242	APELLGGPSWLFPPKPKDTLMISRTPEVTCVVVDVSVPPWMVKFNWYVD GVEVHNAKTKSLTSQHNSTVRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH2D.2
2243	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDMWEYVKFNWYVD GVEVHNAKTKPWVKQLNSTWRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	Clone CH2D.3
2244	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDDWTWVKFNWYVD GVEVHNAKTKPWIAQPNSTWRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH2D.4
2245	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDDWEWVKFNWYVD GVEVHNAKTKPWKLQLNSTWRWSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH2D.5
2246	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPWVWFYWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCSVVNIALW WSIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH2E3.1
2247	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPWGFRWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCRVSNSALTW KIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2E3.2
2248	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPWGFRWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCRVSNSALSW RIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2E3.3
2249	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPIVGFRWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCRVSNSALRW RIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH2E3.4

2250	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPAVGFEWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCQVFNWALD WVIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH2E3.5
2251	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	Fc sequence with hole mutations
2252	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	Fc sequence with hole and LALA mutations
2253	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	Fc sequence with hole and YTE mutations
2254	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	Fc sequence with hole, LALA, and YTE mutations
2255	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	Fc sequence with knob mutation
2256	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	Fc sequence with knob and LALA mutations
2257	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	Fc sequence with knob and YTE mutations
2258	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	Fc sequence with knob, LALA, and YTE mutations

2259	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21 with knob mutation
2260	APEAAGGPSWLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21 with knob and LALA mutations
2261	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21 with knob and YTE mutations
2262	APEAAGGPSWLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21 with knob, LALA, and YTE mutations
2263	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQV	Clone CH3C.35.21 with hole mutations
2264	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21 with hole and LALA mutations
2265	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21 with hole and YTE mutations
2266	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21 with hole, LALA, and YTE mutations
2267	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob mutation
2268	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob and LALA mutations

2269	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob and LALAPG mutations
2270	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob and YTE mutations
2271	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob, LALA, and YTE mutations
2272	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob, LALAPG, and YTE mutations
2273	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole mutations
2274	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole and LALA mutations
2275	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAV EWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSC SVMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole and LALAPG mutations
2276	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole and YTE mutations
2277	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole, LALA, and YTE mutations

2278	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL GAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole, LALAPG, and YTE mutations
2279	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob mutation
2280	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob and LALA mutations
2281	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob and LALAPG mutations
2282	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob and YTE mutations
2283	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob, LALA, and YTE mutations
2284	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob, LALAPG, and YTE mutations
2285	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole mutations
2286	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole and LALA mutations
2287	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAV EWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFS CSVMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole and LALAPG mutations

2288	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole and YTE mutations
2289	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole, LALA, and YTE mutations
2290	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL GAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole, LALAPG, and YTE mutations
2291	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob mutation
2292	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob and LALA mutations
2293	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob and LALAPG mutations
2294	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob and YTE mutations
2295	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob, LALA, and YTE mutations
2296	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob, LALAPG, and YTE mutations

2297	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole mutations
2298	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole and LALA mutations
2299	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAV EWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFS CSVMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole and LALAPG mutations
2300	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole and YTE mutations
2301	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole, LALA, and YTE mutations
2302	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL GAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMH EALHNHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole, LALAPG, and YTE mutations
2303	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob mutation
2304	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob and LALA mutations
2305	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob and LALAPG mutations
2306	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob and YTE mutations

2307	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob, LALA, and YTE mutations
2308	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob, LALAPG, and YTE mutations
2309	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole mutations
2310	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole and LALA mutations
2311	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCS VMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole and LALAPG mutations
2312	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole and YTE mutations
2313	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole, LALA, and YTE mutations
2314	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole, LALAPG, and YTE mutations
2315	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob mutation
2316	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob and LALA mutations

2317	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob and LALAPG mutations
2318	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob and YTE mutations
2319	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob, LALA, and YTE mutations
2320	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob, LALAPG, and YTE mutations
2321	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLWE SYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole mutations
2322	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole and LALA mutations
2323	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCS VMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole and LALAPG mutations
2324	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLWE SYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole and YTE mutations
2325	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole, LALA, and YTE mutations

2326	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole, LALAPG, and YTE mutations
2327	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23 with knob mutation
2328	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23 with knob and LALA mutations
2329	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23 with knob and LALAPG mutations
2330	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23 with knob and YTE mutations
2331	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23 with knob, LALA, and YTE mutations
2332	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23 with knob, LALAPG, and YTE mutations
2333	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23 with hole mutations
2334	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23 with hole and LALA mutations

2335	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAV EWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSC SVMHEALHNHYTQKSLSLSPGK	Clone CH3C.35.23 with hole and LALAPG mutations
2336	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23 with hole and YTE mutations
2337	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23 with hole, LALA, and YTE mutations
2338	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL GAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23 with hole, LALAPG, and YTE mutations
2339	YxTEWSS	CH3C motif
2340	TxxExxxxF	CH3C motif
2341	GGACAGGGATCCAGAGTTCC	mulgGI 3' VH PCR primer
2342	AGCTGGGAAGGTGTGCACAC	mu3/4G2 3' VH PCR primer
2343	CAGGGGCCAGTGGATAGAC	mu3/4G3 3' VH PCR primer
2344	GACATTGATGTCTTTGGGGT	muCkappa.1 3' VL PCR primer
2345	TTCACTGCCATCAATCTTCC	muCkappa.2 3' VL PCR primer
2346	EVQLQQSGPELVKPGASVKMSCKASGYTFTDYNMHWVKQSHGKSLEWIG YINPNNGGTTYNQKEKGKATLTVNKSSSTAYMELRSLTSEDSAVYYCATY NNHYFDSWGQGTTLTVSS	7B10.A2 VH amino acid sequence
2347	GYTFTDYNMH	7B10.A2 CDR-H1
2348	YINPNNGGTTYNQKFKG	7B10.A2 CDR-H2
2349	ATYNNHYFDS	7B10.A2 CDR-H3
2350	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYT SNLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYSNLPYTFGGGTK LEIK	7B10.A2 VL amino acid sequence

2351	SASQGISNYLN	7B10.A2 CDR-L1
2352	YTSNLHS	7B10.A2 CDR-L2
2353	QQYSNLPYT	7B10.A2 CDR-L3
2354	QVHLQQSGPEWRPGVSVKISCKGSGYTFTDYGMHWVKQSHAKSLEWIGV ISTYNGNTSYNQKYKGKATVTVDKPSSTAYMELVRLTSEDSAIYYCARDF GYVPFDYWGQGTTLTVSS	51D4 VH amino acid sequence
2355	GYTFTDYGMH	51D4 CDR-H1
2356	VISTYNGNTSYNQKYKG	51D4 CDR-H2
2357	ARDFGYVPFDY	51D4 CDR-H3
2358	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRP GQSPKRLIYLVSYLDSGVPDRFTGSGSGTDFTLKISRVEADDLGV YYCWQGTHFPYTFGGGTKLEIK	51D4 VL amino acid sequence
2359	LVSYLDS	51D4 CDR-L2
2360	GX2X3X4X5X6X7X8X9X10X11, wherein X2 is Y or F; X3 is T, N, or S; X4 is F, L, or I; X5 is T, S, or K; X6 is D, S, or E; X7 is D or absent; X8 is H, Y, or T; X9 is A, N, G, V, W, T, or Y; X10 is M, I, or W; and X is H, Q, or N	CDR-H1 consensus sequence
2361	GYX3X4X5X6X7X8X9X10X11, wherein X3 is T or S; X4 is F, L, or I; X5 is Tor S; X6 is D, S, or E; X7 is D or absent; X8 is H or Y; X9 is A, N, G, V, W, T, or A; X10 is M, I, or W; and X11 is H, Q, or N	CDR-H1 consensus sequence
2362	GX2X3X4X5X6X8X9X10X11, wherein X is Y or F;X3 is T or N; X4 is F, L, or I; X is T, S, or K; X6 is D, S, or E; X8 is H, Y, or T; X is A, N, G, V, W, T, Y, or A; Xi is M or I; and X is H or Q	CDR-H1 consensus sequence
2363	GYTX4X5X6X8X9X10X11, wherein X4 is F or L; X is T or S; X6 is D, S, or E; X_8 is H, Y; X_9 is A, N, G, V, W, T; X10 is M or I; and X11 is H or Q	CDR-H1 consensus sequence
2364	X1X2X3X4X5X6X7X8X9X10YX12X13X14X15X16X17, wherein X1 is D, V, Y, R, G, or T; X2 is I, S, or V; X3 is L, S, N, D, I, or Y; X4 is P, T, or absent; X5 is S, Y, N, T, A, G, or F; X6 is I, S, N, T, or D; X7 is G or D; X8 is G, D, N, R, or S; X9 is R, T, or A; X10 is I, G, S, K, T, N, or R; X12 is G, N, D, or T; X13 is V, Q, E, or P; X14 is K or S; X15 is F, Y or L; X16 is K, R, Q, or is absent; and X17 is G, T, D, S, or is absent	CDR-H2 consensus sequence
2365	X1X2X3X4X5X6X7X8X9X10YX12X13X14X15X16X17, wherein Xi is V, Y, R, G, or T; X2 is I, S, or V; X3 is S, N, D, I, or Y; X4 is P, T, or absent; X5 is Y, N, T, A, G, or F; X6 is S, N, T, or D; X7 is G or D; X8 is G, D, N, R, or S; X9 is T, or A; X10 is I, G, S, K, T, N, or R; X12 is N, D, or T; X13 is Q, E, or P; X14 is K or S; X15 is F, Y or L; X16 is K, R, or Q; and Xi is G, T, D, or S	CDR-H2 consensus sequence
2366	X1X2X3X4X5X6X7X8X9X10YX12X13KX15X16X17, wherein Xi is V, Y, R, G, or T; X2 is I, S, or V; X3 is S, N, D, I, or Y ; X4 is P or T; X5 is Y, N, T, A, or G; X6 is S, N, T, or D; X7 is G or D; X8 is G, D, or N; X9 is T, or A; X10 is G, S, K, T, N, or R; X12 is N, D, or T; X13 is Q, E, or P; X15 is F or Y; X16 is K, R, or Q; and X17 is G, T, or D	CDR-H2 consensus sequence

2367	ARX3X4X5X6X7X8X9X10YAX13DY, wherein X3 is G or N; X4 is D or G; X5 is D or I; X6 is S or T; X7 is Y or T; X8 is R or A; X9 is R or G; X10 is G or Y; and X13 is L or M	CDR-H3 consensus sequence
2368	X1SSX4SLX7X8X9X10X11X12X13X14X15LX17, wherein X1 is R or K; X4 is Q or K; X7 is V or L; X8 is H, D, or Y; X9 is I, N, or S; X10 is S or absent; X11 is D or N; X12 is G or Q; X13 is N, I, or K; X14 is T or S; X15 is Y or F; and X17 is Q, H, Y, N, or A	CDR-L1 consensus sequence
2369	X1ASX4X5IX7X8X9LX11, wherein X1 is R, K, or S; X4 is E or Q; X5 is N, D, or G; X7 is Y or S; X8 is S or N; X9 is N, R, or Y; and X11 is A or N	CDR-L1 consensus sequence
2370	X1X2SX4X5X6S, wherein Xi is K, Q, Y, V, or L; X2 is V, M, or T; X4 is N, K, or Y; X5 is R or L; and X6 is F, A, H, or D	CDR-L2 consensus sequence
2371	X1X2X3X4X5X6X7X8T, wherein Xi is S, W, or Q; X2 is Q or H; X3 is S, T, G, Y, or F; X4 is T, F, W, S; X5 is H, S, G, or N; X6 is V, A, F, Y, T, or L; X7 is P, T, or L; and X8 is Y, F, P, or W	CDR-L3 consensus sequence
2372	QX2X3X4X5X6PX8T, wherein X2 is Q or H; X3 is Y or F; X4 is F, W, or S; X5 is S, G, or N; X6 is Y, T, or L; and X8 is P, Y, or W	CDR-L3 consensus sequence
2373	SGAHNTTVFQGVAGQSLQVSCPYDSMKHWGRRKAWCRQLGEK GPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLGGTLTITLRNLQP HDAGLYQCQSLHGSEADTLRKVLVEVLADPLDHRDAGDLWFPG ESESFEDAHVEHSISRSLLEGEIPFPPTS	Human TREM2 extracellular domain (ECD) amino acid sequence (without signal peptide and His tag)
2374	DLWFPGESES	Human TREM2 peptide
2375	DLWFPGESE	Human TREM2 peptide 9-mer amino acid sequence
2376	DLWFP	Human TREM2 peptide sequence (residues 140-144 of full-length TREM2)
2377	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESWGFVWSTYKTTPPVLDSDGSFFLYSKLTVPKSNWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.18.3.4-1 (CH3C.3.4-1)
2378	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESWGHVWSTYKTTPPVLDSDGSFFLYSKLTVPKSNWQQGYVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.18.3.4-19 (CH3C.3.4-19)
2379	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESLGHVWVEQKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.18.3.2-3 (CH3C.3.2-3)

2380	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVGVKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.18.3.2-14 (CH3C.3.2-14)
2381	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVHTKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.18.3.2-24 (CH3C.3.2-24)
2382	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SWGTVWGTYKTTPPVLDSDGSFFLYSKLTVPKSNWQQGYVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.18.3.4-26 (CH3C.3.4-26)
2383	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SLGHVWVGTKTTPPVLDSDGSFFLYSKLTVPKSTWQQGWVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.18.3.2-17 (CH3C.3.2-17)
2384	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1
2385	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1
2386	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1
2387	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.S413
2388	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWVNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.3.1
2389	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.N390.1

2390	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWVNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.6.1
2391	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21 with knob and LALAPG mutations
2392	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21 with knob, LALAPG, and YTE mutations
2393	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21 with hole and LALAPG mutations
2394	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.21 with hole, LALAPG, and YTE mutations
2395	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob mutation
2396	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob and LALA mutations
2397	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob and LALAPG mutations
2398	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob and YTE mutations
2399	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob, LALA, and YTE mutations

2400	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob, LALAPG, and YTE mutations
2401	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole mutations
2402	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole and LALA mutations
2403	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole and LALAPG mutations
2404	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole and YTE mutations
2405	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole, LALA, and YTE mutations
2406	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL GAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole, LALAPG, and YTE mutations
2407	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob mutation
2408	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob and LALA mutations
2409	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob and LALAPG mutations

2410	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob and YTE mutations
2411	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob, LALA, and YTE mutations
2412	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob, LALAPG, and YTE mutations
2413	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole mutations
2414	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole and LALA mutations
2415	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole and LALAPG mutations
2416	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole and YTE mutations
2417	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole, LALA, and YTE mutations
2418	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL GAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole, LALAPG, and YTE mutations
2419	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob mutation

2420	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob and LALA mutations
2421	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob and LALAPG mutations
2422	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob and YTE mutations
2423	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob, LALA, and YTE mutations
2424	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob, LALAPG, and YTE mutations
2425	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole mutations
2426	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole and LALA mutations
2427	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole and LALAPG mutations
2428	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEAL HNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole and YTE mutations
2429	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHEA LHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole, LALA, and YTE mutations

2430	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL GAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVMHE ALHNHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole, LALAPG, and YTE mutations
2431	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEALH SHYTQKSLSLSPGK	Clone CH3C.35.20.1 M428L and N434S mutations
2432	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob and M428L and N434S mutations
2433	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob, LALA, and M428L and N434S mutations
2434	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.20.1 with knob, LALAPG, and M428L and N434S mutations
2435	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEALH SHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole and M428L and N434S mutations
2436	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole, LALA, and M428L and N434S mutations
2437	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.20.1 with hole, LALAPG, and M428L and N434S mutations
2438	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEALH SHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with M428L and N434S mutations
2439	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob and M428L and N434S mutations

2440	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob, LALA, and M428L and N434S mutations
2441	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with knob, LALAPG, and M428L and N434S mutations
2442	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEALH SHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole and M428L and N434S mutations
2443	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole, LALA, and M428L and N434S mutations
2444	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.20.1.1 with hole, LALAPG, and M428L and N434S mutations
2445	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.21 with M428L and N434S mutations
2446	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.21 with knob and M428L and N434S mutations
2447	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.21 with knob, LALA, and M428L and N434S mutations
2448	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.21 with knob, LALAPG, and M428L and N434S mutations
2449	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVWW ESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.21 with hole and M428L and N434S mutations

2450	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.21 with hole, LALA, and M428L and N434S mutations
2451	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVW WESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.21 with hole, LALAPG, and M428L and N434S mutations
2452	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVLWE SYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with M428L and N434S mutations
2453	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob and M428L and N434S mutations
2454	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob, LALA, and M428L and N434S mutations
2455	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with knob, LALAPG, and M428L and N434S mutations
2456	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLWE SYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole and M428L and N434S mutations
2457	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole, LALA, and M428L and N434S mutations
2458	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVLW ESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.21. 17.2 with hole, LALAPG, and M428L and N434S mutations

2459	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23 with M428L and N434S mutations
2460	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23 with knob and M428L and N434S mutations
2461	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23 with knob, LALA, and M428L and N434S mutations
2462	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23 with knob, LALAPG, and M428L and N434S mutations
2463	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23 with hole and M428L and N434S mutations
2464	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23 with hole, LALA, and M428L and N434S mutations
2465	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23 with hole, LALAPG, and M428L and N434S mutations
2466	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEALH SHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with M428L and N434S mutations
2467	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob and M428L and N434S mutations
2468	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob, LALA, and M428L and N434S mutations

2469	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with knob, LALAPG, and M428L and N434S mutations
2470	IAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole and M428L and N434S mutations
2471	IAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole, LALA, and M428L and N434S mutations
2472	IAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23. 1.1 with hole, LALAPG, and M428L and N434S mutations
2473	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.2 with M428L and N434S mutations
2474	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob and M428L and N434S mutations
2475	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob, LALA, and M428L and N434S mutations
2476	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.2 with knob, LALAPG, and M428L and N434S mutations
2477	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole and M428L and N434S mutations
2478	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole, LALA, and M428L and N434S mutations

2479	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.2 with hole, LALAPG, and M428L and N434S mutations
2480	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with M428L and N434S mutations
2481	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob and M428L and N434S mutations
2482	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob, LALA, and M428L and N434S mutations
2483	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with knob, LALAPG, and M428L and N434S mutations
2484	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole and M428L and N434S mutations
2485	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole, LALA, and M428L and N434S mutations
2486	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.2.1 with hole, LALAPG, and M428L and N434S mutations
2487	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.3 with M428L and N434S mutations
2488	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob and M428L and N434S mutations

2489	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob, LALA, and M428L and N434S mutations
2490	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.3 with knob, LALAPG, and M428L and N434S mutations
2491	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole and M428L and N434S mutations
2492	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole, LALA, and M428L and N434S mutations
2493	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQGFVFSCSVLHEA LHSHYTQKSLSLSPGK	Clone CH3C.35.23.3 with hole, LALAPG, and M428L and N434S mutations
2494	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.4 with M428L and N434S mutations
2495	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob and M428L and N434S mutations
2496	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob, LALA, and M428L and N434S mutations
2497	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQGFVFSCSVLHE ALHSHYTQKSLSLSPGK	Clone CH3C.35.23.4 with knob, LALAPG, and M428L and N434S mutations
2498	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE SYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole and M428L and N434S mutations

2499	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole, LALA, and M428L and N434S mutations
2500	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALG APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQGFVFSCSVLHEAL HSHYTQKSLSLSPGK	Clone CH3C.35.23.4 with hole, LALAPG, and M428L and N434S mutations
2501	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVLHEA LHSHYTQKSLSLSPGK	Fc sequence with hole and M428L and N434S mutations
2502	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVLHEA LHSHYTQKSLSLSPGK	Fc sequence with hole, LALA, and M428L and N434S mutations
2503	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHE ALHSHYTQKSLSLSPGK	Fc sequence with knob and M428L and N434S mutations
2504	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHE ALHSHYTQKSLSLSPGK	Fc sequence with knob, LALA, and M428L and N434S mutations
2505	MPALLSLVSLLSVLLMGCVAETGGSGHHHHHHHSGTHNTTVFQGVAGQSL QVSCPYDSMKHWGRRKAWCRQLGEKGPCQRWSTHNLWLLSFLRRWNGS TAITDDTLGGTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADP LDHRDAGDLWFPGESESFEDAHVEHSISRSLLEGEIPFPPTSAS	SS2_NHis_TREM2

[00253] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in in the above tables as well as specific combinations thereof and other embodiments of the anti-TREM2 antibody described in the '841 application and herein may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

H. PCT Patent Application Publication No. WO2019/118513A1

[00254] In some embodiments, the TREM2 agonist is an antibody or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. WO2019/118513A1 ("the '513 application"), which is incorporated by reference herein, in its entirety.

[00255] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3, and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 disclosed in the '513 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '513 application specification.

[00256] In some embodiments, the antibody comprises a CDR-H1 comprising the sequence set forth in SEQ ID NO: 2514, a CDR-H2 comprising the sequence set forth in SEQ ID NO:2515, a CDR-H3 comprising the sequence set forth in SEQ ID NO:11, a CDR-L1 comprising the sequence set forth in SEQ ID NO: 2517, a CDR-L2 comprising the sequence set forth in SEQ ID NO: 2518, and a CDR-L3 comprising the sequence set forth in SEQ ID NO: 2519.

[00257] In some embodiments, the antibody is afucosylated and comprises the VH sequence shown in SEQ ID NO: 2506; the VL sequence shown in SEQ ID NO: 2507; and an active human IgG1 Fc region.

[00258] In some embodiments, the antibody comprises all 3 heavy chain CDRs of the sequence shown in SEQ ID NO:2512 and all 3 light chain CDRs of the sequence shown in SEQ ID NO:2513.

[00259] In some embodiments, the antibody comprises an A to T substitution at position 97 of the sequence shown in SEQ ID NO:2512; and a K to R substitution at position 98 of the sequence shown in SEQ ID NO:2512.

[00260] In some embodiments, the antibody comprises the VH sequence shown in SEQ ID NO: 2506, 2508, or 2510.

[00261] In some embodiments, the antibody comprises the VH sequence shown in SEQ ID NO: 2506, 2508, or 2510 and the VL sequence shown in SEQ ID NO: 2507, 2509, or 2511. In some embodiments, the antibody comprises the VH sequence shown in SEQ ID NO: 2506.

[00262] In some embodiments, the antibody comprises the VH sequence shown in SEQ ID NO: 2506 and the VL sequence shown in SEQ ID NO: 2507.

[00263] In some embodiments, the antibody is the 37012 antibody (see Table 16A).

[00264] In some embodiments, the antibody is an antibody having a VL, VH, full heavy chain sequence or full light chain sequence disclosed in Table 1A or a CDR sequence as disclosed in Table 1B of PCT Patent Application Publication No. WO2019/118513A1, which are reproduced below as **Tables 16A** and **16B** respectively.

Table 16A

SEQ ID NO:	Name	Sequence
2506	37012 VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSLTNS GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTREWAGSGYFDY WGQGTLVTVSS
2507	37012 VL	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIYYTSNR FTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFGQGTKLEIK
2508	37013VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSLTNS GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTREWAGSGYFDY WGQGTLVTVSS
2509	37013VL	DIQMTQSPSSLSASVGDRVTMTCKASQNVGNNLAWYQQKPGKAPKLLLYYTSNR FTGVPSRFSGSGSGTDFTLTISSVQPEDFATYYCQRIYNSPWTFGQGTKLELK
2510	37014VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVASLTNS GGSTYYADSVKGRFTLSRDNSKNTLYLQMNSLRAEDTAVYYCTREWAGSGYFDY WGQGTLVTVSS
2511	37014VL	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIYYTSNR FTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFGQGTKLEIK
2512	37017VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSLTNS GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEWAGSGYFDY WGQGTLVTVSS
2513	37017VL	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIYYTSNR FTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFGQGTKLEIK
2529	Full 37012_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSLTNS GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTREWAGSGYFDY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
2530	Full 37012 L	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIYYTSNR FTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

2531	Full 37013_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSLTNS GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTREWAGSGYFDY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
2532	Full 37013 L	DIQMTQSPSSLSASVGDRVTMTCKASQNVGNNLAWYQQKPGKAPKLLLYYTSNR FTGVPSRFSGSGSGTDFTLTISSVQPEDFATYYCQRIYNSPWTFGQGTKLELKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
2533	Full 37014_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVASLTNS GGSTYYADSVKGRFTLSRDNSKNTLYLQMNSLRAEDTAVYYCTREWAGSGYFDY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
2534	Full 37014 L	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIYYTSNR FTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
2535	Full 37017_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSLTNS GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEWAGSGYFDY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
2536	Full 37017_L	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIYYTSNRFT GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Table 16B – CDR's of humanized antibodies

CDR	Sequence	SEQ ID NO
CDR-H1	FSNYYMA	2514
CDR-H2	SLTNSGGSTY	2515
CDR-H3	EWAGSGY	2516
CDR-L1	NVGNNLA	2517
CDR-L2	YTSNRFT	2518
CDR-L3	RIYNSPW	2519

[00265] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in in the above tables as well as specific combinations thereof and other embodiments of the anti-TREM2 antibody described in the '513 application and herein may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

I. PCT Patent Application Publication No. WO2020/055975A1

[00266] In some embodiments, the TREM2 agonist is an antibody or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. WO2020/055975A1 ("the '975 application"), which is incorporated by reference herein, in its entirety.

[00267] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3, and a heavy chain variable domain comprising a CDRH1, CDRH2, and CDRH3 disclosed in the '975 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '975 application specification.

[00268] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 derived from SEQ ID NO: 2539, an L2 derived from SEQ ID NO: 2539, an L3 derived from of SEQ ID NO: 2539, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 derived from SEQ ID NO: 2540, an H2 derived from SEQ ID NO: 2540, an H3 derived from SEQ ID NO: 2540, or any combination thereof.

[00269] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 of SEQ ID NO: 2541, an L2 comprising the amino acid sequence IVS, an L3 of SEQ ID NO: 2542, or any combination thereof; and/or (b) a heavy chain variable region

comprising an H1 comprising SEQ ID NO: 2543, an H2 comprising SEQ ID NO: 2544, an H3 comprising SEQ ID NO: 2545, or any combination thereof.

[00270] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 derived from SEQ ID NO: 2546, an L2 derived from SEQ ID NO: 2546, an L3 derived from of SEQ ID NO: 2546, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 derived from SEQ ID NO: 2547, an H2 derived from SEQ ID NO: 2547, an H3 derived from of SEQ ID NO: 2547, or any combination thereof.

[00271] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 of SEQ ID NO: 2548, an L2 comprising the amino acid sequence KVS, an L3 of SEQ ID NO: 2549, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 comprising SEQ ID NO: 2550, an H2 comprising SEQ ID NO: 2551, an H3 comprising SEQ ID NO: 2552, or any combination thereof.

[00272] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 derived from SEQ ID NO: 2553, an L2 derived from SEQ ID NO: 2553, an L3 derived from of SEQ ID NO: 2553, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 derived from SEQ ID NO: 2554, an H2 derived from SEQ ID NO: 2554, an H3 derived from of SEQ ID NO: 2554, or any combination thereof.

[00273] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 of SEQ ID NO: 2555, an L2 comprising the amino acid sequence KVS, an L3 of SEQ ID NO: 2556, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 comprising SEQ ID NO: 2557, an H2 comprising SEQ ID NO: 2558, an H3 comprising SEQ ID NO: 2559, or any combination thereof.

[00274] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 derived from SEQ ID NO: 2560, an L2 derived from SEQ ID NO: 2560, an L3 derived from of SEQ ID NO: 2560, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 derived from SEQ ID NO: 2561, an H2 derived from SEQ ID NO: 2561, an H3 derived from of SEQ ID NO: 2561, or any combination thereof.

[00275] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 of SEQ ID NO: 2562, an L2 comprising the amino acid sequence KVS, an L3

of SEQ ID NO: 2563, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 comprising SEQ ID NO: 2564, an H2 comprising SEQ ID NO: 2565, an H3 comprising SEQ ID NO: 2566, or any combination thereof.

[00276] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 derived from SEQ ID NO: 2567, an L2 derived from SEQ ID NO: 2567, an L3 derived from of SEQ ID NO: 2567, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 derived from SEQ ID NO: 2568, an H2 derived from SEQ ID NO: 2568, an H3 derived from of SEQ ID NO: 2568, or any combination thereof. Compositions comprising the antibody, including but not limited to pharmaceutical compositions, are contemplated herein. In certain embodiments the antibody is a humanized antibody.

[00277] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 of SEQ ID NO: 2569, an L2 comprising the amino acid sequence KVS, an L3 of SEQ ID NO: 2570, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 comprising SEQ ID NO: 2571, an H2 comprising SEQ ID NO: 2572, an H3 comprising SEQ ID NO: 2573, or any combination thereof.

[00278] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 derived from SEQ ID NO: 2574, an L2 derived from SEQ ID NO: 2574, an L3 derived from of SEQ ID NO: 2574, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 derived from SEQ ID NO: 2575, an H2 derived from SEQ ID NO: 2575, an H3 derived from of SEQ ID NO: 2575, or any combination thereof.

[00279] In some embodiments, the antibody comprises (a) a light chain variable region comprising an L1 of SEQ ID NO: 2576, an L2 comprising the amino acid sequence WAS, an L3 of SEQ ID NO: 2577, or any combination thereof; and/or (b) a heavy chain variable region comprising an H1 comprising SEQ ID NO: 2578, an H2 comprising SEQ ID NO: 2579, an H3 comprising SEQ ID NO: 2580, or any combination thereof.

[00280] In some embodiments, the antibody is HJ23.4, HJ23.7, HJ23.8, HJ23.9, HJ23.10, or HJ23.13. In some embodiments, the antibody is a humanized antibody derived from HJ23.4, HJ23.7, HJ23.8, HJ23.9, HJ23.10, or HJ23.13. The accession number for the hybridoma that produced antibodies HJ23.4, HJ23.7, HJ23.8, HJ23.9, HJ23.10, and HJ23.13, and their respective light chain variable and heavy chain variable regions are noted below:

Table 17A

Antibody (ATCC # of the hybridoma)	Light chain variable region	Heavy chain variable region
HJ23.4 (PTA-125168)	SEQ ID NO: 2539	SEQ ID NO: 2540
HJ23.7 (PTA-125169)	SEQ ID NO: 2546	SEQ ID NO: 2547
HJ23.8 (PTA-125170)	SEQ ID NO: 2552	SEQ ID NO: 2553
HJ23.9 (PTA-125171)	SEQ ID NO: 2561	SEQ ID NO: 2562
HJ23.10 (PTA-125172)	SEQ ID NO: 2567	SEQ ID NO: 2568
HJ23.13 (PTA-125173)	SEQ ID NO: 2574	SEQ ID NO: 2575

[00281] In some embodiments, the antibody is an antibody disclosed in Tables A and B or the summary table appended to Example 2 of PCT Patent Application Publication No. WO2020/055975A1, reproduced below as **Tables 17B**, **17C** and **17D**.

Table 17B

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
1	SEQ ID NO: 2541					
2	SEQ ID NO: 2541	IVS				
3	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542			
4		IVS				
5		IVS	SEQ ID NO: 2542			
6			SEQ ID NO: 2542			
7	SEQ ID NO: 2541		SEQ ID NO: 2542			
8				SEQ ID NO: 2543		
9				SEQ ID NO: 2543	SEQ ID NO: 2544	
10				SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
11					SEQ ID NO: 2544	
12					SEQ ID NO: 2544	SEQ ID NO: 2545
13						SEQ ID NO: 2545
14				SEQ ID NO: 2543		SEQ ID NO: 2545
15	SEQ ID NO: 2541			SEQ ID NO: 2543		
16	SEQ ID NO: 2541			SEQ ID NO: 2543	SEQ ID NO: 2544	
17	SEQ ID NO: 2541			SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
18	SEQ ID NO: 2541				SEQ ID NO: 2544	
19	SEQ ID NO: 2541				SEQ ID NO: 2544	SEQ ID NO: 2545

20	SEQ ID NO: 2541					SEQ ID NO: 2545
21	SEQ ID NO: 2541			SEQ ID NO: 2543		SEQ ID NO: 2545
22	SEQ ID NO: 2541	IVS		SEQ ID NO: 2543		
23	SEQ ID NO: 2541	IVS		SEQ ID NO: 2543	SEQ ID NO: 2544	
24	SEQ ID NO: 2541	IVS		SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
25	SEQ ID NO: 2541	IVS			SEQ ID NO: 2544	
26	SEQ ID NO: 2541	IVS			SEQ ID NO: 2544	SEQ ID NO: 2545
27	SEQ ID NO: 2541	IVS				SEQ ID NO: 2545
28	SEQ ID NO: 2541	IVS		SEQ ID NO: 2543		SEQ ID NO: 2545
29	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542	SEQ ID NO: 2543		
30	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	
31	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
32	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542		SEQ ID NO: 2544	
33	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542		SEQ ID NO: 2544	SEQ ID NO: 2545
34	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542	SEQ ID NO: 2543		SEQ ID NO: 2545
35	SEQ ID NO: 2541	IVS	SEQ ID NO: 2542			SEQ ID NO: 2545
36		IVS		SEQ ID NO: 2543		
37		IVS		SEQ ID NO: 2543	SEQ ID NO: 2544	
38		IVS		SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
39		IVS			SEQ ID NO: 2544	
40		IVS			SEQ ID NO: 2544	SEQ ID NO: 2545
41		IVS				SEQ ID NO: 2545
42		IVS		SEQ ID NO: 2543		SEQ ID NO: 2545
43		IVS	SEQ ID NO: 2542	SEQ ID NO: 2543		
44		IVS	SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	
45		IVS	SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
46		IVS	SEQ ID NO: 2542		SEQ ID NO: 2544	
47		IVS	SEQ ID NO: 2542		SEQ ID NO: 2544	SEQ ID NO: 2545
48		IVS	SEQ ID NO: 2542			SEQ ID NO: 2545
49		IVS	SEQ ID NO: 2542	SEQ ID NO: 2543		SEQ ID NO: 2545
50			SEQ ID NO: 2542	SEQ ID NO: 2543		
51			SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	
52			SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
53			SEQ ID NO: 2542		SEQ ID NO: 2544	
54			SEQ ID NO: 2542		SEQ ID NO: 2544	SEQ ID NO: 2545
55			SEQ ID NO: 2542			SEQ ID NO: 2545
56			SEQ ID NO: 2542	SEQ ID NO: 2543		SEQ ID NO: 2545
57	SEQ ID NO: 2541		SEQ ID NO: 2542	SEQ ID NO: 2543		
58	SEQ ID NO: 2541		SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	
59	SEQ ID NO: 2541		SEQ ID NO: 2542	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
60	SEQ ID NO: 2541		SEQ ID NO: 2542		SEQ ID NO: 2544	
61	SEQ ID NO: 2541		SEQ ID NO: 2542		SEQ ID NO: 2544	SEQ ID NO: 2545
62	SEQ ID NO: 2541		SEQ ID NO: 2542			SEQ ID NO: 2545

63	SEQ ID NO: 2541		SEQ ID NO: 2542	SEQ ID NO: 2543		SEQ ID NO: 2545
64	SEQ ID NO: 2548					
65	SEQ ID NO: 2548	KVS				
66	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549			
67		KVS				
68		KVS	SEQ ID NO: 2549			
69			SEQ ID NO: 2549			
70	SEQ ID NO: 2548		SEQ ID NO: 2549			
71				SEQ ID NO: 2550		
72				SEQ ID NO: 2550	SEQ ID NO: 2551	
73				SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
74					SEQ ID NO: 2551	
75					SEQ ID NO: 2551	SEQ ID NO: 2552
76						SEQ ID NO: 2552
77				SEQ ID NO: 2550		SEQ ID NO: 2552
78	SEQ ID NO: 2548			SEQ ID NO: 2550		
79	SEQ ID NO: 2548			SEQ ID NO: 2550	SEQ ID NO: 2551	
80	SEQ ID NO: 2548			SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
81	SEQ ID NO: 2548				SEQ ID NO: 2551	
82	SEQ ID NO: 2548				SEQ ID NO: 2551	SEQ ID NO: 2552
83	SEQ ID NO: 2548					SEQ ID NO: 2552
84	SEQ ID NO: 2548			SEQ ID NO: 2550		SEQ ID NO: 2552
85	SEQ ID NO: 2548	KVS		SEQ ID NO: 2550		
86	SEQ ID NO: 2548	KVS		SEQ ID NO: 2550	SEQ ID NO: 2551	
87	SEQ ID NO: 2548	KVS		SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
88	SEQ ID NO: 2548	KVS			SEQ ID NO: 2551	
89	SEQ ID NO: 2548	KVS			SEQ ID NO: 2551	SEQ ID NO: 2552
90	SEQ ID NO: 2548	KVS				SEQ ID NO: 2552
91	SEQ ID NO: 2548	KVS		SEQ ID NO: 2550		SEQ ID NO: 2552
92	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549	SEQ ID NO: 2550		
93	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	
94	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
95	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549		SEQ ID NO: 2551	
96	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549		SEQ ID NO: 2551	SEQ ID NO: 2552
97	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549			SEQ ID NO: 2552
98	SEQ ID NO: 2548	KVS	SEQ ID NO: 2549	SEQ ID NO: 2550		SEQ ID NO: 2552
99		KVS		SEQ ID NO: 2550		
100		KVS		SEQ ID NO: 2550	SEQ ID NO: 2551	
101		KVS		SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
102		KVS			SEQ ID NO: 2551	
103		KVS			SEQ ID NO: 2551	SEQ ID NO: 2552
104		KVS				SEQ ID NO: 2552
105		KVS		SEQ ID NO: 2550		SEQ ID NO: 2552

106		KVS	SEQ ID NO: 2549	SEQ ID NO: 2550		
107		KVS	SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	
108		KVS	SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
109		KVS	SEQ ID NO: 2549		SEQ ID NO: 2551	
110		KVS	SEQ ID NO: 2549		SEQ ID NO: 2551	SEQ ID NO: 2552
111		KVS	SEQ ID NO: 2549			SEQ ID NO: 2552
112		KVS	SEQ ID NO: 2549	SEQ ID NO: 2550		SEQ ID NO: 2552
113			SEQ ID NO: 2549	SEQ ID NO: 2550		
114			SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	
115			SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
116			SEQ ID NO: 2549		SEQ ID NO: 2551	
117			SEQ ID NO: 2549		SEQ ID NO: 2551	SEQ ID NO: 2552
118			SEQ ID NO: 2549			SEQ ID NO: 2552
119			SEQ ID NO: 2549	SEQ ID NO: 2550		SEQ ID NO: 2552
120	SEQ ID NO: 2548		SEQ ID NO: 2549	SEQ ID NO: 2550		
121	SEQ ID NO: 2548		SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	
122	SEQ ID NO: 2548		SEQ ID NO: 2549	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
123	SEQ ID NO: 2548		SEQ ID NO: 2549		SEQ ID NO: 2551	
124	SEQ ID NO: 2548		SEQ ID NO: 2549		SEQ ID NO: 2551	SEQ ID NO: 2552
125	SEQ ID NO: 2548		SEQ ID NO: 2549			SEQ ID NO: 2552
126	SEQ ID NO: 2548		SEQ ID NO: 2549	SEQ ID NO: 2550		SEQ ID NO: 2552
127	SEQ ID NO: 2555					
128	SEQ ID NO: 2555	KVS				
129	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556			
130		KVS				
131		KVS	SEQ ID NO: 2556			
132			SEQ ID NO: 2556			
133	SEQ ID NO: 2555		SEQ ID NO: 2556			
134				SEQ ID NO: 2557		
135				SEQ ID NO: 2557	SEQ ID NO: 2558	
136				SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
137					SEQ ID NO: 2558	
138					SEQ ID NO: 2558	SEQ ID NO: 2559
139						SEQ ID NO: 2559
140				SEQ ID NO: 2557		SEQ ID NO: 2559
141	SEQ ID NO: 2555			SEQ ID NO: 2557		
142	SEQ ID NO: 2555			SEQ ID NO: 2557	SEQ ID NO: 2558	
143	SEQ ID NO: 2555			SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
144	SEQ ID NO: 2555				SEQ ID NO: 2558	
145	SEQ ID NO: 2555				SEQ ID NO: 2558	SEQ ID NO: 2559
146	SEQ ID NO: 2555					SEQ ID NO: 2559
147	SEQ ID NO: 2555			SEQ ID NO: 2557		SEQ ID NO: 2559
148	SEQ ID NO: 2555	KVS		SEQ ID NO: 2557		

149	SEQ ID NO: 2555	KVS		SEQ ID NO: 2557	SEQ ID NO: 2558	
150	SEQ ID NO: 2555	KVS		SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
151	SEQ ID NO: 2555	KVS			SEQ ID NO: 2558	
152	SEQ ID NO: 2555	KVS			SEQ ID NO: 2558	SEQ ID NO: 2559
153	SEQ ID NO: 2555	KVS				SEQ ID NO: 2559
154	SEQ ID NO: 2555	KVS		SEQ ID NO: 2557		SEQ ID NO: 2559
155	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556	SEQ ID NO: 2557		
156	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	
157	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
158	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556		SEQ ID NO: 2558	
159	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556		SEQ ID NO: 2558	SEQ ID NO: 2559
160	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556	SEQ ID NO: 2557		SEQ ID NO: 2559
161	SEQ ID NO: 2555	KVS	SEQ ID NO: 2556			SEQ ID NO: 2559
162		KVS		SEQ ID NO: 2557		
163		KVS		SEQ ID NO: 2557	SEQ ID NO: 2558	
164		KVS		SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
165		KVS			SEQ ID NO: 2558	
166		KVS			SEQ ID NO: 2558	SEQ ID NO: 2559
167		KVS				SEQ ID NO: 2559
168		KVS		SEQ ID NO: 2557		SEQ ID NO: 2559
169		KVS	SEQ ID NO: 2556	SEQ ID NO: 2557		
170		KVS	SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	
171		KVS	SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
172		KVS	SEQ ID NO: 2556		SEQ ID NO: 2558	
173		KVS	SEQ ID NO: 2556		SEQ ID NO: 2558	SEQ ID NO: 2559
174		KVS	SEQ ID NO: 2556			SEQ ID NO: 2559
175		KVS	SEQ ID NO: 2556	SEQ ID NO: 2557		SEQ ID NO: 2559
176			SEQ ID NO: 2556	SEQ ID NO: 2557		
177			SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	
178			SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
179			SEQ ID NO: 2556		SEQ ID NO: 2558	
180			SEQ ID NO: 2556		SEQ ID NO: 2558	SEQ ID NO: 2559
181			SEQ ID NO: 2556			SEQ ID NO: 2559
182			SEQ ID NO: 2556	SEQ ID NO: 2557		SEQ ID NO: 2559
183	SEQ ID NO: 2555		SEQ ID NO: 2556	SEQ ID NO: 2557		
184	SEQ ID NO: 2555		SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	
185	SEQ ID NO: 2555		SEQ ID NO: 2556	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
186	SEQ ID NO: 2555		SEQ ID NO: 2556		SEQ ID NO: 2558	
187	SEQ ID NO: 2555		SEQ ID NO: 2556		SEQ ID NO: 2558	SEQ ID NO: 2559
188	SEQ ID NO: 2555		SEQ ID NO: 2556			SEQ ID NO: 2559
189	SEQ ID NO: 2555		SEQ ID NO: 2556	SEQ ID NO: 2557		SEQ ID NO: 2559
190	SEQ ID NO: 2562					
191	SEQ ID NO: 2562	KVS				

192	SEQ ID NO: 2562	KVS	SEQ ID NO: 25			
193		KVS				
194		KVS	SEQ ID NO: 25			
195			SEQ ID NO: 25			
196	SEQ ID NO: 2562		SEQ ID NO: 25			
197				SEQ ID NO: 2564		
198				SEQ ID NO: 2564	SEQ ID NO: 2565	
199				SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
200					SEQ ID NO: 2565	
201					SEQ ID NO: 2565	SEQ ID NO: 2566
202						SEQ ID NO: 2566
203				SEQ ID NO: 2564		SEQ ID NO: 2566
204	SEQ ID NO: 2562			SEQ ID NO: 2564		
205	SEQ ID NO: 2562			SEQ ID NO: 2564	SEQ ID NO: 2565	
206	SEQ ID NO: 2562			SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
207	SEQ ID NO: 2562				SEQ ID NO: 2565	
208	SEQ ID NO: 2562				SEQ ID NO: 2565	SEQ ID NO: 2566
209	SEQ ID NO: 2562					SEQ ID NO: 2566
210	SEQ ID NO: 2562			SEQ ID NO: 2564		SEQ ID NO: 2566
211	SEQ ID NO: 2562	KVS		SEQ ID NO: 2564		
212	SEQ ID NO: 2562	KVS		SEQ ID NO: 2564	SEQ ID NO: 2565	
213	SEQ ID NO: 2562	KVS		SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
214	SEQ ID NO: 2562	KVS			SEQ ID NO: 2565	
215	SEQ ID NO: 2562	KVS			SEQ ID NO: 2565	SEQ ID NO: 2566
216	SEQ ID NO: 2562	KVS				SEQ ID NO: 2566
217	SEQ ID NO: 2562	KVS		SEQ ID NO: 2564		SEQ ID NO: 2566
218	SEQ ID NO: 2562	KVS	SEQ ID NO: 25	SEQ ID NO: 2564		
219	SEQ ID NO: 2562	KVS	SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	
220	SEQ ID NO: 2562	KVS	SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
221	SEQ ID NO: 2562	KVS	SEQ ID NO: 25		SEQ ID NO: 2565	
222	SEQ ID NO: 2562	KVS	SEQ ID NO: 25		SEQ ID NO: 2565	SEQ ID NO: 2566
223	SEQ ID NO: 2562	KVS	SEQ ID NO: 25	SEQ ID NO: 2564		SEQ ID NO: 2566
224	SEQ ID NO: 2562	KVS	SEQ ID NO: 25			SEQ ID NO: 2566
225		KVS		SEQ ID NO: 2564		
226		KVS		SEQ ID NO: 2564	SEQ ID NO: 2565	
227		KVS		SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
228		KVS			SEQ ID NO: 2565	
229		KVS			SEQ ID NO: 2565	SEQ ID NO: 2566
230		KVS				SEQ ID NO: 2566
231		KVS		SEQ ID NO: 2564		SEQ ID NO: 2566
232		KVS	SEQ ID NO: 25	SEQ ID NO: 2564		
233		KVS	SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	
234		KVS	SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566

235		KVS	SEQ ID NO: 25		SEQ ID NO: 2565	
236		KVS	SEQ ID NO: 25		SEQ ID NO: 2565	SEQ ID NO: 2566
237		KVS	SEQ ID NO: 25			SEQ ID NO: 2566
238		KVS	SEQ ID NO: 25	SEQ ID NO: 2564		SEQ ID NO: 2566
239			SEQ ID NO: 25	SEQ ID NO: 2564		
240			SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	
241			SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
242			SEQ ID NO: 25		SEQ ID NO: 2565	
243			SEQ ID NO: 25		SEQ ID NO: 2565	SEQ ID NO: 2566
244			SEQ ID NO: 25			SEQ ID NO: 2566
245			SEQ ID NO: 25	SEQ ID NO: 2564		SEQ ID NO: 2566
246	SEQ ID NO: 2562		SEQ ID NO: 25	SEQ ID NO: 2564		
247	SEQ ID NO: 2562		SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	
248	SEQ ID NO: 2562		SEQ ID NO: 25	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
249	SEQ ID NO: 2562		SEQ ID NO: 25		SEQ ID NO: 2565	
250	SEQ ID NO: 2562		SEQ ID NO: 25		SEQ ID NO: 2565	SEQ ID NO: 2566
251	SEQ ID NO: 2562		SEQ ID NO: 25			SEQ ID NO: 2566
252	SEQ ID NO: 2562		SEQ ID NO: 25	SEQ ID NO: 2564		SEQ ID NO: 2566
253	SEQ ID NO: 2569					
254	SEQ ID NO: 2569	KVS				
255	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570			
256		KVS				
257		KVS	SEQ ID NO: 2570			
258			SEQ ID NO: 2570			
259	SEQ ID NO: 2569		SEQ ID NO: 2570			
260				SEQ ID NO: 2571		
261				SEQ ID NO: 2571	SEQ ID NO: 2572	
262				SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
263					SEQ ID NO: 2572	
264					SEQ ID NO: 2572	SEQ ID NO: 2573
265						SEQ ID NO: 2573
266				SEQ ID NO: 2571		SEQ ID NO: 2573
267	SEQ ID NO: 2569			SEQ ID NO: 2571		
268	SEQ ID NO: 2569			SEQ ID NO: 2571	SEQ ID NO: 2572	
269	SEQ ID NO: 2569			SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
270	SEQ ID NO: 2569				SEQ ID NO: 2572	
271	SEQ ID NO: 2569				SEQ ID NO: 2572	SEQ ID NO: 2573
272	SEQ ID NO: 2569					SEQ ID NO: 2573
273	SEQ ID NO: 2569			SEQ ID NO: 2571		SEQ ID NO: 2573
274	SEQ ID NO: 2569	KVS		SEQ ID NO: 2571		
275	SEQ ID NO: 2569	KVS		SEQ ID NO: 2571	SEQ ID NO: 2572	
276	SEQ ID NO: 2569	KVS		SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
277	SEQ ID NO: 2569	KVS			SEQ ID NO: 2572	

278	SEQ ID NO: 2569	KVS			SEQ ID NO: 2572	SEQ ID NO: 2573
279	SEQ ID NO: 2569	KVS				SEQ ID NO: 2573
280	SEQ ID NO: 2569	KVS		SEQ ID NO: 2571		SEQ ID NO: 2573
281	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570	SEQ ID NO: 2571		
282	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	
283	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
284	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570		SEQ ID NO: 2572	
285	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570		SEQ ID NO: 2572	SEQ ID NO: 2573
286	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570	SEQ ID NO: 2571		SEQ ID NO: 2573
287	SEQ ID NO: 2569	KVS	SEQ ID NO: 2570			SEQ ID NO: 2573
288		KVS		SEQ ID NO: 2571		
289		KVS		SEQ ID NO: 2571	SEQ ID NO: 2572	
290		KVS		SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
291		KVS			SEQ ID NO: 2572	
292		KVS			SEQ ID NO: 2572	SEQ ID NO: 2573
293		KVS				SEQ ID NO: 2573
294		KVS		SEQ ID NO: 2571		SEQ ID NO: 2573
295		KVS	SEQ ID NO: 2570	SEQ ID NO: 2571		
296		KVS	SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	
297		KVS	SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
298		KVS	SEQ ID NO: 2570		SEQ ID NO: 2572	
299		KVS	SEQ ID NO: 2570		SEQ ID NO: 2572	SEQ ID NO: 2573
300		KVS	SEQ ID NO: 2570			SEQ ID NO: 2573
301		KVS	SEQ ID NO: 2570	SEQ ID NO: 2571		SEQ ID NO: 2573
302			SEQ ID NO: 2570	SEQ ID NO: 2571		
303			SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	
304			SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
305			SEQ ID NO: 2570		SEQ ID NO: 2572	
306			SEQ ID NO: 2570		SEQ ID NO: 2572	SEQ ID NO: 2573
307			SEQ ID NO: 2570			SEQ ID NO: 2573
308			SEQ ID NO: 2570	SEQ ID NO: 2571		SEQ ID NO: 2573
309	SEQ ID NO: 2569		SEQ ID NO: 2570	SEQ ID NO: 2571		
310	SEQ ID NO: 2569		SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	
311	SEQ ID NO: 2569		SEQ ID NO: 2570	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
312	SEQ ID NO: 2569		SEQ ID NO: 2570		SEQ ID NO: 2572	
313	SEQ ID NO: 2569		SEQ ID NO: 2570		SEQ ID NO: 2572	SEQ ID NO: 2573
314	SEQ ID NO: 2569		SEQ ID NO: 2570			SEQ ID NO: 2573
315	SEQ ID NO: 2569		SEQ ID NO: 2570	SEQ ID NO: 2571		SEQ ID NO: 2573
316	SEQ ID NO: 2576					
317	SEQ ID NO: 2576	WAS				
318	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577			
319		WAS				
320		WAS	SEQ ID NO: 2577			

321			SEQ ID NO: 2577			
322	SEQ ID NO: 2576		SEQ ID NO: 2577			
323				SEQ ID NO: 2578		
324				SEQ ID NO: 2578	SEQ ID NO: 2579	
325				SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
326					SEQ ID NO: 2579	
327					SEQ ID NO: 2579	SEQ ID NO: 2580
328						SEQ ID NO: 2580
329				SEQ ID NO: 2578		SEQ ID NO: 2580
330	SEQ ID NO: 2576			SEQ ID NO: 2578		
331	SEQ ID NO: 2576			SEQ ID NO: 2578	SEQ ID NO: 2579	
332	SEQ ID NO: 2576			SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
333	SEQ ID NO: 2576				SEQ ID NO: 2579	
334	SEQ ID NO: 2576				SEQ ID NO: 2579	SEQ ID NO: 2580
335	SEQ ID NO: 2576					SEQ ID NO: 2580
336	SEQ ID NO: 2576			SEQ ID NO: 2578		SEQ ID NO: 2580
337	SEQ ID NO: 2576	WAS		SEQ ID NO: 2578		
338	SEQ ID NO: 2576	WAS		SEQ ID NO: 2578	SEQ ID NO: 2579	
339	SEQ ID NO: 2576	WAS		SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
340	SEQ ID NO: 2576	WAS			SEQ ID NO: 2579	
341	SEQ ID NO: 2576	WAS			SEQ ID NO: 2579	SEQ ID NO: 2580
342	SEQ ID NO: 2576	WAS				SEQ ID NO: 2580
343	SEQ ID NO: 2576	WAS		SEQ ID NO: 2578		SEQ ID NO: 2580
344	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577	SEQ ID NO: 2578		
345	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	
346	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
347	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577		SEQ ID NO: 2579	
348	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577		SEQ ID NO: 2579	SEQ ID NO: 2580
349	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577	SEQ ID NO: 2578		SEQ ID NO: 2580
350	SEQ ID NO: 2576	WAS	SEQ ID NO: 2577			SEQ ID NO: 2580
351		WAS		SEQ ID NO: 2578		
352		WAS		SEQ ID NO: 2578	SEQ ID NO: 2579	
353		WAS		SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
354		WAS			SEQ ID NO: 2579	
355		WAS			SEQ ID NO: 2579	SEQ ID NO: 2580
356		WAS				SEQ ID NO: 2580
357		WAS		SEQ ID NO: 2578		SEQ ID NO: 2580
358		WAS	SEQ ID NO: 2577	SEQ ID NO: 2578		
359		WAS	SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	
360		WAS	SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
361		WAS	SEQ ID NO: 2577		SEQ ID NO: 2579	
362		WAS	SEQ ID NO: 2577		SEQ ID NO: 2579	SEQ ID NO: 2580
363		WAS	SEQ ID NO: 2577			SEQ ID NO: 2580

364		WAS	SEQ ID NO: 2577	SEQ ID NO: 2578		SEQ ID NO: 2580
365			SEQ ID NO: 2577	SEQ ID NO: 2578		
366			SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	
367			SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
368			SEQ ID NO: 2577		SEQ ID NO: 2579	
369			SEQ ID NO: 2577		SEQ ID NO: 2579	SEQ ID NO: 2580
370			SEQ ID NO: 2577			SEQ ID NO: 2580
371			SEQ ID NO: 2577	SEQ ID NO: 2578		SEQ ID NO: 2580
372	SEQ ID NO: 2576		SEQ ID NO: 2577	SEQ ID NO: 2578		
373	SEQ ID NO: 2576		SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	
374	SEQ ID NO: 2576		SEQ ID NO: 2577	SEQ ID NO: 2578	SEQ ID NO: 2579	SEQ ID NO: 2580
375	SEQ ID NO: 2576		SEQ ID NO: 2577		SEQ ID NO: 2579	
376	SEQ ID NO: 2576		SEQ ID NO: 2577		SEQ ID NO: 2579	SEQ ID NO: 2580
377	SEQ ID NO: 2576		SEQ ID NO: 2577			SEQ ID NO: 2580
378	SEQ ID NO: 2576		SEQ ID NO: 2577	SEQ ID NO: 2578		SEQ ID NO: 2580

Table 17C

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	**L2**	**L3**	**H1**	**H2**	**H3**
1	SEQ ID NO: 2582					
2	SEQ ID NO: 2582	(I/V)KS				
3	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583			
4		(I/V)KS				
5		(I/V)KS	SEQ ID NO: 2583			
6			SEQ ID NO: 2583			
7	SEQ ID NO: 2582		SEQ ID NO: 2583			
8	SEQ ID NO: 2582			SEQ ID NO: 2543		
9	SEQ ID NO: 2582			SEQ ID NO: 2543	SEQ ID NO: 2544	
10	SEQ ID NO: 2582			SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
11	SEQ ID NO: 2582				SEQ ID NO: 2544	
12	SEQ ID NO: 2582				SEQ ID NO: 2544	SEQ ID NO: 2545
13	SEQ ID NO: 2582					SEQ ID NO: 2545
14	SEQ ID NO: 2582			SEQ ID NO: 2543		SEQ ID NO: 2545
15	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2543		
16	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2543	SEQ ID NO: 2544	
17	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
18	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2544	
19	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2544	SEQ ID NO: 2545
20	SEQ ID NO: 2582	(I/V)KS				SEQ ID NO: 2545
21	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2543		SEQ ID NO: 2545
22	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543		
23	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	

24	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
25	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2544	
26	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2544	SEQ ID NO: 2545
27	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543		SEQ ID NO: 2545
28	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2545
29		(I/V)KS		SEQ ID NO: 2543		
30		(I/V)KS		SEQ ID NO: 2543	SEQ ID NO: 2544	
31		(I/V)KS		SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
32		(I/V)KS			SEQ ID NO: 2544	
33		(I/V)KS			SEQ ID NO: 2544	SEQ ID NO: 2545
34		(I/V)KS				SEQ ID NO: 2545
35		(I/V)KS		SEQ ID NO: 2543		SEQ ID NO: 2545
36		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543		
37		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	
38		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
39		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2544	
40		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2544	SEQ ID NO: 2545
41		(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2545
42		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2543		SEQ ID NO: 2545
43			SEQ ID NO: 2583	SEQ ID NO: 2543		
44			SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	
45			SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
46			SEQ ID NO: 2583		SEQ ID NO: 2544	
47			SEQ ID NO: 2583		SEQ ID NO: 2544	SEQ ID NO: 2545
48			SEQ ID NO: 2583			SEQ ID NO: 2545
49			SEQ ID NO: 2583	SEQ ID NO: 2543		SEQ ID NO: 2545
50	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2543		
51	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	
52	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2543	SEQ ID NO: 2544	SEQ ID NO: 2545
53	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2544	
54	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2544	SEQ ID NO: 2545
55	SEQ ID NO: 2582		SEQ ID NO: 2583			SEQ ID NO: 2545
56	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2543		SEQ ID NO: 2545
57	SEQ ID NO: 2582			SEQ ID NO: 2550		
58	SEQ ID NO: 2582			SEQ ID NO: 2550	SEQ ID NO: 2551	
59	SEQ ID NO: 2582			SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
60	SEQ ID NO: 2582				SEQ ID NO: 2551	
61	SEQ ID NO: 2582				SEQ ID NO: 2551	SEQ ID NO: 2552
62	SEQ ID NO: 2582					SEQ ID NO: 2552
63	SEQ ID NO: 2582			SEQ ID NO: 2550		SEQ ID NO: 2552
64	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2550		
65	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2550	SEQ ID NO: 2551	
66	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552

67	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2551	
68	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2551	SEQ ID NO: 2552
69	SEQ ID NO: 2582	(I/V)KS				SEQ ID NO: 2552
70	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2550		SEQ ID NO: 2552
71	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550		
72	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	
73	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
74	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2551	
75	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2551	SEQ ID NO: 2552
76	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2552
77	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550		SEQ ID NO: 2552
78		(I/V)KS		SEQ ID NO: 2550		
79		(I/V)KS		SEQ ID NO: 2550	SEQ ID NO: 2551	
80		(I/V)KS		SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
81		(I/V)KS			SEQ ID NO: 2551	
82		(I/V)KS			SEQ ID NO: 2551	SEQ ID NO: 2552
83		(I/V)KS				SEQ ID NO: 2552
84		(I/V)KS		SEQ ID NO: 2550		SEQ ID NO: 2552
85		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550		
86		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	
87		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
88		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2551	
89		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2551	SEQ ID NO: 2552
90		(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2552
91		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2550		SEQ ID NO: 2552
92			SEQ ID NO: 2583	SEQ ID NO: 2550		
93			SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	
94			SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
95			SEQ ID NO: 2583		SEQ ID NO: 2551	
96			SEQ ID NO: 2583		SEQ ID NO: 2551	SEQ ID NO: 2552
97			SEQ ID NO: 2583			SEQ ID NO: 2552
98			SEQ ID NO: 2583	SEQ ID NO: 2550		SEQ ID NO: 2552
99	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2550		
100	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	
101	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2550	SEQ ID NO: 2551	SEQ ID NO: 2552
102	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2551	
103	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2551	SEQ ID NO: 2552
104	SEQ ID NO: 2582		SEQ ID NO: 2583			SEQ ID NO: 2552
105	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2550		SEQ ID NO: 2552
106	SEQ ID NO: 2582			SEQ ID NO: 2557		
107	SEQ ID NO: 2582			SEQ ID NO: 2557	SEQ ID NO: 2558	
108	SEQ ID NO: 2582			SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
109	SEQ ID NO: 2582				SEQ ID NO: 2558	

110	SEQ ID NO: 2582				SEQ ID NO: 2558	SEQ ID NO: 2559
111	SEQ ID NO: 2582					SEQ ID NO: 2559
112	SEQ ID NO: 2582			SEQ ID NO: 2557		SEQ ID NO: 2559
113	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2557		
114	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2557	SEQ ID NO: 2558	
115	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
116	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2558	
117	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2558	SEQ ID NO: 2559
118	SEQ ID NO: 2582	(I/V)KS				SEQ ID NO: 2559
119	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2557		SEQ ID NO: 2559
120	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557		
121	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	
122	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
123	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2558	
124	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2558	SEQ ID NO: 2559
125	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557		SEQ ID NO: 2559
126	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2559
127		(I/V)KS		SEQ ID NO: 2557		
128		(I/V)KS		SEQ ID NO: 2557	SEQ ID NO: 2558	
129		(I/V)KS		SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
130		(I/V)KS			SEQ ID NO: 2558	
131		(I/V)KS			SEQ ID NO: 2558	SEQ ID NO: 2559
132		(I/V)KS				SEQ ID NO: 2559
133		(I/V)KS		SEQ ID NO: 2557		SEQ ID NO: 2559
134		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557		
135		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	
136		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
137		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2558	
138		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2558	SEQ ID NO: 2559
139		(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2559
140		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2557		SEQ ID NO: 2559
141			SEQ ID NO: 2583	SEQ ID NO: 2557		
142			SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	
143			SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
144			SEQ ID NO: 2583		SEQ ID NO: 2558	
145			SEQ ID NO: 2583		SEQ ID NO: 2558	SEQ ID NO: 2559
146			SEQ ID NO: 2583			SEQ ID NO: 2559
147			SEQ ID NO: 2583	SEQ ID NO: 2557		SEQ ID NO: 2559
148	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2557		
149	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	
150	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2557	SEQ ID NO: 2558	SEQ ID NO: 2559
151	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2558	
152	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2558	SEQ ID NO: 2559

153	SEQ ID NO: 2582		SEQ ID NO: 2583			SEQ ID NO: 2559
154	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2557		SEQ ID NO: 2559
155	SEQ ID NO:2582			SEQ ID NO: 2564		
156	SEQ ID NO: 2582			SEQ ID NO: 2564	SEQ ID NO: 2565	
157	SEQ ID NO: 2582			SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
158	SEQ ID NO: 2582				SEQ ID NO: 2565	
159	SEQ ID NO: 2582				SEQ ID NO: 2565	SEQ ID NO: 2566
160	SEQ ID NO: 2582					SEQ ID NO: 2566
161	SEQ ID NO: 2582			SEQ ID NO: 2564		SEQ ID NO: 2566
162	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2564		
163	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2564	SEQ ID NO: 2565	
164	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
165	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2565	
166	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2565	SEQ ID NO: 2566
167	SEQ ID NO: 2582	(I/V)KS				SEQ ID NO: 2566
168	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2564		SEQ ID NO: 2566
169	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564		
170	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	
171	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
172	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2565	
173	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2565	SEQ ID NO: 2566
174	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564		SEQ ID NO: 2566
175	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2566
176		(I/V)KS		SEQ ID NO: 2564		
177		(I/V)KS		SEQ ID NO: 2564	SEQ ID NO: 2565	
178		(I/V)KS		SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
179		(I/V)KS			SEQ ID NO: 2565	
180		(I/V)KS			SEQ ID NO: 2565	SEQ ID NO: 2566
181		(I/V)KS				SEQ ID NO: 2566
182		(I/V)KS		SEQ ID NO: 2564		SEQ ID NO: 2566
183		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564		
184		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	
185		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
186		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2565	
187		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2565	SEQ ID NO: 2566
188		(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2566
189		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2564		SEQ ID NO: 2566
190			SEQ ID NO: 2583	SEQ ID NO: 2564		
191			SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	
192			SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
193			SEQ ID NO: 2583		SEQ ID NO: 2565	
194			SEQ ID NO: 2583		SEQ ID NO: 2565	SEQ ID NO: 2566
195			SEQ ID NO: 2583			SEQ ID NO: 2566

196			SEQ ID NO: 2583	SEQ ID NO: 2564		SEQ ID NO: 2566
197	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2564		
198	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	
199	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2564	SEQ ID NO: 2565	SEQ ID NO: 2566
200	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2565	
201	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2565	SEQ ID NO: 2566
202	SEQ ID NO: 2582		SEQ ID NO: 2583			SEQ ID NO: 2566
203	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2564		SEQ ID NO: 2566
204	SEQ ID NO:2582			SEQ ID NO: 2571		
205	SEQ ID NO: 2582			SEQ ID NO: 2571	SEQ ID NO: 2572	
206	SEQ ID NO: 2582			SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
207	SEQ ID NO: 2582				SEQ ID NO: 2572	
208	SEQ ID NO: 2582				SEQ ID NO: 2572	SEQ ID NO: 2573
209	SEQ ID NO: 2582					SEQ ID NO: 2573
210	SEQ ID NO: 2582			SEQ ID NO: 2571		SEQ ID NO: 2573
211	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2571		
212	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2571	SEQ ID NO: 2572	
213	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
214	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2572	
215	SEQ ID NO: 2582	(I/V)KS			SEQ ID NO: 2572	SEQ ID NO: 2573
216	SEQ ID NO: 2582	(I/V)KS				SEQ ID NO: 2573
217	SEQ ID NO: 2582	(I/V)KS		SEQ ID NO: 2571		SEQ ID NO: 2573
218	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571		
219	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	
220	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
221	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2572	
222	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2572	SEQ ID NO: 2573
223	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571		SEQ ID NO: 2573
224	SEQ ID NO: 2582	(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2573
225		(I/V)KS		SEQ ID NO: 2571		
226		(I/V)KS		SEQ ID NO: 2571	SEQ ID NO: 2572	
227		(I/V)KS		SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
228		(I/V)KS			SEQ ID NO: 2572	
229		(I/V)KS			SEQ ID NO: 2572	SEQ ID NO: 2573
230		(I/V)KS				SEQ ID NO: 2573
231		(I/V)KS		SEQ ID NO: 2571		SEQ ID NO: 2573
232		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571		
233		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	
234		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
235		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2572	
236		(I/V)KS	SEQ ID NO: 2583		SEQ ID NO: 2572	SEQ ID NO: 2573
237		(I/V)KS	SEQ ID NO: 2583			SEQ ID NO: 2573
238		(I/V)KS	SEQ ID NO: 2583	SEQ ID NO: 2571		SEQ ID NO: 2573

239			SEQ ID NO: 2583	SEQ ID NO: 2571		
240			SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	
241			SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
242			SEQ ID NO: 2583		SEQ ID NO: 2572	
243			SEQ ID NO: 2583		SEQ ID NO: 2572	SEQ ID NO: 2573
244			SEQ ID NO: 2583			SEQ ID NO: 2573
245			SEQ ID NO: 2583	SEQ ID NO: 2571		SEQ ID NO: 2573
246	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2571		
247	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	
248	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2571	SEQ ID NO: 2572	SEQ ID NO: 2573
249	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2572	
250	SEQ ID NO: 2582		SEQ ID NO: 2583		SEQ ID NO: 2572	SEQ ID NO: 2573
251	SEQ ID NO: 2582		SEQ ID NO: 2583			SEQ ID NO: 2573
252	SEQ ID NO: 2582		SEQ ID NO: 2583	SEQ ID NO: 2571		SEQ ID NO: 2573

Table 17D

SEQ ID NO	Comments	Sequence
2539	HJ23.4 light chain variable region	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQK PGQSPKLLIYIVSNRFSGVPDRFSGSGSGTDFTLEISRVEAEDL GVYFCSQSTHVPLTFGAGTKLELK
2540	HJ23.4 heavy chain variable region	EVQLQQSGPDLVKPGASVKMSCKASGYTFTDYNIHWVKQSHGKT LEWIGYINPNTGGTYYNQKFKGKATMTVNKSSSTAYMELRSLTS EDSAVYYCVATRWDGVNWAQGTLVTVSA
2541	HJ23.4 L3	QNLVHSNGNTY
	HJ23.4 L2	IVS
2542	HJ23.4 L3	SQSTHVPLT
2543	HJ23.4 H1	GYTFTDYN
2544	HJ23.4 H2	INPNTGGT
2545	HJ23.4 H3	VATRWDGVN
2546	HJ23.7 light chain variable	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQK PGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDL GVYFCSQSTHVPLTFGAGTKLELK
2547	HJ23.7 heavy chain variable	VEQLQQSGAELVKPGASVKLSCTSSGFNIKGYYIHWVKQRTEQ GLEWIGRIDPEDGETKNAPKFQGKATFGTDTFSNTAYLRLSSLT SEDTGVYYCVRTETRGAYWGPGTLVTVSA
2548	HJ23.7 L1	QSLVHSNGNTY
	HJ23.7 L2	KVS
2549	HJ23.7 L 3	SQSTHVPLT
2550	HJ23.7 H1	GFNIKGYY
2551	HJ23.7 H2	IDPEDGET

2552	HJ23.7 H3	VRTETRGAY
2553	HJ23.8 light chain variable	VDVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGDTYLHVVYLQ KRGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAED LGVYFCSQTTHVPLTFGAGTKLELK
2554	HJ23.8 heavy chain variable	VQPLQQPGAEFVKPGASVKLSCKASAYTFTRYVVMHVVVKQRPG RGLEWIGRIDPNSGGTNYNEKFKSKATFTVDKPSSTSYMQLSSL TSEDSAVYFCVFTGTLFDYWGQGTTLTVSS
2555	HJ23.8 L1	QSLVHSNGDTY
	HJ23.8 L2	KVS
2556	HJ23.8 L3	SQTTHVPLT
2557	HJ23.8 H1	AYTFTRYW
2558	HJ23.8 H2	IDPNSGGT
2559	HJ23.8 H3	VFTGTLFDY
2560	HJ23.9 light chain variable	VDVMTQTPLSLPVSLGDQASISCKSSQSLVHSNGNTYLHWYLQ KPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAED LGVYFCSQSTHVPPTFGGGTKLEIK
2561	HJ23.9 heavy chain variable	VEQLQHSGPVLVKPGASVKMSCKSSGYTFTDYYLNVVVKQSHG KSPEWIGVINPNTGSTSYNQKFKGKATLTVDKSSSTAYMDLNSL TSEDSAVYYCATHYYGSIYKQAWFAYWGQGTLVT
2562	HJ23.9 L1	QSLVHSNGNTY
2563	HJ23.9 L2	KVS
2564	HJ23.9 L3	SQSTHVPPT
2565	HJ23.9 H1	GYTFTDYY
2566	HJ23.9 H2	INPNTGST
2567	HJ23.9 H3	ATHYYGSIYKQAWFAY
2568	HJ23.10 light chain variable	VDVMTQTPLSLPVSLGDQASISCKSSQSLVHSNGNTYLHVVYLQ KPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAED LGIYFCSQSTHVPPTFGGGTKLEIK
2569	HJ23.10 heavy chain variable region	EVQLQHSGPVLVKPGASVKMSCKASGYTFTDYYMNVVVKQSHG KSPEWIGVINPNTGSTSYNQKFKGKATLTVDKSSSTAYMDLNSL TSEDSAVYYCATHYYGSIYKQAWFAYWGQGTLVTV
2556	HJ23.10 L1	QSLVHSNGNTY
	HJ23.10 L2	KVS
2570	HJ23.10 L3	SQSTHVPPT
2571	HJ23.10 H1	GYTFTDYY
2572	HJ23.10 H2	INPNTGST
2573	HJ23.10 H3	ATHYYGSIYKQAWFAY

2574	HJ23.13 light chain variable	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNLKNYLAWFQ QKPGQSPKLLIYWASIRESGVPDRFTGSGSGTDFTLTINSVKAE DLAVYYCQQYYTFPLTFGAGTKLELK
2575	HJ23.13 heavy chain variable region	VQLVETGGGLVQPKGSLKLSCAASGFSFNINAMHWVRQAPGT GLKVVVARIRSGSNDFATYYADSVKDRFTISRDDSHSMLYLQMN NLKTEDTAIYFCVREYVNYFVHWGQGTLVTVSA
2576	HJ23.13 L1	QSLLYSSNLKNY
	HJ23.13 L2	WAS
2577	HJ23.13 L3	QQYYTFPLT
2578	HJ23.13 H1	GFSFNINA
2579	HJ23.13 H2	IRSGSNDFAT
2580	HJ23.13 H3	VREYVNYFVH
2581		DHRDAGDLWFPGES
2582	Consensus L1	QX1LVHSNGX2TY, where X1 is S, T, N, or Q and X2 is D or N
	Consensus L2	X1VS, where X1 is I or K
2583	Consensus L3	SQX1THVPX2T, where X1 is S, T, N, or Q and X2 is P or L

[00282] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed above, including those in **Table 17B** (e.g., antibody 1-378) and **Table 17C** (antibody 1-252) may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

J. PCT Patent Application Publication No. WO2020/079580A1

[00283] In some embodiments, the TREM2 agonist is an antibody, or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. WO2020/079580A1 ("the '580 application"), which is incorporated by reference herein, in its entirety.

[00284] In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain comprising a CDRL1, CDRL2, and CDRL3, and a heavy chain

variable domain comprising a CDRH1, CDRH2, and CDRH3 disclosed in the '580 application specification. In some embodiments, the TREM2 binding agent comprises an antibody that comprises a light chain variable domain and a heavy chain variable domain disclosed in the '580 application specification.

[00285] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a heavy chain variable region CDR1 comprising SEQ ID NO: 2623 or SEQ ID NO: 2626 or SEQ ID NO: 2627 or SEQ ID NO: 2629; a heavy chain variable region CDR2 comprising SEQ ID NO: 2624 or SEQ ID NO: 2628, or SEQ ID NO: 2630; a heavy chain variable region CDR3 comprising SEQ ID NO: 2625 or SEQ ID NO: 2631; a light chain variable region CDR1 comprising SEQ ID NO: 2636 or SEQ ID NO: 2639 or SEQ ID NO: 2642; a light chain variable region CDR2 comprising SEQ ID NO: 2637 or SEQ ID NO: 2640; and a light chain variable region CDR3 comprising SEQ ID NO: 2638 or SEQ ID NO: 2641;

b) a heavy chain variable region CDR1 comprising SEQ ID NO: 2586 or SEQ ID NO: 2589 or SEQ ID NO: 2590 or SEQ ID NO: 2592; a heavy chain variable region CDR2 comprising SEQ ID NO: 2587 or SEQ ID NO: 2591 or SEQ ID NO: 2593; a heavy chain variable region CDR3 comprising SEQ ID NO: 2588 or SEQ ID NO: 2594; a light chain variable region CDR1 comprising SEQ ID NO: 2599 or SEQ ID NO: 2602 or SEQ ID NO: 2605; a light chain variable region CDR2 comprising SEQ ID NO: 2600 or SEQ ID NO: 2603; and a light chain variable region CDR3 comprising SEQ ID NO: 2601 or SEQ ID NO: 2604;

c) a heavy chain variable region CDR1 comprising SEQ ID NO: 2586 or SEQ ID NO: 2589 or SEQ ID NO: 2590 or SEQ ID NO: 2592; a heavy chain variable region CDR2 comprising SEQ ID NO: 2587 or SEQ ID NO: 2591 or SEQ ID NO: 2593; a heavy chain variable region CDR3 comprising SEQ ID NO: 2588 or SEQ ID NO: 2594; a light chain variable region CDR1 comprising SEQ ID NO: 2599 or SEQ ID NO: 2602 or SEQ ID NO: 2605; a light chain variable region CDR2 comprising SEQ ID NO: 2600 or SEQ ID NO: 2603; and a light chain variable region CDR3 comprising SEQ ID NO: 2660 or SEQ ID NO: 2661; or

d) a heavy chain variable region CDR1 comprising SEQ ID NO: 2666 or SEQ ID NO: 2669 or SEQ ID NO: 2670 or SEQ ID NO: 2672; a heavy chain variable region CDR2 comprising SEQ ID NO: 2667 or SEQ ID NO: 2671 or SEQ ID NO: 2673; a heavy chain variable region CDR3 comprising SEQ ID NO: 2668 or SEQ ID NO: 2674; a light chain variable region CDR1 comprising SEQ ID NO: 2679 or SEQ ID NO: 2682 or SEQ ID NO: 2685; a light chain variable

region CDR2 comprising SEQ ID NO: 2680 or SEQ ID NO: 2683; and a light chain variable region CDR3 comprising SEQ ID NO: 2681 or SEQ ID NO: 2684.

[00286] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a VH polypeptide sequence having at least 95% sequence identity to SEQ ID NO: 2595 or to SEQ ID NO: 2632, and a VL polypeptide sequence having at least 95% sequence identity to SEQ ID NO: 2606 or to SEQ ID NO: 2643; or

b) a VH polypeptide sequence having at least 95% sequence identity to SEQ ID NO: 2595 or to SEQ ID NO: 2675, and a VL polypeptide sequence having at least 95% sequence identity to SEQ ID NO: 2662 or to SEQ ID NO: 2686.

[00287] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

[00288] a) a heavy chain variable region CDR1 comprising SEQ ID NO: 2589; a heavy chain variable region CDR2 comprising SEQ ID NO: 2587; a heavy chain variable region CDR3 comprising SEQ ID NO: 2588; a light chain variable region CDR1 comprising SEQ ID NO: 2599; a light chain variable region CDR2 comprising SEQ ID NO: 2600; and a light chain variable region CDR3 comprising SEQ ID NO: 2601; b) a heavy chain variable region CDR1 comprising SEQ ID NO: 2626; a heavy chain variable region CDR2 comprising SEQ ID NO: 2624; a heavy chain variable region CDR3 comprising SEQ ID NO: 2625; a light chain variable region CDR1 comprising SEQ ID NO: 2636; a light chain variable region CDR2 comprising, e.g., consisting of SEQ ID NO: 2637; and a light chain variable region CDR3 comprising SEQ ID NO: 2638; c) a heavy chain variable region CDR1 comprising SEQ ID NO: 2589; a heavy chain variable region CDR2 comprising SEQ ID NO: 2587; a heavy chain variable region CDR3 comprising SEQ ID NO: 2588; a light chain variable region CDR1 comprising SEQ ID NO: 2599; a light chain variable region CDR2 comprising SEQ ID NO: 2600; and a light chain variable region CDR3 comprising SEQ ID NO: 2660; or d) a heavy chain variable region CDR1 comprising SEQ ID NO: 2669; a heavy chain variable region CDR2 comprising SEQ ID NO: 2667; a heavy chain variable region CDR3 comprising SEQ ID NO: 2668; a light chain variable region CDR1 comprising SEQ ID NO: 2679; a light chain variable region CDR2 comprising SEQ ID NO: 2680; and a light chain variable region CDR3 comprising SEQ ID NO: 2681.

[00289] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a heavy chain variable region CDR1 of SEQ ID NO: 2590; a heavy chain variable region CDR2 comprising SEQ ID NO: 2591; a heavy chain variable region CDR3 comprising SEQ ID

NO: 2588; a light chain variable region CDR1 comprising SEQ ID NO: 2602; a light chain variable region CDR2 comprising SEQ ID NO: 2603; and a light chain variable region CDR3 comprising SEQ ID NO: 2604;

b) a heavy chain variable region CDR1 comprising SEQ ID NO: 2627; a heavy chain variable region CDR2 comprising SEQ ID NO: 2628; a heavy chain variable region CDR3 comprising SEQ ID NO: 2625; a light chain variable region CDR1 comprising SEQ ID NO: 2639; a light chain variable region CDR2 comprising SEQ ID NO: 2640; and a light chain variable region CDR3 comprising SEQ ID NO: 2641;

c) a heavy chain variable region CDR1 comprising SEQ ID NO: 2590; a heavy chain variable region CDR2 comprising SEQ ID NO: 2591; a heavy chain variable region CDR3 comprising SEQ ID NO: 2588; a light chain variable region CDR1 comprising SEQ ID NO: 2602; a light chain variable region CDR2 comprising SEQ ID NO: 2603; and a light chain variable region CDR3 comprising SEQ ID NO: 2661; or

d) a heavy chain variable region CDR1 comprising SEQ ID NO: 2670; a heavy chain variable region CDR2 comprising SEQ ID NO: 2671; a heavy chain variable region CDR3 comprising SEQ ID NO: 2668; a light chain variable region CDR1 comprising SEQ ID NO: 2682; a light chain variable region CDR2 comprising SEQ ID NO: 2683; and a light chain variable region CDR3 comprising SEQ ID NO: 2684.

[00290] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a heavy chain variable region CDR1 comprising SEQ ID NO: 2592; a heavy chain variable region CDR2 comprising SEQ ID NO: 2593; a heavy chain variable region CDR3 comprising SEQ ID NO: 2594; a light chain variable region CDR1 comprising SEQ ID NO: 2605; a light chain variable region CDR2 comprising SEQ ID NO: 2603; and a light chain variable region CDR3 comprising SEQ ID NO: 2601;

b) a heavy chain variable region CDR1 comprising SEQ ID NO: 2629; a heavy chain variable region CDR2 comprising SEQ ID NO: 2630; a heavy chain variable region CDR3 comprising SEQ ID NO: 2631; a light chain variable region CDR1 comprising SEQ ID NO: 2642; a light chain variable region CDR2 comprising SEQ ID NO: 2640; and a light chain variable region CDR3 comprising SEQ ID NO: 2638;

c) a heavy chain variable region CDR1 comprising SEQ ID NO: 2592; a heavy chain variable region CDR2 comprising SEQ ID NO: 2593; a heavy chain variable region CDR3

comprising SEQ ID NO: 2594; a light chain variable region CDR1 comprising SEQ ID NO: 2605; a light chain variable region CDR2 comprising SEQ ID NO: 2603; and a light chain variable region CDR3 comprising SEQ ID NO: 2660; or

d) a heavy chain variable region CDR1 comprising SEQ ID NO: 2672; a heavy chain variable region CDR2 comprising SEQ ID NO: 2673; a heavy chain variable region CDR3 comprising SEQ ID NO: 2674; a light chain variable region CDR1 comprising SEQ ID NO: 2685; a light chain variable region CDR2 comprising SEQ ID NO: 2683; and a light chain variable region CDR3 comprising SEQ ID NO: 2681.

[00291] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a heavy chain variable region CDR1 comprising SEQ ID NO: 2586; a heavy chain variable region CDR2 comprising SEQ ID NO: 2587; a heavy chain variable region CDR3 comprising SEQ ID NO: 2588; a light chain variable region CDR1 comprising SEQ ID NO: 2599; a light chain variable region CDR2 comprising SEQ ID NO: 2600; and a light chain variable region CDR3 comprising SEQ ID NO: 2601;

b) a heavy chain variable region CDR1 comprising SEQ ID NO: 2623; a heavy chain variable region CDR2 comprising SEQ ID NO: 2624; a heavy chain variable region CDR3 comprising SEQ ID NO: 2625; a light chain variable region CDR1 comprising SEQ ID NO: 2636; a light chain variable region CDR2 comprising SEQ ID NO: 2637; and a light chain variable region CDR3 comprising SEQ ID NO: 2638;

c) a heavy chain variable region CDR1 comprising SEQ ID NO: 2586; a heavy chain variable region CDR2 comprising SEQ ID NO: 2587; a heavy chain variable region CDR3 comprising SEQ ID NO: 2588; a light chain variable region CDR1 comprising SEQ ID NO: 2599; a light chain variable region CDR2 comprising SEQ ID NO: 2600; and a light chain variable region CDR3 comprising SEQ ID NO: 2660; or

d) a heavy chain variable region CDR1 comprising SEQ ID NO: 2666; a heavy chain variable region CDR2 comprising SEQ ID NO: 2667; a heavy chain variable region CDR3 comprising SEQ ID NO: 2668; a light chain variable region CDR1 comprising SEQ ID NO: 2679; a light chain variable region CDR2 comprising SEQ ID NO: 2680; and a light chain variable region CDR3 comprising SEQ ID NO: 2681.

[00292] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a VH comprising SEQ ID NO: 2595 and a VL comprising SEQ ID NO: 2606; or

b) a VH comprising SEQ ID NO: 2632 and a VL comprising SEQ ID NO: 2643; or

c) a VH comprising a sequence having at least 95% homology to SEQ ID NO: 2595 and a VL comprising a sequence having at least 95% homology to SEQ ID NO: 2606; or

d) a VH comprising a sequence having at least 95% homology to SEQ ID NO: 2632 and a VL comprising a sequence having at least 95% homology to SEQ ID NO: 2643; or

e) a VH comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2595 and a VL comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2606; or

f) a VH comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2632 and a VL comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2643. g) a VH comprising SEQ ID NO: 2595 and a VL comprising SEQ ID NO: 2662; or

h) a VH comprising SEQ ID NO: 2675 and a VL comprising SEQ ID NO: 2686; or

i) a VH comprising a sequence having at least 95% homology to SEQ ID NO: 2595 and a VL comprising a sequence having at least 95% homology to SEQ ID NO: 2662; or

j) a VH comprising a sequence having at least 95% homology to SEQ ID NO: 2675 and a VL comprising a sequence having at least 95% homology to SEQ ID NO: 2686; or

k) a VH comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2595 and a VL comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2662; or

l) a VH comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2675 and a VL comprising, e.g. consisting of, a sequence that differs by at least 1, 2, 3, 4, 5, or 6 amino acids from SEQ ID NO: 2686.

[00293] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a heavy chain amino acid sequence comprising SEQ ID NO: 2597, SEQ ID NO: 2611, SEQ ID NO: 2615, SEQ ID NO: 2617, SEQ ID NO: 2619, or SEQ ID NO: 2621, and a light chain amino acid sequence comprising SEQ ID NO: 2608; b) a heavy chain amino acid sequence comprising SEQ ID NO: 2634, SEQ ID NO: 2648, SEQ ID NO: 2652, SEQ ID NO: 2654, SEQ ID NO: 2656, or SEQ ID NO: 2658, and a light chain amino acid sequence comprising SEQ ID NO: 2645; c) a heavy chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2597, SEQ ID NO: 2611, SEQ ID NO: 2615, SEQ ID NO: 2617, SEQ ID NO: 2619, or SEQ

ID NO: 2621, and a light chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2608;

d) a heavy chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2634, SEQ ID NO: 2648, SEQ ID NO: 2652, SEQ ID NO: 2654, SEQ ID NO: 2656, or SEQ ID NO: 2658, and a light chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2645;

e) a heavy chain amino acid sequence comprising SEQ ID NO: 2597, and a light chain amino acid sequence comprising SEQ ID NO: 2664;

f) a heavy chain amino acid sequence comprising SEQ ID NO: 2677, and a light chain amino acid sequence comprising SEQ ID NO: 2688;

g) a heavy chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2597, and a light chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2664; or

h) a heavy chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2677, and a light chain amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2688.

[00294] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

a) a heavy chain sequence comprising SEQ ID NO: 2597 and a light chain sequence comprising SEQ ID NO: 2608;

b) a heavy chain sequence comprising SEQ ID NO: 2611 and a light chain sequence comprising SEQ ID NO: 2608;

c) a heavy chain sequence comprising SEQ ID NO: 2615 and a light chain sequence comprising SEQ ID NO: 2608;

d) a heavy chain sequence comprising SEQ ID NO: 2617 and a light chain sequence comprising SEQ ID NO: 2608;

e) a heavy chain sequence comprising SEQ ID NO: 2619 and a light chain sequence comprising SEQ ID NO: 2608;

f) a heavy chain sequence comprising SEQ ID NO: 2621 and a light chain sequence comprising SEQ ID NO: 2608;

g) a heavy chain sequence comprising SEQ ID NO: 2634 and a light chain sequence comprising SEQ ID NO: 2645;

h) a heavy chain sequence comprising SEQ ID NO: 2648 and light chain sequence comprising SEQ ID NO: 2645;

i) a heavy chain sequence comprising SEQ ID NO: 2652 and light chain sequence comprising SEQ ID NO: 2645;

j) a heavy chain sequence comprising SEQ ID NO: 2654 and light chain sequence comprising SEQ ID NO: 2645;

k) a heavy chain sequence comprising SEQ ID NO: 2656 and light chain sequence comprising SEQ ID NO: 2645;

l) a heavy chain sequence comprising SEQ ID NO: 2658 and light chain sequence comprising SEQ ID NO: 2645;

m) a heavy chain sequence comprising SEQ ID NO: 2597 and light chain sequence comprising SEQ ID NO: 2664; or

n) a heavy chain sequence comprising SEQ ID NO: 2677 and light chain sequence comprising SEQ ID NO: 2688.

[00295] In some embodiments, the antibody is an antibody disclosed in Table 1 of PCT Patent Application Publication No. WO2020/079580A1, reproduced below as **Table 18**.

Table 18. Sequences of Exemplary Monoclonal Antibodies That Bind Human TREM2

MOR44698A		
SEQ ID NO: 2586	HCDR1 (Combined)	GYTFTGYHMS
SEQ ID NO: 2587	HCDR2 (Combined)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Combined)	IPSYTYAFDY
SEQ ID NO: 2589	HCDR1 (Kabat)	GYHMS
SEQ ID NO: 2587	HCDR2 (Kabat)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Kabat)	IPSYTYAFDY
SEQ ID NO: 2590	HCDR1 (Chothia)	GYTFTGY
SEQ ID NO: 2591	HCDR2 (Chothia)	NPVSGN
SEQ ID NO: 2588	HCDR3 (Chothia)	IPSYTYAFDY
SEQ ID NO: 2592	HCDR1 (IMGT)	GYTFTGYH
SEQ ID NO: 2593	HCDR2 (IMGT)	INPVSGNT
SEQ ID NO: 2594	HCDR3 (IMGT)	ARIPSYTYAFDY

SEQ ID NO: 2595	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMG VINPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCAR IPSYTYAFDYWGQGTLVTVSS
SEQ ID NO: 2596	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCC AGCGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTAC CATATGTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATG GGCGTTATCAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTT CAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTAT ATGGAACTGAGCCGTCTGCGTAGCGAAGATACGGCCGTGTATTATTGC GCGCGTATCCCGTCTTACACTTACGCTTTCGATTACTGGGGCCAAGGC ACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 2597	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWM GVINPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYC ARIPSYTYAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
SEQ ID NO: 2598	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCA GCGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTACCA TATGTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATGGGC GTTATCAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTTCAGG GCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGA ACTGAGCCGTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGT ATCCCGTCTTACACTTACGCTTTCGATTACTGGGGCCAAGGCACCCTGG TGACTGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCG CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGC ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGG TGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAGCAGCGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAA CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGG GAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTT CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 2599	LCDR1 (Combined)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Combined)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Combined)	FQYRHMPSQT
SEQ ID NO: 2599	LCDR1 (Kabat)	RASQDISNYLA

SEQ ID NO: 2600	LCDR2 (Kabat)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Kabat)	FQYRHMPSQT
SEQ ID NO: 2602	LCDR1 (Chothia)	SQDISNY
SEQ ID NO: 2603	LCDR2 (Chothia)	RAS
SEQ ID NO: 2604	LCDR3 (Chothia)	YRHMPSQ
SEQ ID NO: 2605	LCDR1 (IMGT)	QDISNY
SEQ ID NO: 2603	LCDR2 (IMGT)	RAS
SEQ ID NO: 2601	LCDR3 (IMGT)	FQYRHMPSQT
SEQ ID NO: 2606	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIY RASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQT FGQGTKVEIK
SEQ ID NO: 2607	DNA VL	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCG ATCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCT GGCTTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTAC CGTGCTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCG GATCCGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGA CTTTGCGACCTATTATTGCTTCCAGTACCGTCATATGCCGTCTCAGACC TTTGGCCAGGGCACGAAAGTTGAAATTAAA
SEQ ID NO: 2608	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIY RASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQT FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
SEQ ID NO: 2609	DNA Light Chain	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCG ATCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCT GGCTTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTAC CGTGCTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCG GATCCGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGA CTTTGCGACCTATTATTGCTTCCAGTACCGTCATATGCCGTCTCAGACC TTTGGCCAGGGCACGAAAGTTGAAATTAAACGTACGGTGGCCGCTCCCA GCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGC CAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTG CAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCG TCACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCT GACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAG GTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGG GCGAGTGT
MOR44698B		
SEQ ID NO: 2586	HCDR1 (Combined)	GYTFTGYHMS
SEQ ID NO: 2587	HCDR2 (Combined)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Combined)	IPSYTYAFDY
SEQ ID NO: 2589	HCDR1 (Kabat)	GYHMS
SEQ ID NO: 2587	HCDR2 (Kabat)	VINPVSGNTVYAQKFQG

SEQ ID NO: 2588	HCDR3 (Kabat)	IPSYTYAFDY
SEQ ID NO: 2590	HCDR1 (Chothia)	GYTFTGY
SEQ ID NO: 2591	HCDR2 (Chothia)	NPVSGN
SEQ ID NO: 2588	HCDR3 (Chothia)	IPSYTYAFDY
SEQ ID NO: 2592	HCDR1 (IMGT)	GYTFTGYH
SEQ ID NO: 2593	HCDR2 (IMGT)	INPVSGNT
SEQ ID NO: 2594	HCDR3 (IMGT)	ARIPSYTYAFDY
SEQ ID NO: 2595	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSS
SEQ ID NO: 2610	DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCG
SEQ ID NO: 2611	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 2612	DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCGGCCTCCACTAAGGGCCCAAGTGTGTTTCCCCTGGCCCCCAGCA GCAAGTCTACTTCCGGCGGAACTGCTGCCCTGGGTTGCCTGGTGAAGGAC TACTTCCCCGAGCCCGTGACAGTGTCCTGGAACTCTGGGGCTCTGACTTC CGGCGTGCACACCTTCCCCGCCGTGCTGCAGAGCAGCGGCCTGTACAGCC TGAGCAGCGTGGTGACAGTGCCCTCCAGCTCTCTGGGAACCCAGACCTAT ATCTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGT GGAGCCCAAGAGCTGCGACAAGACCCACACCTGCCCCCCCTGCCCAGCTC CAGAACTGCTGGGAGGGCCTTCCGTGTTCCTGTTCCCCCCCAAGCCCAAG GACACCCTGATGATCAGCAGGACCCCCGAGGTGACCTGCGTGGTGGTGGA CGTGTCCCACGAGGACCCAGAGGTGAAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCACAACGCCAAGACCAAGCCCAGAGAGGAGCAGTACAACAGC ACCTACAGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAA CGGCAAAGAATACAAGTGCAAAGTCTCCAACAAGGCCCTGCCAGCCCCAA TCGAAAAGACAATCAGCAAGGCCAAGGGCCAGCCACGGGAGCCCCAGGTG TACACCCTGCCCCCCAGCCGGGAGGAGATGACCAAGAACCAGGTGTCCCT GACCTGTCTGGTGAAGGGCTTCTACCCCAGCGATATCGCCGTGGAGTGGG AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCAGTGCTG GACAGCGACGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGT CCAGGTGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGAGGC CCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGCAAG
SEQ ID NO: 2599	LCDR1 (Combined)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Combined)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Combined)	FQYRHMPSQT
SEQ ID NO: 2599	LCDR1 (Kabat)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Kabat)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Kabat)	FQYRHMPSQT
SEQ ID NO: 2602	LCDR1 (Chothia)	SQDISNY
SEQ ID NO: 2603	LCDR2 (Chothia)	RAS
SEQ ID NO: 2604	LCDR3 (Chothia)	YRHMPSQ
SEQ ID NO: 2605	LCDR1 (IMGT)	QDISNY
SEQ ID NO: 2603	LCDR2 (IMGT)	RAS
SEQ ID NO: 2601	LCDR3 (IMGT)	FQYRHMPSQT
SEQ ID NO: 2606	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIK

SEQ ID NO: 2613	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2608	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID NO: 2614	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTT CATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGG TGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCA GGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCA AGGCCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAG GGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44698C		
SEQ ID NO: 2586	HCDR1 (Combined)	GYTFTGYHMS
SEQ ID NO: 2587	HCDR2 (Combined)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Combined)	IPSYTYAFDY
SEQ ID NO: 2589	HCDR1 (Kabat)	GYHMS
SEQ ID NO: 2587	HCDR2 (Kabat)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Kabat)	IPSYTYAFDY
SEQ ID NO: 2590	HCDR1 (Chothia)	GYTFTGY
SEQ ID NO: 2591	HCDR2 (Chothia)	NPVSGN
SEQ ID NO: 2588	HCDR3 (Chothia)	IPSYTYAFDY
SEQ ID NO: 2592	HCDR1 (IMGT)	GYTFTGYH
SEQ ID NO: 2593	HCDR2 (IMGT)	INPVSGNT
SEQ ID NO: 2594	HCDR3 (IMGT)	ARIPSYTYAFDY
SEQ ID NO: 2595	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSS

SEQ ID NO: 2610	DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCG
SEQ ID NO: 2615	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 2616	DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCT CGAAGTCAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGAC TATTTCCCGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAG CGGAGTGCATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCC TGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTAC ATTTGCAACGTCAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGT GGAGCCCAAGTCCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCAC CTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAA GACACCCTGATGATCTCCCGCACTCCGGAAGTCACTTGCGTGGTCGTGGC CGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAG TGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCC ACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCACTGGCTGCCCCTA TCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTG TACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAACCAGGTGTCGCT GACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCCGTGGAATGGG AGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACCACCTGTCCTG GACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTGGACAAGTC GCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGATGCACGAAGCCC TGCACAACCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGAAAG
SEQ ID NO: 2599	LCDR1 (Combined)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Combined)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Combined)	FQYRHMPSQT
SEQ ID NO: 2599	LCDR1 (Kabat)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Kabat)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Kabat)	FQYRHMPSQT
SEQ ID NO: 2602	LCDR1 (Chothia)	SQDISNY
SEQ ID NO: 2603	LCDR2 (Chothia)	RAS

SEQ ID NO: 2604	LCDR3 (Chothia)	YRHMPSQ
SEQ ID NO: 2605	LCDR1 (IMGT)	QDISNY
SEQ ID NO: 2603	LCDR2 (IMGT)	RAS
SEQ ID NO: 2601	LCDR3 (IMGT)	FQYRHMPSQT
SEQ ID NO: 2606	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIK
SEQ ID NO: 2613	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2608	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID NO: 2614	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTT CATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGG TGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCA GGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCA AGGCCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAG GGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44698D		
SEQ ID NO: 2586	HCDR1 (Combined)	GYTFTGYHMS
SEQ ID NO: 2587	HCDR2 (Combined)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Combined)	IPSYTYAFDY
SEQ ID NO: 2589	HCDR1 (Kabat)	GYHMS
SEQ ID NO: 2587	HCDR2 (Kabat)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Kabat)	IPSYTYAFDY
SEQ ID NO: 2590	HCDR1 (Chothia)	GYTFTGY
SEQ ID NO: 2591	HCDR2 (Chothia)	NPVSGN
SEQ ID NO: 2588	HCDR3 (Chothia)	IPSYTYAFDY
SEQ ID NO: 2592	HCDR1 (IMGT)	GYTFTGYH
SEQ ID NO: 2593	HCDR2 (IMGT)	INPVSGNT

SEQ ID NO: 2594	HCDR3 (IMGT)	ARIPSYTYAFDY
SEQ ID NO: 2595	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSS
SEQ ID NO: 2610	DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCG
SEQ ID NO: 2617	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
SEQ ID NO: 2618	DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCT CGAAGTCAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGAC TATTTCCCGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAG CGGAGTGCATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCC TGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTAC ATTTGCAACGTCAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGT GGAGCCCAAGTCCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCAC CTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAA GACACCCTGATGATCTCCCGCACTCCGGAAGTCACTTGCGTGGTCGTGGA CGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAG TGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCC ACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCACTGCCAGCCCCTA TCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTG TACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAACCAGGTGTCGCT GACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCCGTGGAATGGG AGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACCACCTGTCCTG GACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTGGACAAGTC GCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGCTGCACGAAGCCC TGCACAGCCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGAAAG
SEQ ID NO: 2599	LCDR1 (Combined)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Combined)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Combined)	FQYRHMPSQT
SEQ ID NO: 2599	LCDR1 (Kabat)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Kabat)	RASSLQS

SEQ ID NO: 2601	LCDR3 (Kabat)	FQYRHMPSQT
SEQ ID NO: 2602	LCDR1 (Chothia)	SQDISNY
SEQ ID NO: 2603	LCDR2 (Chothia)	RAS
SEQ ID NO: 2604	LCDR3 (Chothia)	YRHMPSQ
SEQ ID NO: 2605	LCDR1 (IMGT)	QDISNY
SEQ ID NO: 2603	LCDR2 (IMGT)	RAS
SEQ ID NO: 2601	LCDR3 (IMGT)	FQYRHMPSQT
SEQ ID NO: 2606	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIK
SEQ ID NO: 2613	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2608	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID NO: 2614	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTT CATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGG TGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCA GGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCA AGGCCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAG GGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44698E		
SEQ ID NO: 2586	HCDR1 (Combined)	GYTFTGYHMS
SEQ ID NO: 2587	HCDR2 (Combined)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Combined)	IPSYTYAFDY
SEQ ID NO: 2589	HCDR1 (Kabat)	GYHMS
SEQ ID NO: 2587	HCDR2 (Kabat)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Kabat)	IPSYTYAFDY

SEQ ID NO: 2590	HCDR1 (Chothia)	GYTFTGY
SEQ ID NO: 2591	HCDR2 (Chothia)	NPVSGN
SEQ ID NO: 2588	HCDR3 (Chothia)	IPSYTYAFDY
SEQ ID NO: 2592	HCDR1 (IMGT)	GYTFTGYH
SEQ ID NO: 2593	HCDR2 (IMGT)	INPVSGNT
SEQ ID NO: 2594	HCDR3 (IMGT)	ARIPSYTYAFDY
SEQ ID NO: 2595	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSS
SEQ ID NO: 2610	DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCG
SEQ ID NO: 2619	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
SEQ ID NO: 2620	DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCT CGAAGTCAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGAC TATTTCCCGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAG CGGAGTGCATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCC TGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTAC ATTTGCAACGTCAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGT GGAGCCCAAGTCCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCAC CTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAA GACACCCTGATGATCTCCCGCACTCCGGAAGTCACTTGCGTGGTCGTGGC CGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAG TGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCC ACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCACTGGCTGCCCCTA TCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTG TACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAACCAGGTGTCGCT GACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCCGTGGAATGGG AGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACCACCTGTCCTG GACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTGGACAAGTC GCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGCTGCACGAAGCCC TGCACAGCCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGAAAG

SEQ ID NO: 2599	LCDR1 (Combined)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Combined)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Combined)	FQYRHMPSQT
SEQ ID NO: 2599	LCDR1 (Kabat)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Kabat)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Kabat)	FQYRHMPSQT
SEQ ID NO: 2602	LCDR1 (Chothia)	SQDISNY
SEQ ID NO: 2603	LCDR2 (Chothia)	RAS
SEQ ID NO: 2604	LCDR3 (Chothia)	YRHMPSQ
SEQ ID NO: 2605	LCDR1 (IMGT)	QDISNY
SEQ ID NO: 2603	LCDR2 (IMGT)	RAS
SEQ ID NO: 2601	LCDR3 (IMGT)	FQYRHMPSQT
SEQ ID NO: 2606	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIK
SEQ ID NO: 2613	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2608	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID NO: 2614	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTT CATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGG TGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCA GGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCA AGGCCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAG GGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44698F		
SEQ ID NO: 2586	HCDR1 (Combined)	GYTFTGYHMS
SEQ ID NO: 2587	HCDR2 (Combined)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Combined)	IPSYTYAFDY

SEQ ID NO: 2589	HCDR1 (Kabat)	GYHMS
SEQ ID NO: 2587	HCDR2 (Kabat)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Kabat)	IPSYTYAFDY
SEQ ID NO: 2590	HCDR1 (Chothia)	GYTFTGY
SEQ ID NO: 2591	HCDR2 (Chothia)	NPVSGN
SEQ ID NO: 2588	HCDR3 (Chothia)	IPSYTYAFDY
SEQ ID NO: 2592	HCDR1 (IMGT)	GYTFTGYH
SEQ ID NO: 2593	HCDR2 (IMGT)	INPVSGNT
SEQ ID NO: 2594	HCDR3 (IMGT)	ARIPSYTYAFDY
SEQ ID NO: 2595	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSS
SEQ ID NO: 2610	DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTC AGCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCC CGTCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCAC CGTGTCCTCG
SEQ ID NO: 2621	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 2622	DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACA TGTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTC ATCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCG CGTGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCA GCCGGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCG TCCTACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGT GTCCTCGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCT CGAAGTCAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGAC TATTTCCCGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAG CGGAGTGCATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCC TGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTAC ATTTGCAACGTCAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGT GGAGCCCAAGTCCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCAC CTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAA GACACCCTGTATATCACTCGCGAACCGGAAGTCACTTGCGTGGTCGTGGA CGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAG TGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCC ACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCACTGCCAGCCCCTA TCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTG TACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAACCAGGTGTCGCT GACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCCGTGGAATGGG AGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACCACCTGTCCTG GACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTGGACAAGTC GCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGATGCACGAAGCCC TGCACAACCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGAAAG
SEQ ID NO: 2599	LCDR1 (Combined)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Combined)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Combined)	FQYRHMPSQT
SEQ ID NO: 2599	LCDR1 (Kabat)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Kabat)	RASSLQS
SEQ ID NO: 2601	LCDR3 (Kabat)	FQYRHMPSQT
SEQ ID NO: 2602	LCDR1 (Chothia)	SQDISNY
SEQ ID NO: 2603	LCDR2 (Chothia)	RAS
SEQ ID NO: 2604	LCDR3 (Chothia)	YRHMPSQ
SEQ ID NO: 2605	LCDR1 (IMGT)	QDISNY
SEQ ID NO: 2603	LCDR2 (IMGT)	RAS
SEQ ID NO: 2601	LCDR3 (IMGT)	FQYRHMPSQT
SEQ ID NO: 2606	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIK

SEQ ID NO: 2613	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2608	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFG QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID NO: 2614	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGG CCTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGG GCGTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGA CAGGGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTT CATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGG TGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCA GGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCA AGGCCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAG GGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44746A		
SEQ ID NO: 2623	HCDR1 (Combined)	GDSVSSSSAAWN
SEQ ID NO: 2624	HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Combined)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2626	HCDR1 (Kabat)	SSSAAWN
SEQ ID NO: 2624	HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Kabat)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2627	HCDR1 (Chothia)	GDSVSSSSA
SEQ ID NO: 2628	HCDR2 (Chothia)	GYRSKWY
SEQ ID NO: 2625	HCDR3 (Chothia)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2629	HCDR1 (IMGT)	GDSVSSSSAA
SEQ ID NO: 2630	HCDR2 (IMGT)	IGYRSKWYN
SEQ ID NO: 2631	HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI
SEQ ID NO: 2632	VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSS

SEQ ID NO: 2633	DNA VH	CAGGTGCAATTGCAGCAGAGCGGTCCGGGCCTGGTGAAACCGAGCCAGAC CCTGAGCCTGACCTGCGCGATTTCCGGAGATAGCGTGAGCTCTTCTTCTG CTGCTTGGAACTGGATTCGTCAGAGCCCGAGCCGTGGCCTCGAGTGGCTG GGCCATATCGGTTACCGTAGCAAATGGTACAACGAATATGCCGTGAGCGT GAAAAGCCGCATTACCATTAACCCGGATACTTCGAAAAACCAGTTTAGCC TGCAACTGAACAGCGTGACCCCGGAAGATACGGCCGTGTATTATTGCGCG CGTGGTATGTACGGTTCTGTTCCCTACAAAGAAGGTTACTACTTCGATAT TTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 2634	Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
SEQ ID NO: 2635	DNA Heavy Chain	CAGGTGCAATTGCAGCAGAGCGGTCCGGGCCTGGTGAAACCGAGCCAGAC CCTGAGCCTGACCTGCGCGATTTCCGGAGATAGCGTGAGCTCTTCTTCTG CTGCTTGGAACTGGATTCGTCAGAGCCCGAGCCGTGGCCTCGAGTGGCTG GGCCATATCGGTTACCGTAGCAAATGGTACAACGAATATGCCGTGAGCGT GAAAAGCCGCATTACCATTAACCCGGATACTTCGAAAAACCAGTTTAGCC TGCAACTGAACAGCGTGACCCCGGAAGATACGGCCGTGTATTATTGCGCG CGTGGTATGTACGGTTCTGTTCCCTACAAAGAAGGTTACTACTTCGATAT TTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTC CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT GTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTG TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCC CAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAA CTCACACATGCCCACCGTGCCCAGCACCTGAAGCAGCGGGGGGACCGTCA GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCT CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA GGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT CTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG AGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 2636	LCDR1 (Combined)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Combined)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Combined)	QQYTDESMT
SEQ ID NO: 2636	LCDR1 (Kabat)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Kabat)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Kabat)	QQYTDESMT

SEQ ID NO: 2639	LCDR1 (Chothia)	SQGISSD
SEQ ID NO: 2640	LCDR2 (Chothia)	AAS
SEQ ID NO: 2641	LCDR3 (Chothia)	YTDESM
SEQ ID NO: 2642	LCDR1 (IMGT)	QGISSD
SEQ ID NO: 2640	LCDR2 (IMGT)	AAS
SEQ ID NO: 2638	LCDR3 (IMGT)	QQYTDESMT
SEQ ID NO: 2643	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIK
SEQ ID NO: 2644	DNA VL	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGGTATTTCTTCTGACCTGA ACTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACGCT GCTTCTAACCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATC CGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTG CGACCTATTATTGCCAGCAGTACACTGACGAATCTATGACCTTTGGCCAG GGCACGAAAGTTGAAATTAAA
SEQ ID NO: 2645	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
SEQ ID NO: 2646	DNA Light Chain	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGGTATTTCTTCTGACCTGA ACTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACGCT GCTTCTAACCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATC CGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTG CGACCTATTATTGCCAGCAGTACACTGACGAATCTATGACCTTTGGCCAG GGCACGAAAGTTGAAATTAAACGTACGGTGGCCGCTCCCAGCGTGTTCAT CTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGT GCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTG GACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGA CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGG CCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGC CTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGT
MOR44746B		
SEQ ID NO: 2623	HCDR1 (Combined)	GDSVSSSSAAWN
SEQ ID NO: 2624	HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Combined)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2626	HCDR1 (Kabat)	SSSAAWN
SEQ ID NO: 2624	HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Kabat)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2627	HCDR1 (Chothia)	GDSVSSSSA

SEQ ID NO: 2628	HCDR2 (Chothia)	GYRSKWY
SEQ ID NO: 2625	HCDR3 (Chothia)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2629	HCDR1 (IMGT)	GDSVSSSSAA
SEQ ID NO: 2630	HCDR2 (IMGT)	IGYRSKWYN
SEQ ID NO: 2631	HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI
SEQ ID NO: 2632	VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSS
SEQ ID NO: 2647	DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCG
SEQ ID NO: 2648	Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
SEQ ID NO: 2649	DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCC CAAGTGTGTTTCCCCTGGCCCCCAGCAGCAAGTCTACTTCCGGCGGAACT GCTGCCCTGGGTTGCCTGGTGAAGGACTACTTCCCCGAGCCCGTGACAGT GTCCTGGAACTCTGGGGCTCTGACTTCCGGCGTGCACACCTTCCCCGCCG TGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACAGTGCCC TCCAGCTCTCTGGGAACCCAGACCTATATCTGCAACGTGAACCACAAGCC CAGCAACACCAAGGTGGACAAGAGAGTGGAGCCCAAGAGCTGCGACAAGA CCCACACCTGCCCCCCCTGCCCAGCTCCAGAACTGCTGGGAGGGCCTTCC GTGTTCCTGTTCCCCCCCAAGCCCAAGGACACCCTGATGATCAGCAGGAC CCCCGAGGTGACCTGCGTGGTGGTGGACGTGTCCCACGAGGACCCAGAGG TGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACC AAGCCCAGAGAGGAGCAGTACAACAGCACCTACAGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAATACAAGTGCAAAG TCTCCAACAAGGCCCTGCCAGCCCCAATCGAAAAGACAATCAGCAAGGCC AAGGGCCAGCCACGGGAGCCCCAGGTGTACACCCTGCCCCCCAGCCGGGA GGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAGGGCTTCT ACCCCAGCGATATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAAC AACTACAAGACCACCCCCCCAGTGCTGGACAGCGACGGCAGCTTCTTCCT GTACAGCAAGCTGACCGTGGACAAGTCCAGGTGGCAGCAGGGCAACGTGT TCAGCTGCAGCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAG TCCCTGAGCCTGAGCCCCGGCAAG

SEQ ID NO: 2636	LCDR1 (Combined)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Combined)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Combined)	QQYTDESMT
SEQ ID NO: 2636	LCDR1 (Kabat)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Kabat)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Kabat)	QQYTDESMT
SEQ ID NO: 2639	LCDR1 (Chothia)	SQGISSD
SEQ ID NO: 2640	LCDR2 (Chothia)	AAS
SEQ ID NO: 2641	LCDR3 (Chothia)	YTDESM
SEQ ID NO: 2642	LCDR1 (IMGT)	QGISSD
SEQ ID NO: 2640	LCDR2 (IMGT)	AAS
SEQ ID NO: 2638	LCDR3 (IMGT)	QQYTDESMT
SEQ ID NO: 2643	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIK
SEQ ID NO: 2650	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2645	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
SEQ ID NO: 2651	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCAT CTTCCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGT GCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTG GACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGA CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGG CCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGC CTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44746C		
SEQ ID NO: 2623	HCDR1 (Combined)	GDSVSSSSAAWN

SEQ ID NO: 2624	HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Combined)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2626	HCDR1 (Kabat)	SSSAAWN
SEQ ID NO: 2624	HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Kabat)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2627	HCDR1 (Chothia)	GDSVSSSSA
SEQ ID NO: 2628	HCDR2 (Chothia)	GYRSKWY
SEQ ID NO: 2625	HCDR3 (Chothia)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2629	HCDR1 (IMGT)	GDSVSSSSAA
SEQ ID NO: 2630	HCDR2 (IMGT)	IGYRSKWYN
SEQ ID NO: 2631	HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI
SEQ ID NO: 2632	VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSS
SEQ ID NO: 2647	DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCG
SEQ ID NO: 2652	Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK

SEQ ID NO: 2653	DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCC CGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACT GCCGCACTGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGT CTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGG TGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCC TCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCC AAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGA CCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCC GTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGATGATCTCCCGCAC TCCGGAAGTCACTTGCGTGGTCGTGGCCGTGTCCCACGAGGACCCCGAGG TCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAACGCCAAGACC AAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCT GACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAG TGTCCAACAAGGCACTGGCTGCCCCTATCGAAAAGACTATCTCCAAGGCC AAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGA AGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCT ACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCTGAGAAC AACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTCTTCCT GTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAACGTGT TCTCTTGCTCCGTGATGCACGAAGCCCTGCACAACCACTACACCCAAAAG TCGCTCAGCCTCTCCCCCGGAAAG
SEQ ID NO: 2636	LCDR1 (Combined)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Combined)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Combined)	QQYTDESMT
SEQ ID NO: 2636	LCDR1 (Kabat)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Kabat)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Kabat)	QQYTDESMT
SEQ ID NO: 2639	LCDR1 (Chothia)	SQGISSD
SEQ ID NO: 2640	LCDR2 (Chothia)	AAS
SEQ ID NO: 2641	LCDR3 (Chothia)	YTDESM
SEQ ID NO: 2642	LCDR1 (IMGT)	QGISSD
SEQ ID NO: 2640	LCDR2 (IMGT)	AAS
SEQ ID NO: 2638	LCDR3 (IMGT)	QQYTDESMT
SEQ ID NO: 2643	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIK

SEQ ID NO: 2650	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2645	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
SEQ ID NO: 2651	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCAT CTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGT GCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTG GACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGA CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGG CCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGC CTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44746D		
SEQ ID NO: 2623	HCDR1 (Combined)	GDSVSSSSAAWN
SEQ ID NO: 2624	HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Combined)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2626	HCDR1 (Kabat)	SSSAAWN
SEQ ID NO: 2624	HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Kabat)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2627	HCDR1 (Chothia)	GDSVSSSSA
SEQ ID NO: 2628	HCDR2 (Chothia)	GYRSKWY
SEQ ID NO: 2625	HCDR3 (Chothia)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2629	HCDR1 (IMGT)	GDSVSSSSAA
SEQ ID NO: 2630	HCDR2 (IMGT)	IGYRSKWYN
SEQ ID NO: 2631	HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI
SEQ ID NO: 2632	VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSS

SEQ ID NO: 2647	DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCG
SEQ ID NO: 2654	Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQK SLSLSPGK
SEQ ID NO: 2655	DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCC CGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACT GCCGCACTGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGT CTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGG TGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCC TCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCC AAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGA CCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCC GTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGATGATCTCCCGCAC TCCGGAAGTCACTTGCGTGGTCGTGGACGTGTCCCACGAGGACCCCGAGG TCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAACGCCAAGACC AAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCT GACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAG TGTCCAACAAGGCACTGCCAGCCCCTATCGAAAAGACTATCTCCAAGGCC AAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGA AGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCT ACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCTGAGAAC AACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTCTTCCT GTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAACGTGT TCTCTTGCTCCGTGCTGCACGAAGCCCTGCACAGCCACTACACCCAAAAG TCGCTCAGCCTCTCCCCCGGAAAG
SEQ ID NO: 2636	LCDR1 (Combined)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Combined)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Combined)	QQYTDESMT
SEQ ID NO: 2636	LCDR1 (Kabat)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Kabat)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Kabat)	QQYTDESMT
SEQ ID NO: 2639	LCDR1 (Chothia)	SQGISSD

SEQ ID NO: 2640	LCDR2 (Chothia)	AAS
SEQ ID NO: 2641	LCDR3 (Chothia)	YTDESM
SEQ ID NO: 2642	LCDR1 (IMGT)	QGISSD
SEQ ID NO: 2640	LCDR2 (IMGT)	AAS
SEQ ID NO: 2638	LCDR3 (IMGT)	QQYTDESMT
SEQ ID NO: 2643	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIK
SEQ ID NO: 2650	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2645	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
SEQ ID NO: 2651	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCAT CTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGT GCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTG GACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGA CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGG CCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGC CTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44746E		
SEQ ID NO: 2623	HCDR1 (Combined)	GDSVSSSSAAWN
SEQ ID NO: 2624	HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Combined)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2626	HCDR1 (Kabat)	SSSAAWN
SEQ ID NO: 2624	HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Kabat)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2627	HCDR1 (Chothia)	GDSVSSSSA
SEQ ID NO: 2628	HCDR2 (Chothia)	GYRSKWY

SEQ ID NO: 2625	HCDR3 (Chothia)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2629	HCDR1 (IMGT)	GDSVSSSSAA
SEQ ID NO: 2630	HCDR2 (IMGT)	IGYRSKWYN
SEQ ID NO: 2631	HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI
SEQ ID NO: 2632	VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSS
SEQ ID NO: 2647	DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCG
SEQ ID NO: 2656	Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQK SLSLSPGK
SEQ ID NO: 2657	DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCC CGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACT GCCGCACTGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGT CTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGG TGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCC TCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCC AAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGA CCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCC GTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGATGATCTCCCGCAC TCCGGAAGTCACTTGCGTGGTCGTGGCCGTGTCCCACGAGGACCCCGAGG TCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAACGCCAAGACC AAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCT GACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAG TGTCCAACAAGGCACTGGCTGCCCCTATCGAAAAGACTATCTCCAAGGCC AAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGA AGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCT ACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCTGAGAAC AACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTCTTCCT GTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAACGTGT TCTCTTGCTCCGTGCTGCACGAAGCCCTGCACAGCCACTACACCCAAAAG TCGCTCAGCCTCTCCCCCGGAAAG
SEQ ID NO: 2636	LCDR1 (Combined)	RASQGISSDLN

SEQ ID NO: 2637	LCDR2 (Combined)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Combined)	QQYTDESMT
SEQ ID NO: 2636	LCDR1 (Kabat)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Kabat)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Kabat)	QQYTDESMT
SEQ ID NO: 2639	LCDR1 (Chothia)	SQGISSD
SEQ ID NO: 2640	LCDR2 (Chothia)	AAS
SEQ ID NO: 2641	LCDR3 (Chothia)	YTDESM
SEQ ID NO: 2642	LCDR1 (IMGT)	QGISSD
SEQ ID NO: 2640	LCDR2 (IMGT)	AAS
SEQ ID NO: 2638	LCDR3 (IMGT)	QQYTDESMT
SEQ ID NO: 2643	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIK
SEQ ID NO: 2650	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2645	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
SEQ ID NO: 2651	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCAT CTTCCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGT GCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTG GACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGA CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGG CCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGC CTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR44746F		
SEQ ID NO: 2623	HCDR1 (Combined)	GDSVSSSSAAWN
SEQ ID NO: 2624	HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS

SEQ ID NO: 2625	HCDR3 (Combined)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2626	HCDR1 (Kabat)	SSSAAWN
SEQ ID NO: 2624	HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS
SEQ ID NO: 2625	HCDR3 (Kabat)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2627	HCDR1 (Chothia)	GDSVSSSSA
SEQ ID NO: 2628	HCDR2 (Chothia)	GYRSKWY
SEQ ID NO: 2625	HCDR3 (Chothia)	GMYGSVPYKEGYYFDI
SEQ ID NO: 2629	HCDR1 (IMGT)	GDSVSSSSAA
SEQ ID NO: 2630	HCDR2 (IMGT)	IGYRSKWYN
SEQ ID NO: 2631	HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI
SEQ ID NO: 2632	VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSS
SEQ ID NO: 2647	DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCG
SEQ ID NO: 2658	Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWL GHIGYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCA RGMYGSVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK

SEQ ID NO: 2659	DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAG CCGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTG GGCCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGT GAAGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCC TCCAGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCG CGGGGCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACAT TTGGGGCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCC CGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACT GCCGCACTGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGT CTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGG TGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCC TCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCC AAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGA CCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCC GTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGTATATCACTCGCGA ACCGGAAGTCACTTGCGTGGTCGTGGACGTGTCCCACGAGGACCCCGAGG TCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAACGCCAAGACC AAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCT GACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAG TGTCCAACAAGGCACTGCCAGCCCCTATCGAAAAGACTATCTCCAAGGCC AAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGA AGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCT ACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCTGAGAAC AACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTCTTCCT GTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAACGTGT TCTCTTGCTCCGTGATGCACGAAGCCCTGCACAACCACTACACCCAAAAG TCGCTCAGCCTCTCCCCCGGAAAG
SEQ ID NO: 2636	LCDR1 (Combined)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Combined)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Combined)	QQYTDESMT
SEQ ID NO: 2636	LCDR1 (Kabat)	RASQGISSDLN
SEQ ID NO: 2637	LCDR2 (Kabat)	AASNLQS
SEQ ID NO: 2638	LCDR3 (Kabat)	QQYTDESMT
SEQ ID NO: 2639	LCDR1 (Chothia)	SQGISSD
SEQ ID NO: 2640	LCDR2 (Chothia)	AAS
SEQ ID NO: 2641	LCDR3 (Chothia)	YTDESM
SEQ ID NO: 2642	LCDR1 (IMGT)	QGISSD
SEQ ID NO: 2640	LCDR2 (IMGT)	AAS
SEQ ID NO: 2638	LCDR3 (IMGT)	QQYTDESMT
SEQ ID NO: 2643	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIK

SEQ ID NO: 2650	DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAG
SEQ ID NO: 2645	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYA ASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
SEQ ID NO: 2651	DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGA CAGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGA ACTGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCC GCGTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAG CGGGACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCG CTACCTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAG GGCACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCAT CTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGT GCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTG GACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGA CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGG CCGACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGC CTGTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC
MOR042596		
SEQ ID NO: 2586	HCDR1 (Combined)	GYTFTGYHMS
SEQ ID NO: 2587	HCDR2 (Combined)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Combined)	IPSYTYAFDY
SEQ ID NO: 2589	HCDR1 (Kabat)	GYHMS
SEQ ID NO: 2587	HCDR2 (Kabat)	VINPVSGNTVYAQKFQG
SEQ ID NO: 2588	HCDR3 (Kabat)	IPSYTYAFDY
SEQ ID NO: 2590	HCDR1 (Chothia)	GYTFTGY
SEQ ID NO: 2591	HCDR2 (Chothia)	NPVSGN
SEQ ID NO: 2588	HCDR3 (Chothia)	IPSYTYAFDY
SEQ ID NO: 2592	HCDR1 (IMGT)	GYTFTGYH
SEQ ID NO: 2593	HCDR2 (IMGT)	INPVSGNT
SEQ ID NO: 2594	HCDR3 (IMGT)	ARIPSYTYAFDY
SEQ ID NO: 2595	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSS

SEQ ID NO: 2596	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAG CGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTACCATA TGTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATGGGCGTT ATCAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTTCAGGGCCG GGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGA GCCGTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTATCCCG TCTTACACTTACGCTTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGT TAGCTCA
SEQ ID NO: 2597	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIP SYTYAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 2598	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAG CGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTACCATA TGTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATGGGCGTT ATCAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTTCAGGGCCG GGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGA GCCGTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTATCCCG TCTTACACTTACGCTTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGT TAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCCCCTGGCACCCTCCT CCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGT TGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCAC CTGAAGCAGCGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGA CGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC ACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGC CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGT GGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
SEQ ID NO: 2599	LCDR1 (Combined)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Combined)	RASSLQS
SEQ ID NO: 2660	LCDR3 (Combined)	QQHGHSPTT
SEQ ID NO: 2599	LCDR1 (Kabat)	RASQDISNYLA
SEQ ID NO: 2600	LCDR2 (Kabat)	RASSLQS
SEQ ID NO: 2660	LCDR3 (Kabat)	QQHGHSPTT
SEQ ID NO: 2602	LCDR1 (Chothia)	SQDISNY

SEQ ID NO: 2603	LCDR2 (Chothia)	RAS
SEQ ID NO: 2661	LCDR3 (Chothia)	HGHSPT
SEQ ID NO: 2605	LCDR1 (IMGT)	QDISNY
SEQ ID NO: 2603	LCDR2 (IMGT)	RAS
SEQ ID NO: 2660	LCDR3 (IMGT)	QQHGHSPTT
SEQ ID NO: 2662	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHGHSPTTFGQ GTKVEIK
SEQ ID NO: 2663	DNA VL	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCTGG CTTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACCGT GCTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATC CGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTG CGACCTATTATTGCCAGCAGCATGGTCATTCTCCGACTACCTTTGGCCAG GGCACGAAAGTTGAAATTAAA
SEQ ID NO: 2664	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYR ASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHGHSPTTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
SEQ ID NO: 2665	DNA Light Chain	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCTGG CTTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACCGT GCTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATC CGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTG CGACCTATTATTGCCAGCAGCATGGTCATTCTCCGACTACCTTTGGCCAG GGCACGAAAGTTGAAATTAAACGTACGGTGGCCGCTCCCAGCGTGTTCAT CTTCCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGT GCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTG GACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGA CAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGG CCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGC CTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGT
MOR041877		
SEQ ID NO: 2666	HCDR1 (Combined)	GFSLSTSGVGVS
SEQ ID NO: 2667	HCDR2 (Combined)	LIFSDHDKIYSTSLKT
SEQ ID NO: 2668	HCDR3 (Combined)	TLIDRSVYFDY
SEQ ID NO: 2669	HCDR1 (Kabat)	TSGVGVS
SEQ ID NO: 2667	HCDR2 (Kabat)	LIFSDHDKIYSTSLKT
SEQ ID NO: 2668	HCDR3 (Kabat)	TLIDRSVYFDY
SEQ ID NO: 2670	HCDR1 (Chothia)	GFSLSTSGV
SEQ ID NO: 2671	HCDR2 (Chothia)	FSDHD
SEQ ID NO: 2668	HCDR3 (Chothia)	TLIDRSVYFDY

SEQ ID NO: 2672	HCDR1 (IMGT)	GFSLSTSGVG
SEQ ID NO: 2673	HCDR2 (IMGT)	IFSDHDK
SEQ ID NO: 2674	HCDR3 (IMGT)	ARTLIDRSVYFDY
SEQ ID NO: 2675	VH	QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVSWIRQPPGKALEWL ALIFSDHDKIYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCART LIDRSVYFDYWGQGTLVTVSS
SEQ ID NO: 2676	DNA VH	CAGGTGCAATTGAAAGAAAGCGGTCCGGCGCTGGTGAAACCGACCCAGAC CCTGACCCTGACGTGCACCTTTTCCGGATTCAGCCTGTCTACTTCCGGTG TTGGTGTGAGCTGGATTCGCCAGCCGCCGGGCAAAGCGCTCGAGTGGCTG GCGCTGATCTTCTCTGACCATGACAAGATCTATAGCACCAGCCTGAAAAC CCGTCTGACCATTAGCAAAGATACTTCGAAAAACCAGGTGGTGCTGACCA TGACCAACATGGACCCGGTGGATACCGCGACCTATTATTGCGCGCGTACT CTGATCGACCGTTCTGTTTACTTCGATTACTGGGGCCAAGGCACCCTGGT GACTGTTAGCTCA
SEQ ID NO: 2677	Heavy Chain	QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVSWIRQPPGKALEWL ALIFSDHDKIYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCART LIDRSVYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
SEQ ID NO: 2678	DNA Heavy Chain	CAGGTGCAATTGAAAGAAAGCGGTCCGGCGCTGGTGAAACCGACCCAGAC CCTGACCCTGACGTGCACCTTTTCCGGATTCAGCCTGTCTACTTCCGGTG TTGGTGTGAGCTGGATTCGCCAGCCGCCGGGCAAAGCGCTCGAGTGGCTG GCGCTGATCTTCTCTGACCATGACAAGATCTATAGCACCAGCCTGAAAAC CCGTCTGACCATTAGCAAAGATACTTCGAAAAACCAGGTGGTGCTGACCA TGACCAACATGGACCCGGTGGATACCGCGACCTATTATTGCGCGCGTACT CTGATCGACCGTTCTGTTTACTTCGATTACTGGGGCCAAGGCACCCTGGT GACTGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCT ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAA GAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCC CAGCACCTGAAGCAGCGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGT GGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGG ACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC AACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTG GCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA CAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGG AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT AAA
SEQ ID NO: 2679	LCDR1 (Combined)	SGSSSNIGHHYVS
SEQ ID NO: 2680	LCDR2 (Combined)	DNTNRPS

SEQ ID NO: 2681	LCDR3 (Combined)	ATWDGLMNSIV
SEQ ID NO: 2679	LCDR1 (Kabat)	SGSSSNIGHHYVS
SEQ ID NO: 2680	LCDR2 (Kabat)	DNTNRPS
SEQ ID NO: 2681	LCDR3 (Kabat)	ATWDGLMNSIV
SEQ ID NO: 2682	LCDR1 (Chothia)	SSSNIGHHY
SEQ ID NO: 2683	LCDR2 (Chothia)	DNT
SEQ ID NO: 2684	LCDR3 (Chothia)	WDGLMNSI
SEQ ID NO: 2685	LCDR1 (IMGT)	SSNIGHHY
SEQ ID NO: 2683	LCDR2 (IMGT)	DNT
SEQ ID NO: 2681	LCDR3 (IMGT)	ATWDGLMNSIV
SEQ ID NO: 2686	VL	DIVLTQPPSVSGAPGQRVTISCSGSSSNIGHHYVSWYQQLPGTAPKLLIY DNTNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCATWDGLMNSIV FGGGTKLTVL
SEQ ID NO: 2687	DNA VL	GATATCGTGCTGACCCAGCCGCCGAGCGTGAGCGGTGCACCGGGCCAGCG CGTGACCATTAGCTGTAGCGGCAGCAGCAGCAACATTGGTCATCATTACG TGTCTTGGTACCAGCAGCTGCCGGGCACGGCGCCGAAACTGCTGATCTAC GACAACACTAACCGCCCGAGCGGCGTGCCGGATCGCTTTAGCGGATCCAA AAGCGGCACCAGCGCCAGCCTGGCGATTACCGGCCTGCAAGCAGAAGACG AAGCGGATTATTACTGCGCTACTTGGGACGGTCTGATGAACTCTATCGTG TTTGGCGGCGGCACGAAGTTAACCGTCCTA
SEQ ID NO: 2688	Light Chain	DIVLTQPPSVSGAPGQRVTISCSGSSSNIGHHYVSWYQQLPGTAPKLLIY DNTNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCATWDGLMNSIV FGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS
SEQ ID NO: 2689	DNA Light Chain	GATATCGTGCTGACCCAGCCGCCGAGCGTGAGCGGTGCACCGGGCCAGCG CGTGACCATTAGCTGTAGCGGCAGCAGCAGCAACATTGGTCATCATTACG TGTCTTGGTACCAGCAGCTGCCGGGCACGGCGCCGAAACTGCTGATCTAC GACAACACTAACCGCCCGAGCGGCGTGCCGGATCGCTTTAGCGGATCCAA AAGCGGCACCAGCGCCAGCCTGGCGATTACCGGCCTGCAAGCAGAAGACG AAGCGGATTATTACTGCGCTACTTGGGACGGTCTGATGAACTCTATCGTG TTTGGCGGCGGCACGAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCC CTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGG CCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTG GCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCC TGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCA

[00296] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed above, including those in **Table 18** above, may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete

antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

K. KR Patent Application Publication No. KR20200048069A

[00297] In some embodiments, the TREM2 agonist is an antibody, or an antigen-binding fragment thereof, as described in KR Patent Application Publication No. KR20200048069A, which is incorporated by reference herein, in its entirety.

[00298] In some embodiments, the TREM2 antibody comprises the CDR L1, CDR L2 and CDR L3 in the light chain variable region of the antibody produced by hybridoma cells with accession number KCTC 13471BP or hybridoma cells with accession number KTC 13470BP.

[00299] In some embodiments, the TREM2 antibody comprises the CDR H1, CDR H2 and CDR H3 in the heavy chain variable region of the antibody produced by hybridoma cells with accession number KCTC 13471BP or hybridoma cells with accession number KTC 13470BP.

[00300] In some embodiments, the TREM2 antibody comprises the CDR L1, CDR L2 and CDR L3 in the light chain variable region and the CDR H1, CDR H2 and CDR H3 in the heavy chain variable region of the antibody produced by hybridoma cells with accession number KCTC 13471BP or hybridoma cells with accession number KTC 13470BP.

[00301] In some embodiments, the TREM2 antibody comprises the light chain variable region and the heavy chain variable region of the antibody produced by hybridoma cells with accession number KCTC 13471BP or hybridoma cells with accession number KTC 13470BP.

[00302] In some embodiments, the TREM2 agonist is an antibody produced by hybridoma cells with accession number KCTC 13471BP or hybridoma cells with accession number KTC 13470BP.

[00303] In some embodiments, the light chain variable regions and the heavy chain variable regions describe above for the antibody produced by hybridoma cells with accession number KCTC 13471BP or hybridoma cells with accession number KTC 13470BP may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete

antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

L. PCT Patent Application Publication No. WO2020/172450A1

[00304] In some embodiments, the TREM2 agonist is an antibody, or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. WO2020/172450A1 ("the '450 application"), which is incorporated by reference herein, in its entirety.

[00305] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

(a) a CDR-H1 sequence comprising the sequence of GFSIEDFYIH (SEQ ID NO: 2717);

(b) a CDR-H2 sequence comprising the sequence of Y-I-D-P-E-β_6-G-β_8-S-K-Y-A-P-K-F-Q-G (SEQ ID NO: 2735), wherein β_6 is N or Q and β_8 is D or E;

(c) a CDR-H3 sequence comprising the sequence of HADHGNYGSTMDY (SEQ ID NO: 2719);

(d) CDR-L1 sequence comprising the sequence of HASQHINVWLS (SEQ ID NO: 2720);

(e) a CDR-L2 sequence comprising the sequence of KASNLHT (SEQ ID NO: 2721); and

(f) a CDR-L3 sequence comprising the sequence of QQGQTYPRT (SEQ ID NO: 2722).

[00306] In some embodiments, the CDR-H2 sequence is selected from SEQ ID NOS: 2718, 2727, 2729, and 2731.

[00307] In some embodiments, the antibody or antigen-binding fragment comprises:

(a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2718, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722; or

(b) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2727, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722; or

(c) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2729, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722; or

(d) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2731, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722.

[00308] In some embodiments, the antibody or antigen-binding fragment comprises a V H sequence that has at least 85% sequence identity to any one of SEQ ID NOS: 2715, 2723, 2725, 2726, 2728, 2730, 2732, 2733, and 2734. In some embodiments, the V H sequence has at least 90% sequence identity to SEQ ID NO: 2715. In some embodiments, the V_H sequence has at least 95% sequence identity to SEQ ID NO: 2715. In some embodiments, the V_H sequence comprises SEQ ID NO: 2715. In some embodiments, the V_H sequence has at least 90% sequence identity to SEQ ID NO: 2730. In some embodiments, the V_H sequence has at least 95% sequence identity to SEQ ID NO: 2730. In some embodiments, the V_H sequence comprises SEQ ID NO: 2730. In some embodiments, the V_H sequence has at least 90% sequence identity to SEQ ID NO: 2733. In some embodiments, the V_H sequence has at least 95% sequence identity to SEQ ID NO: 2733. In some embodiments, the V_H sequence comprises SEQ ID NO: 2733.

[00309] In some embodiments, the antibody or antigen-binding fragment comprises a V_L sequence that has at least 85% sequence identity to SEQ ID NO: 2716 or SEQ ID NO: 2724. In some embodiments, the V_L sequence has at least 90% sequence identity to SEQ ID NO: 2716. In some embodiments, the V_L sequence has at least 95% sequence identity to SEQ ID NO: 2716. In some embodiments, the V_L sequence comprises SEQ ID NO: 2716. In some embodiments, the V_L sequence has at least 90% sequence identity to SEQ ID NO: 2724. In some embodiments, the V_L sequence has at least 95% sequence identity to SEQ ID NO: 2724. In some embodiments, the V_L sequence comprises SEQ ID NO: 2724.

[00310] In some embodiments, the antibody or antigen-binding fragment comprises:

(a) a VH sequence comprising SEQ ID NO: 2715 and a V_L sequence comprising SEQ ID NO: 2716; or

(b) a VH sequence comprising SEQ ID NO: 2723 and a V_L sequence comprising SEQ ID NO: 2724; or

(c) a VH sequence comprising SEQ ID NO: 2725 and a V_L sequence comprising SEQ ID NO: 2724; or

(d) a VH sequence comprising SEQ ID NO: 2726 and a V_L sequence comprising SEQ ID NO: 2724; or

(e) a VH sequence comprising SEQ ID NO: 2728 and a V_L sequence comprising SEQ ID NO: 2724; or

(f) a VH sequence comprising SEQ ID NO: 2730 and a V_L sequence comprising SEQ ID NO: 2724; or

(g) a VH sequence comprising SEQ ID NO: 2732 and a V_L sequence comprising SEQ ID NO: 2724; or

(h) a VH sequence comprising SEQ ID NO: 2733 and a VL sequence comprising SEQ ID NO: 2724; or

(i) a VH sequence comprising SEQ ID NO: 2734 and a VL sequence comprising SEQ ID NO: 2724.

[00311] In some embodiments, an antibody or antigen-binding fragment thereof that specifically binds to TREM2 comprises:

(a) a CDR-H1 sequence comprising the sequence of G-F-T-F-T-α_6-F-Y-M-S (SEQ ID NO: 2736), wherein α_6 is D or N;

(b) a CDR-H2 sequence comprising the sequence of V-I-R-N-β_5-β_6-N-β_8-Y-T-β_{11}-β_{12}-Y-N-P-S-V-K-G (SEQ ID NO: 2737), wherein β_5 is K or R; β_6 is A or P; β_8 is G or A; β_{11} is A or T; and β_{12} is G or D;

(c) a CDR-H3 sequence comprising the sequence of γ_1-R-L-γ_4-Y-G-F-D-Y (SEQ ID NO: 2738), wherein γ_1 is A or T; and γ_4 is T or S;

(d) a CDR-L1 sequence comprising the sequence of Q-S-S-K-S-L-L-H-S-δ_{10} -G-K-T-Y-L-N (SEQ ID NO: 2739), wherein δ_{10} is N or T;

(e) a CDR-L2 sequence comprising the sequence of WMSTRAS (SEQ ID NO: 2696); and

(f) a CDR-L3 sequence comprising the sequence of Q-Q-F-L-ϕ_6-P-F-T (SEQ ID NO: 2740), wherein ϕ_6 is Y or F.

[00312] In some embodiments, the CDR-H1 sequence is selected from any one of SEQ ID NOS: 2692 and 2700. In some embodiments, the CDR-H2 sequence is selected from any one of SEQ ID NOS: 2693, 2701, and 2713. In some embodiments, the CDR-H3 sequence is selected from any one of SEQ ID NOS: 2694, 2702, and 2705. In some embodiments, the CDR-L1 sequence is selected from any one of SEQ ID NOS: 2695 and 2711. In some embodiments, the CDR-L3 sequence is selected from any one of SEQ ID NOS: 2697 and 2706.

[00313] In some embodiments, the antibody or antigen-binding fragment comprises:

(a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2693, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(b) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2693, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2711, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(c) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2713, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(d) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2713, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2711, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(e) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2693, a CDR-H3 comprising the amino acid

sequence of SEQ ID NO: 2694, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2697; or

(f) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2700, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2701, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2702, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2697; or

(g) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2713, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2697.

[00314] In some embodiments, the antibody or antigen-binding fragment comprises a VH sequence that has at least 85% sequence identity to any one of SEQ ID NOS: 2690, 2698, 2703, 2708, 2709, 2712, 2714, and 2752. In some embodiments, the VH sequence has at least 90% sequence identity to SEQ ID NO: 2703. In some embodiments, the V_H sequence has at least 95% sequence identity to SEQ ID NO: 2703. In some embodiments, the VH sequence comprises SEQ ID NO: 2703. In some embodiments, the VH sequence has at least 90% sequence identity to SEQ ID NO: 2712. In some embodiments, the V_H sequence has at least 95% sequence identity to SEQ ID NO: 2712. In some embodiments, the VH sequence comprises SEQ ID NO: 2712. In some embodiments, the VH sequence has at least 90% sequence identity to SEQ ID NO: 79. In some embodiments, the VH sequence has at least 95% sequence identity to SEQ ID NO: 79. In some embodiments, the VH sequence comprises SEQ ID NO: 79.

[00315] In some embodiments, the antibody or antigen-binding fragment comprises a VL sequence that has at least 85% sequence identity to any one of SEQ ID NOS: 2691, 2699, 2704, 2708, 2710, and 2741. In some embodiments, the VL sequence has at least 90% sequence identity to SEQ ID NO: 2704. In some embodiments, the VL sequence has at least 95% sequence identity to SEQ ID NO: 2704. In some embodiments, the VL sequence comprises SEQ ID NO: 2704. In some embodiments, the VL sequence has at least 90% sequence identity to SEQ ID NO: 2710. In some embodiments, the VL sequence has at least 95% sequence identity to SEQ ID NO:

2710. In some embodiments, the VL sequence comprises SEQ ID NO: 2710. In some embodiments, the VL sequence has at least 90% sequence identity to SEQ ID NO: 2741. In some embodiments, the VL sequence has at least 95% sequence identity to SEQ ID NO: 2741. In some embodiments, the VL sequence comprises SEQ ID NO: 2741.

[00316] In some embodiments, the antibody or antigen-binding fragment comprises:

(a) a VH sequence comprising SEQ ID NO: 2703 and a VL sequence comprising SEQ ID NO: 2704; or

(b) a VH sequence comprising SEQ ID NO: 2707 and a VL sequence comprising SEQ ID NO: 2708; or

(c) a VH sequence comprising SEQ ID NO: 2709 and a VL sequence comprising SEQ ID NO: 2708; or

(d) a VH sequence comprising SEQ ID NO: 2707 and a VL sequence comprising SEQ ID NO: 2710; or

(e) a VH sequence comprising SEQ ID NO: 79 and a VL sequence comprising SEQ ID NO: 2710; or

(f) a VH sequence comprising SEQ ID NO: 2712 and a VL sequence comprising SEQ ID NO: 2708; or

(g) a VH sequence comprising SEQ ID NO: 2714 and a VL sequence comprising SEQ ID NO: 2708; or

(h) a VH sequence comprising SEQ ID NO: 2712 and a VL sequence comprising SEQ ID NO: 2710; or

(i) a VH sequence comprising SEQ ID NO: 2714 and a VL sequence comprising SEQ ID NO: 2710; or

(j) a VH sequence comprising SEQ ID NO: 2690 and a VL sequence comprising SEQ ID NO: 2691; or

(k) a VH sequence comprising SEQ ID NO: 2698 and a VL sequence comprising SEQ ID NO: 2699; or

(l) a VH sequence comprising SEQ ID NO: 2712 and a VL sequence comprising SEQ ID NO: 2741.

[00317] In some embodiments, an antibody or antigen-binding fragment thereof that specifically binds to TREM2 comprises:

(a) a CDR-H1 sequence comprising the amino acid sequence of any one of SEQ ID NOS: 2692, 2700, and 2717;

(b) a CDR-H2 sequence comprising the amino acid sequence of any one of SEQ ID NOS: 2693, 2701, 2713, 2718, 2727, 2729, and 2731;

(c) a CDR-H3 sequence comprising the amino acid sequence of any one of SEQ ID NOS: 2694, 2702, 2705, and 2719;

(d) a CDR-L1 sequence comprising the amino acid sequence of any one of SEQ ID NOS: 2695, 2711, and 2720;

(e) a CDR-L2 sequence comprising the amino acid sequence of any one of SEQ ID NOS: 2696 and 2721; and

(f) a CDR-L3 sequence comprising the amino acid sequence of any one of SEQ ID NOS: 2697, 2706, and 2722.

[00318] In some embodiments, the antibody or antigen-binding fragment comprises:

(a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2693, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2694, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2697; or

(b) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2693, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(c) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2693, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2711, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(d) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2713, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO:

2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(e) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2713, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2711, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2706; or

(f) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2700, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2701, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2702, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2697;

(g) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2718, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722; or

(h) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2727, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722; or

(i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2729, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722; or

(j) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2717, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2731, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2719, a CDR-L1 comprising the amino acid sequence of SEQ ID NO:

2720, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2721, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2722; or

(k) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2692, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2713, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2705, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2695, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2696, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2697.

[00319] In some embodiments, the antibody or antigen-binding fragment comprises:

(a) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2690 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2691; or

(b) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2698 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2699; or

(c) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2703 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2704; or

(d) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2707 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2708; or

a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2709 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2708; or

(f) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2707 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2710; or

(g) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 79 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2710; or

(h) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2712 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2708; or

(i) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2714 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2708; or

(j) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2712 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2710; or

(k) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2714 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2710; or

(l) a VH sequence that has at least 85% sequence identity to SEQ ID

NO: 2715 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2716; or

(m) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2723 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(n) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2725 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(o) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2726 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(p) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2728 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(q) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2730 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(r) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2732 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(s) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2733 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(t) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2734 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2724; or

(u) a VH sequence that has at least 85% sequence identity to SEQ ID NO: 2712 and a VL sequence that has at least 85% sequence identity to SEQ ID NO: 2741.

[00320] In some embodiments, an antibody or antigen-binding fragment thereof that specifically binds to TREM2 recognizes an epitope that is the same or substantially the same as the epitope recognized by antibody clone selected from the group consisting of: CL0020306, Clone CL0020188, Clone CL0020188-1, Clone CL0020188-2, Clone CL0020188-3, Clone CL0020188-4, Clone CL0020188-5, Clone CL0020188-6, Clone CL0020 188-7, Clone CL0020188-8, Clone CL0020307, Clone CL0020123, Clone CL0020 123-1, Clone CL0020123-2, Clone CL0020123-3, Clone CL0020123-4, Clone CL0020123-5, Clone CL0020123-6, Clone CL0020123-7, and Clone CL0020123-8.

[00321] In some embodiments, the antibody or antigen-binding fragment recognizes an epitope that is the same or substantially the same as the epitope recognized by an antibody clone selected from the group consisting of: Clone CL0020123, Clone CL0020123-1, Clone CL0020123-2, Clone CL0020123-3, Clone CL0020123-4, Clone CL0020123-5, Clone

CL0020123-6, Clone CL0020123-7, and Clone CL0020123-8. In particular embodiments, the antibody or antigen-binding fragment recognizes one or more of the following epitopes in SEQ ID NO: 1: (i) amino acid residues 55-63 (GEKGPCQRV (SEQ ID NO: 2743)), (ii) amino acids 96-107 (TLRNLQPHDAGL (SEQ ID NO: 2744)), and (iii) amino acid residues 126-129 (VEVL (SEQ ID NO: 2745)). In another aspect, the disclosure features an isolated antibody or antigen-binding fragment thereof that specifically binds to a human TREM2, wherein the antibody or antigen-binding fragment thereof recognizes an epitope comprising or consisting of one or more of the following epitopes in SEQ ID NO: 1: (i) amino acid residues 55-63 (GEKGPCQRV (SEQ ID NO: 2743)), (ii) amino acids 96-107 (TLRNLQPHDAGL (SEQ ID NO: 2744)), and (iii) amino acid residues 126-129 (VEVL (SEQ ID NO: 2745)). In some embodiments, the antibody or antigen-binding fragment recognizes an epitope that is the same or substantially the same as the epitope recognized by an antibody clone selected from the group consisting of: Clone CL0020188, Clone CL0020188-1, Clone CL0020188-2, Clone CL0020188-3, Clone CL0020188-4, Clone CL0020188-5, Clone CL0020188-6, Clone CL0020 188-7, Clone CL0020188-8, Clone CL0020307, and Clone CL0020306. In particular embodiments, the antibody or antigen-binding fragment recognizes amino acid residues 143149 (FPGESES (SEQ ID NO: 2742)) in SEQ ID NO: 1. In another aspect, the disclosure features an isolated antibody or antigen-binding fragment thereof that specifically binds to a human TREM2, wherein the antibody or antigen-binding fragment thereof recognizes an epitope comprising or consisting of amino acid residues 143-149 (FPGESES (SEQ ID NO: 2742)) in SEQ ID NO: 1.

[00322] In some embodiments, an antibody or antigen-binding fragment as disclosed herein decreases levels of soluble TREM2 protein (sTREM2). In some embodiments, an antibody or antigen-binding fragment as disclosed herein binds soluble TREM2 protein (sTREM2) in healthy human CSF or cynomolgus CSF with better potency compared to a reference antibody. In some embodiments, the reference antibody is represented by a combination of sequences selected from the group consisting of: SEQ ID NOS: 2746 and 2747; SEQ ID NOS: 2748 and 2749; and SEQ ID NOS: 2750 and 2751.

[00323] In some embodiments, the antibody is an antibody having a VL, VH, full heavy chain sequence, full light chain sequence, a CDR sequence, or a full sequence disclosed in the "Informal Sequence Listing" Table IX of PCT Patent Application Publication No. WO 2020/172450 A1, which are reproduced below as **Table 19**.

Table 19

SEQ ID NO	Sequence	Description
1	MEPLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKH WGRRKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAIT DDTLGGTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVL ADPLDHRDAGDLWFPGESESFEDAHVEHSISRSLLEGEIPFPPTSI LLLLACIFLIKILAASALWAAAWHGQKPGTHPPSELDCGHDPGY QLQTLPGLRDT	Human TREM2 Protein
2690	EVKLLDSGGGLVQAGGSLRLSCAGSGFTFTDFYMSWIRQPPGKA PEWLGVIRNKANGYTAGYNPSVKGRFTISRDNTQNILYLQMNTL RAEDTAIYYCARLSYGFDYWGQGVMVTVSS	CL0020306 VH
2691	DIVMTQGALPNPVPSGESASITCQSSKSLLHSNGKTYLNWYLQR PGQSPQLLIYWMSTRASGVSDRFSGSGSGTDFTLKIS SVEAEDVG VYYCQQFLEFPFTFGSGTKLEIK	CL0020306 VL
2692	GFTFTDFYMS	CL0020306 CDR-H1; CDR-H1 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3, CL0020188-4, CL0020188-5, CL0020188-6, CL0020188-7, and CL0020188-8
2693	VIRNKANGYTAGYNPSVKG	CL0020306 CDR-H2; CDR-H2 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3, and CL0020188-4
2694	ARLSYGFDY	CL0020306 CDR-H3
2695	QSSKSLLHSNGKTYLN	CL0020306 CDR-L1; CL0020307 CDR-L1; CL0020307-1 CDR-L1; CDR-L1 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-5, and CL0020188-6
2696	WMSTRAS	CL0020306 CDR-L2; CL0020307 CDR-L2; CL0020307-1 CDR-L2; CDR-L2 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3, CL0020188-4, CL0020188-5, CL0020188-6, CL0020188-7, and CL0020188-8
2697	QQFLEFPFT	CL0020306 CDR-L3; CL0020307 CDR-L3; CL0020307-1 CDR-L3
2698	EVKLLESGGGLVQPGGSLRLSCAASGFTFTNFYMSWIRQPPGRA PEWLGVIRNRPNGYTTDYNPSVKGRFTISRDNTQNILYLQMSTL RADDTAFYYCTRLTYGFDYWGQGVMVTVSS	CL0020307 V_H
2699	DIVMTQGALPNPVPSGESASITCQSSKSLLHSNGKTYLNWYLQR PGQSPQLLIYWMSTRASGVSDRFSGSGSGTDFTLKIS SVEAEVVG VYYCQQFLEFPFTFGSGTKLEIK	CL0020307 VL
2700	GFTFTNFYMS	CL0020307 CDR-H1

2701	VIRNRPNGYTTDYNPSVKG	CL0020307 CDR-H2
2702	TRLTYGFDY	CL0020307 CDR-H3
2703	EVKLLDSGGGLVQAGGSLRLSCAGSGFTFTDFYMSWIRQPPGKA PEWLGVIRNKANGYTAGYNPSVKGRFTISRDNTQNILYLQMNTL RAEDTAIYYCARLTYGFDYWGQGVMVTVSS	CL0020188 VH
2704	DIVMTQGALPNPVPSGESASITCQSSKSLLHSNGKTYLNWYLQR PGQSPQLLIYWMSTRASGVSDRFSGSGSGTDFTLKIS SVEAEDVG VYYCQQFLEYPFTFGSGTKLEIK	CL0020188 VL
2705	ARLTYGFDY	CDR-H3 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3,
2706	QQFLEYPFT	CDR-L3 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3,
2707	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDFYMSWVRQAPGK GLEWVSVIRNKANGYTAGYNPSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARLTYGFDYWGQGTLVTVSS	CL0020188-1 VH; CL0020188-3 VH
2708	DIVMTQTPLSLPVTPGEPASISCQSSKSLLHSNGKTYLNWYLQKP GQSPQLLIYWMSTRASGVPDRFSGSGSGTDFTLKISRVEAEDVG VYYCQQFLEYPFTFGQGTKVEIK	CL0020188-1 VL; CL0020188-2 VL; CL0020188-5 VL;
2709	EVQLVESGGGLVQPGGSLRLSCAGSGFTFTDFYMSWVRQAPGK GLEWVSVIRNKANGYTAGYNPSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARLTYGFDYWGQGTLVTVSS	CL0020188-2 VH
2710	DIVMTQTPLSLPVTPGEPASISCQSSKSLLHSTGKTYLNWYLQKP GQSPQLLIYWMSTRASGVPDRFSGSGSGTDFTLKISRVEAEDVG VYYCQQFLEYPFTFGQGTKVEIK	CL0020188-3 VL; CL0020188-4 VL; CL0020188-7 VL;
2711	QSSKSLLHSTGKTYLN	CDR-L1 for variants CL0020188-3, CL0020188-4, CL0020188-7, and CL0020188-
2712	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDFYMSWVRQAPGK GLEWVSVIRNKANAYTAGYNPSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARLTYGFDYWGQGTLVTVSS	CL0020188-5 VH; CL0020188-7 VH
2713	VIRNKANAYTAGYNPSVKG	CDR-H2 for variants CL0020188-5, CL0020188-6, CL0020188-7, and CL0020188-
2714	EVQLVESGGGLVQPGGSLRLSCAGSGFTFTDFYMSWVRQAPGK GPEWLSVIRNKANAYTAGYNPSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARLTYGFDYWGQGTLVTVSS	CL0020188-6 VH; CL0020188-8 VH
2715	EVQLQQSGAELVRSGASVKLSCTASGFSIEDFYIHWVKQRPEQG LEWIGWIDPENGDSKYAPKFQGKATMTADTSSNTAYLHLSSLTS EDTAVYYCHADHGNYGSTMDYWGQGTSVTVSS	CL0020123 VH
2716	DIQMNQSPSSLSASLGDTVTITCHASQHINVWLSWYQQKPGDHP KLLIYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYCQQ GQTYPRTFGGGTKLEIK	CL0020123 VL
2717	GFSIEDFYIH	CDR-H1 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3,
2718	WIDPENGDSKYAPKFQG	CDR-H2 for CL0020123 and variants CL0020123-1 and CL0020123-2
2719	HADHGNYGSTMDY	CDR-H3 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3,

2720	HASQHINVWLS	CDR-L1 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3,
2721	KASNLHT	CDR-L2 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3,
2722	QQGQTYPRT	CDR-L3 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3,
2723	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPENGDSKYAPKFQGRATITADTSTSTAYMELSSL RSEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-1 VH
2724	DIQMTQSPSSLSASVGDRVTITCHASQHINVWLSWYQQKPGKAP KLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ QGQTYPRTFGQGTKVEIK	CL0020123-1 VL; CL0020123-2 VL; CL0020123-3 VL;
2725	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPENGDSKYAPKFQGRVTITADTSTSTAYMELSSL RSEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-2 VH
2726	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPEQGDSKYAPKFQGRATITADTSTSTAYMELSSL RSEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-3 VH
2727	WIDPEQGDSKYAPKFQG	CDR-H2 for variants CL0020123-3 and CL0020123-6
2728	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPENGESKYAPKFQGRATITADTSTSTAYMELS SLR SEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-4 VH
2729	WIDPENGESKYAPKFQG	CDR-H2 for variants CL0020123-4 and CL0020123-7
2730	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPEQGESKYAPKFQGRATITADTSTSTAYMELS SLR SEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-5 VH
2731	WIDPEQGESKYAPKFQG	CDR-H2 for variants CL0020123-5 and CL0020123-8
2732	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPEQGDSKYAPKFQGRVTITADTSTSTAYMELSSL RSEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-6 VH
2733	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPENGESKYAPKFQGRVTITADTSTSTAYMELS SLR SEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-7 VH
2734	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYIHWVRQAPGQ GLEWMGWIDPEQGESKYAPKFQGRVTITADTSTSTAYMELS SLR SEDTAVYYCHADHGNYGSTMDYWGQGTLVTVSS	CL0020123-8 VH
2735	W-I-D-P-E-β6-G-β8-S-K-Y-A-P-K-F-Q-G, wherein (β6 is N or Q and (β8 is D or E	CDR-H2 consensus sequence
2736	G-F-T-F-T-α6-F-Y-M-S, wherein α6 is D or N	CDR-H1 consensus sequence
2737	V-I-R-N-β5-β6-N-β8-Y-T-β11-β12-Y-N-P-S-V-K-G, wherein β5 is K or R; β6 is A or P; β5 is G or A; Pic is A or T; and (312 is G or D	CDR-H2 consensus sequence

2738	γ1-R-L-γ4-Y-G-F-D-Y, wherein γ1 is A or T; and γ4 is T or S	CDR-H3 consensus sequence
2739	Q-S-S-K-S-L-L-H-S-δ10-G-K-T-Y-L-N, wherein δ10 is N or T	CDR-L1 consensus sequence
2740	Q-Q-F-L-E-ϕ6-P-F-T, wherein ϕ6 is Y or F	CDR-L3 consensus sequence
2741	DIVMTQSPDSLAVSLGERATINCQSSKSLLHSNGKTYLNWYQQK PGQPPKLLIYWMSTRASGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQFLEFPFTFGQGTKVEIK	CL0020307-1 VL
2742	FPGESES	TREM2 epitope
2743	GEKGPCQRV	TREM2 epitope
2744	TLRNLQPHDAGL	TREM2 epitope
2745	VEVL	TREM2 epitope
2746	DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWYQQKPGKAP KLLIYAASSLQVGVPLRFSGSGSGTDFTLTISSLQPEDFATYYCQ QADSFPRNFGQGTKLEIK	Reference antibody #1 VL
2747	EVQLVQSGAEVKKPGESLKISCKGSGHSFTNYWIAWVRQMPGK GLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKA SDTAVYFCARQRTFYYDSSGYFDYWGQGTLVTVSS	Reference antibody #1 VH
2748	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAP KLLIYAASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQ ADSFPRTFGQGTKLEIK	Reference antibody #2 VL
2749	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGK GLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKA SDTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSS	Reference antibody #2 VH
2750	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNRYTYLHWYQQ KPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDV GVYYCSQSTRVPYTFGQGTKLEIK	Reference antibody #3 VL
2751	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWVRQAP GQRLEWIGRIYPGGGDTNYAGKFQGRVTITADTSASTAYMELSS LRSEDTAVYYCARLLRNQPGESYAMDYWGQGTLVTVSS	Reference antibody #3 VH
2752	EVQLVESGGGLVQPGGSLRLSCAGSGFTFTDFYMSWVRQAPGK GPEWLSVIRNKANGYTAGYNPSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARLTYGFDYWGQGTLVTVSS	CL0020188-4 VH

[00324] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in Table 19 as well as specific combinations thereof and other embodiments of the anti-TREM2 antibody described in the '450 application and herein may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain

variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

M. PCT Patent Application Publication No. WO2021/101823A1

[00325] In some embodiments, the TREM2 agonist is an antibody, or an antigen-binding fragment thereof, as described in PCT Patent Application Publication No. *WO2021/101823A1* ("the '823 application"), which is incorporated by reference herein, in its entirety.

[00326] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

(a) a CDR-H1 sequence comprising the sequence of GFSFNTYWIG (SEQ ID NO: 2753);

(b) a CDR-H2 sequence comprising the sequence of IIYPGDQDIRYSPSFQG (SEQ ID NO: 2754;

(c) a CDR-H3 sequence comprising the sequence of ARYGRYIYGYGGYHGMDV (SEQ ID NO: 2755;

(d) CDR-L1 sequence comprising the sequence of RASQAIRDDLG (SEQ ID NO: 2756);

(e) a CDR-L2 sequence comprising the sequence of YAASSLQS (SEQ ID NO: 2757); and

(f) a CDR-L3 sequence comprising the sequence of LQNYNYPHT (SEQ ID NO: 2758).

[00327] In some embodiments, the antibody or antigen-binding fragment comprises a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 2753, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 2754, a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 2755, a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 2756, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2757, and a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 2758

[00328] In some embodiments, the antibody or antigen-binding fragment comprises a V_H sequence that has at least 85% sequence identity to SEQ ID NO: 2759. In some embodiments, the V_H sequence has at least 90% sequence identity to SEQ ID NO: 2759. In some embodiments, the V_H sequence has at least 95% sequence identity to SEQ ID NO: 2759. In some embodiments, the V_H sequence comprises SEQ ID NO: 2759.

[00329] In some embodiments, the antibody or antigen-binding fragment comprises a V_L sequence that has at least 85% sequence identity to SEQ ID NO: 2760. In some embodiments, the V_L sequence has at least 90% sequence identity to SEQ ID NO: 2760. In some embodiments,

the V_L sequence has at least 95% sequence identity to SEQ ID NO: 2760. In some embodiments, the V_L sequence comprises SEQ ID NO: 2760.

[00330] In some embodiments, the antibody or antigen-binding fragment comprises a VH sequence comprising SEQ ID NO: 2759 and a V_L sequence comprising SEQ ID NO: 2760.

[00331] In some embodiments, an antibody or antigen-binding fragment thereof that specifically binds to TREM2 recognizes an epitope that is the same or substantially the same as the epitope recognized by Antibody 1 of the '823 application.

[00332] In some embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a human TREM2. In particular embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a human TREM2 in SEQ ID NO: 2763. In some embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a mouse TREM2. In particular embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a mouse TREM2 in SEQ ID NO: 2764. In some embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a rat TREM2. In particular embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a rat TREM2 in SEQ ID NO: 2765. In some embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a rabbit TREM2. In particular embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a rabbit TREM2 in SEQ ID NO: 2766. In some embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a cynomolgus monkey TREM2. In particular embodiments, the antibody or antigen-binding fragment recognizes an epitope present on the extracellular domain of a cynomolgus monkey TREM2 in SEQ ID NO: 2767.

[00333] In some embodiments, the antibody is an antibody having a VL, VH, full heavy chain sequence, full light chain sequence, a CDR sequence, or a full sequence disclosed in the "SEQUENCE" Table of PCT Patent Application Publication No. *WO2021/101823A1*, which are reproduced below as **Table 20**.

Table 20

SEQ ID NO	Sequence	Description

2753	GFSFNTYWIG	’823 Antibody 1 CDR-H1
2754	IIYPGDQDIRYSPSFQG	’823 Antibody 1 CDR-H2
2755	ARYGRYIYGYGGYHGMDV	’823 Antibody 1 CDR-H3
2756	RASQAIRDDLG	’823 Antibody 1 CDR-L1
2757	YAASSLQS	’823 Antibody 1 CDR-L2
2758	LQNYNYPHT	’823 Antibody 1 CDR-L3
2759	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYWIGWVRQMPGKG LEWMGIIYPGDQDIRYSPSFQGQVTISADKSISTAYLQWSSLKASD TAMYYCARYGRYIYGYGGYHGMDVWGQGTTVTVSS	’823 Antibody 1 VH
2760	DIQMTQSPSSLSASVGDRVTITCRASQAIRDDLGWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQNY NYPHTFGQGTKLEIK	’823 Antibody 1 VL
2761	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYWIGWVRQMPGKG LEWMGIIYPGDQDIRYSPSFQGQVTISADKSISTAYLQWSSLKASD TAMYYCARYGRYIYGYGGYHGMDVWGQGTTVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKR VESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQK SLSLSLG	’823 Antibody 1 Heavy Chain
2762	DIQMTQSPSSLSASVGDRVTITCRASQAIRDDLGWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQ NYNYPHTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	’823 Antibody 1 Light Chain
2763	HNTTVFQGVAGQSLQVSCPYDSMKHWGRRKAWCRQLGEKGP CQRVVSTHNLWLLSFLRRWNGSTAITDDTLGGTLTITLRNLQPH DAGLYQCQSLHGSEADTLRKVLVEVLADPLDHRDAGDLWFPG ESESFEDAHVEHSISRSLLEGEIPFPPTSHHHHHH	Human TREM2 ECD-His
2764	LNTTVLQGMAGQSLRVSCTYDALKHWGRRKAWCRQLGEEGPC QRVVSTHGVWLLAFLKKRNGSTVIADDTLAGTVTITLKNLQAGD AGLYQCQSLRGREAEVLQKVLVEVLEDPLDDQDAGDLWVPEESS SFEGAQVEHSTSRNQETSFPPTSHHHHHH	Mouse TREM2 ECD-His
2765	NTTVFQGVAGQSLRVSCPYDSATHWGRRKAWCRQLGEEGPCER VVSTHSWWLLSFLKRRNGSTAITDDALGGTLTVTLRDLQAQDAG VYQCQSLQGREASTLQKILVEVLTEPLEHEHAGDFWVPEESGSFE DPPVERSSSRSPSEGEPSFPPASGGGGQHHHHHH	Rat TREM2 ECD-His
2766	NTTVLQGVAGQSLRVSCTYDALRHWGRRKAWCRQLAEEGPCQR VVSTHGVWLLAFLRKQNGSTVITDDTLAGTVTITLRNLQAGDAG LYQCQSLRGREAEVLQKVVVEVLEDPLDDQDAGDLWVPEESESF EGAQVEHSTSRSQSGGGGQHHHHHH	Rabbit TREM2 ECD-His
2767	HNTTVFQGVEGQSLQVSCPYDSMKHWGRRKAWCRQLGEKGPC QRVVSTHNLWLLSFLRRRNGSTAITDDTLGGTLTITLRNLQPHDA GFYQCQSLHGSEADTLRKVLVEVLADPLDHRDAGDLWVPGESE SFEDAHVEHSISRPSQGSHLPSCLSKEGGGGQHHHHHH	Cynomolgus monkey TREM2 ECD-His

[00334] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in Table 20 as well as specific combinations thereof and other

embodiments of the anti-TREM2 antibody described in the '823 application and herein may be attached to the light chain constant regions (**Table 4**) and heavy chain constant regions (**Table 5**) to form complete antibody light and heavy chains, respectively, as further discussed below. Further, each of the generated heavy and light chain sequences may be combined to form a complete antibody structure. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed herein.

Antibody Constant Domains and Engineered Constant Regions

[00335] In some embodiments, any of the antigen binding agents, can have a constant domain on the light chain and/or the heavy chain of any origin. The term "constant region" as used herein refers to all domains of an antibody other than the variable region. The constant domain can be that of rodent, primate or other mammals. In some embodiments, the constant domain is of human origin. Accordingly, in some embodiments, any of the antigen binding agents described herein can have a human constant region, some of which are described above.

[00336] In some embodiments, a human constant region is, for example, a human light chain constant region or a human constant heavy chain region.

[00337] The term "light chain" or "immunoglobulin light chain" refers to a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin light chain variable region (VL) and a single immunoglobulin light chain constant domain (CL). The immunoglobulin light chain constant domain (CL) can be a human kappa (κ) or human lambda (λ) constant domain.

[00338] The term "heavy chain" or "immunoglobulin heavy chain" refers to a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin heavy chain variable region (VH), an immunoglobulin heavy chain constant domain 1 (CH1), an immunoglobulin hinge region, an immunoglobulin heavy chain constant domain 2 (CH2), an immunoglobulin heavy chain constant domain 3 (CH3), and optionally an immunoglobulin heavy chain constant domain 4 (CH4). Heavy chains are classified as mu (μ), delta (Δ), gamma (γ), alpha (α), and epsilon (ε), and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. The IgG-class and IgA-class antibodies are further divided into subclasses, namely,

IgG1, IgG2, IgG3, and IgG4, and IgA1 and IgA2, respectively. The heavy chains in IgG, IgA, and IgD antibodies have three domains (CH1, CH2, and CH3), whereas the heavy chains in IgM and IgE antibodies have four domains (CH1, CH2, CH3, and CH4). The immunoglobulin heavy chain constant domains can be from any immunoglobulin isotype, including subtypes. The antibody chains are linked together via inter-polypeptide disulfide bonds between the CL domain and the CH1 domain (i.e. between the light and heavy chain) and between the hinge regions of the antibody heavy chains.

[00339] In some embodiments, the human light chain constant region comprises a human kappa or human lambda constant region. In some embodiments, the antigen binding agents based on any light chain variable region or CDRs of a light chain variable region described herein includes a human light chain constant region, such as a kappa or lambda constant region sequences, which are found in all five antibody isotypes. Examples of human immunoglobulin light chain constant region sequences are shown in the following table.

[00340] Table 4. Exemplary Human Immunoglobulin Light Chain Constant Regions

Designation	SEQ ID NO:	CL Domain Amino Acid Sequence
Human lambda v1	191	GQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
Human lambda v2	192	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
Human lambda v3	193	QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
Human lambda v4	194	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
Human lambda v5	195	GQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS
Human kappa v1	196	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Human kappa v2	197	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

[00341] In some embodiments, a human constant region comprises at least one or all of the following: a human CH1, human Hinge, human CH2, and CH3 domain. In some embodiments, the heavy chain constant region comprises an Fc region, where the Fc portion is a human IgG_1, IgG_2, IgG_3, IgG_4 or IgM isotype. The term "Fc region" refers to the C-terminal region of an immunoglobulin heavy chain which may be generated by papain digestion of an intact antibody. The Fc region of an immunoglobulin generally comprises two constant domains, a CH2 domain and a CH3 domain, and optionally comprises a CH4 domain. In certain embodiments, the Fc region is an Fc region from an IgG1, IgG2, IgG3, or IgG4 immunoglobulin. In some embodiments, the Fc region comprises CH2 and CH3 domains from a human IgG1 or human IgG2 immunoglobulin. The Fc region may retain effector function, such as C1q binding, complement-dependent cytotoxicity (CDC), Fc receptor binding, antibody-dependent cell-mediated cytotoxicity (ADCC), and phagocytosis. In other embodiments, the Fc region may be modified to reduce or eliminate effector function as described in further detail below.

[00342] In some embodiments, the antigen binding agents based on any heavy chain variable region or CDRs of a heavy chain variable region described herein includes a human heavy chain constant region., for example a human constant region comprising at least one or all of a human CH1, human Hinge, human CH2, and CH3 domain. In some embodiments, the antigen binding agents based on any heavy chain variable region or CDRs of a heavy chain variable region described herein includes an Fc region, where the Fc region is a human IgG_1, IgG_2, IgG_3, IgG_4 or IgM isotype. Examples of human IgG1, IgG2, and IgG4 heavy chain constant region sequences are shown below in **Table 5**.

[00343] Table 5. Exemplary Human Immunoglobulin Heavy Chain Constant Regions

Ig isotype	SEQ ID NO:	Heavy Chain Constant Region Amino Acid Sequence
Human IgG1z	198	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1za	199	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS

Ig isotype	SEQ ID NO:	Heavy Chain Constant Region Amino Acid Sequence
		HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1f	200	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1fa	201	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1z aglycosylated v1	202	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1z aglycosylated v2	203	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG2	204	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVER KCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG4	205	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[00344] In some embodiments, the heavy chain constant region, particularly the Fc region, is an engineered heavy chain constant region. In some embodiments, the antigen binding proteins, e.g. monoclonal antibodies, comprise one or more amino acid substitutions in the Fc region to enhance effector function, including ADCC activity, CDC activity, ADCP activity, and/or the clearance or half-life of the antigen binding protein. Exemplary amino acid substitutions (according to EU numbering scheme) that can enhance effector function include, but are not limited to, E233L, L234I, L234Y, L235S, G236A, S239D, F243L, F243V, P247I, D280H, K290S, K290E, K290N, K290Y, R292P, E294L, Y296W, S298A, S298D, S298V, S298G, S298T, T299A, Y300L, V305I, Q311M, K326A, K326E, K326W, A330S, A330L, A330M, A330F, I332E, D333A, E333S, E333A, K334A, K334V, A339D, A339Q, P396L, or combinations of any of the foregoing.

[00345] In some embodiments, the TREM2 antigen binding proteins (e.g. monoclonal antibodies) comprise one or more amino acid substitutions in a heavy chain constant region to reduce effector function. Exemplary amino acid substitutions (according to EU numbering scheme) that can reduce effector function include, but are not limited to, C220S, C226S, C229S, E233P, L234A, L234V, V234A, L234F, L235A, L235E, G237A, P238S, S267E, H268Q, N297A, N297G, N297Q, V309L, E318A, L328F, A330S, A331S, P331S or combinations of any of the foregoing.

[00346] In some embodiments, the TREM2 agonist antigen binding proteins comprise one or more amino acid substitutions that affect the level or type of glycosylation of the binding proteins. Glycosylation can contribute to the effector function of antibodies, particularly IgG1 antibodies. Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[00347] In some embodiments, glycosylation of the TREM2 agonist antigen binding proteins described herein is increased by adding one or more glycosylation sites, e.g., to the Fc region of the binding protein. Addition of glycosylation sites to the antigen binding protein can be conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antigen binding protein amino acid sequence may be altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[00348] The invention also encompasses production of TREM2 antigen binding protein molecules with altered carbohydrate structure resulting in altered effector activity, including antigen binding proteins with absent or reduced fucosylation that exhibit improved ADCC activity. Various methods are known in the art to reduce or eliminate fucosylation. For example, ADCC effector activity is mediated by binding of the antibody molecule to the FcγRIII receptor, which has been shown to be dependent on the carbohydrate structure of the N-linked glycosylation at the N297 residue of the CH2 domain. Non-fucosylated antibodies bind this receptor with increased affinity and trigger FcγRIII-mediated effector functions more efficiently than native, fucosylated antibodies. For example, recombinant production of non-fucosylated antibody in CHO cells in which the alpha-1,6-fucosyl transferase enzyme has been knocked out results in antibody with 100-fold increased ADCC activity (*see* Yamane-Ohnuki *et al.*, Biotechnol Bioeng. 87(5):614-22, 2004). Similar effects can be accomplished through decreasing the activity of alpha-1,6-fucosyl transferase enzyme or other enzymes in the fucosylation pathway, e.g., through siRNA or antisense RNA treatment, engineering cell lines to knockout the enzyme(s), or culturing with selective glycosylation inhibitors (*see* Rothman *et al.*, Mol Immunol. 26(12):1113-23, 1989). Some host cell strains, e.g. Lec13 or rat hybridoma YB2/0 cell line naturally produce antibodies with lower fucosylation levels (*see* Shields *et al.*, J Biol Chem. 277(30):26733-40, 2002 and Shinkawa *et al.*, J Biol Chem. 278(5):3466-73, 2003). An increase in the level of bisected carbohydrate, e.g. through recombinantly producing antibody in cells that overexpress GnTIII enzyme, has also been determined to increase ADCC activity (*see* Umana *et al.*, Nat Biotechnol. 17(2):176-80, 1999).

[00349] In other embodiments, glycosylation of the TREM2 agonist antigen binding proteins described herein is decreased or eliminated by removing one or more glycosylation sites, e.g., from the Fc region of the binding protein. In some embodiments, the TREM2 agonist antigen binding protein is an aglycosylated human monoclonal antibody, e.g. an aglycosylated human IgG1 monoclonal antibody. Amino acid substitutions that eliminate or alter N-linked glycosylation sites can reduce or eliminate N-linked glycosylation of the antigen binding protein. In certain embodiments, the TREM2 agonist antigen binding proteins described herein comprise a mutation at position N297 (according to EU numbering scheme), such as N297Q, N297A, or N297G. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise an Fc region from a human IgG1 antibody with a mutation at position N297. In one particular embodiment, the TREM2 agonist antigen binding proteins of the invention comprise an Fc region from a human IgG1 antibody with a N297G mutation. For instance, in some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a heavy chain constant region comprising the sequence of SEQ ID NO: 202.

[00350] To improve the stability of molecules comprising a N297 mutation, the Fc region of the TREM2 agonist antigen binding proteins may be further engineered. For instance, in some embodiments, one or more amino acids in the Fc region are substituted with cysteine to promote disulfide bond formation in the dimeric state. Residues corresponding to V259, A287, R292, V302, L306, V323, or I332 (according to EU numbering scheme) of an IgG1 Fc region may thus be substituted with cysteine. Preferably, specific pairs of residues are substituted with cysteine such that they preferentially form a disulfide bond with each other, thus limiting or preventing disulfide bond scrambling. Preferred pairs include, but are not limited to, A287C and L306C, V259C and L306C, R292C and V302C, and V323C and I332C. In certain embodiments, the TREM2 agonist antigen binding proteins described herein comprise an Fc region from a human IgG1 antibody with mutations R292C and V302C. In such embodiments, the Fc region may also comprise a N297 mutation, such as a N297G mutation. In some embodiments, the TREM2 agonist antigen binding proteins of the invention comprise a heavy chain constant region comprising the sequence of SEQ ID NO: 203.

[00351] Modifications to the hinge region and/or CH1 domain of the heavy chain and/or the constant region of the light chain of the TREM2 agonist antigen binding proteins (e.g. monoclonal antibodies) of the invention can be made to reduce or eliminate disulfide

heterogeneity. Structural hetereogeneity of IgG2 antibodies has been observed where the disulfide bonds in the hinge and CH1 regions of IgG2 antibodies can be shuffled to create different structural disulfide isoforms (IgG2A, IgG2B, and IgG2A-B), which can have different levels of activity. *See, e.g.*, Dillon *et al.*, J. Biol. Chem., Vol. 283: 16206-16215; Martinez *et al.*, Biochemistry, Vol. 47: 7496-7508, 2008; and White *et al.*, Cancer Cell, Vol. 27: 138-148, 2015. Amino acid substitutions can be made in the hinge region, CH1 domain, and/or light chain constant region to promote the formation of a single disulfide isoform or lock the antigen binding protein (e.g. monoclonal antibody) into a particular disulfide isoform (e.g. IgG2A or IgG2B). Such mutations are described in WO 2009/036209 and White *et al.*, Cancer Cell, Vol. 27: 138-148, 2015, both of which are hereby incorporated by reference in its entirety, and include C131S, C219S, and C220S (according to EU numbering scheme) mutations in the heavy chain and a C214S (according to EU numbering scheme) mutation in the light chain. In certain embodiments, the TREM2 agonist antigen binding proteins of the invention are human IgG2 anti-TREM2 agonist antibodies. In some such embodiments, the TREM2 agonist antibodies comprise a C131S mutation (according to the EU numbering scheme) in their heavy chains. In other embodiments, the TREM2 agonist antibodies comprise a C214S mutation (according to the EU numbering scheme) in their light chains and a C220S mutation (according to the EU numbering scheme) in their heavy chains. In still other embodiments, the TREM2 agonist antibodies comprise a C214S mutation (according to the EU numbering scheme) in their light chains and a C219S mutation (according to the EU numbering scheme) in their heavy chains.

[00352] In other embodiments, the TREM2 agonist antigen binding proteins of the invention are anti-TREM2 agonist antibodies comprising a CH1 region and hinge region from a human IgG2 antibody and an Fc region from a human IgG1 antibody. The unique arrangement of the disulfide bonds in the hinge region of IgG2 antibodies has been reported to impart enhanced stimulatory activity for certain anticancer antibodies (White *et al.*, Cancer Cell, Vol. 27: 138-148, 2015). This enhanced activity could be transferred to IgG1-type antibodies by exchanging the CH1 and hinge regions of the IgG1 antibody for those in the IgG2 antibody (White *et al.*, 2015). The IgG2 hinge region includes the amino acid sequence ERKCCVECPPCP (SEQ ID NO: 206). The amino acid sequence of the CH1 and hinge regions from a human IgG2 antibody may comprise the following amino acid sequence:

ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER
KCCVECPPCP (SEQ ID NO: 207).

[00353] In some embodiments, the antigen binding agents based on any heavy chain variable region or CThus, in some embodiments, the anti-TREM2 agonist antibodies comprise the sequence of SEQ ID NO: 207 in combination with an Fc region from a human IgG1 antibody. In such embodiments, the anti-TREM2 antibodies can comprise one or more of the mutations described above to lock the anti-TREM2 antibodies into a particular disulfide isoform. For instance, in one embodiment, the anti-TREM2 antibody comprises a CH1 region and hinge region from a human IgG2 antibody and an Fc region from a human IgG1 antibody and comprises a C131S mutation (according to the EU numbering scheme) in its heavy chain. In another embodiment, the anti-TREM2 antibody comprises a CH1 region and hinge region from a human IgG2 antibody and an Fc region from a human IgG1 antibody and comprises a C214S mutation (according to the EU numbering scheme) in its light chain and a C220S mutation (according to the EU numbering scheme) in its heavy chain. In yet another embodiment, the anti-TREM2 antibody comprises a CH1 region and hinge region from a human IgG2 antibody and an Fc region from a human IgG1 antibody and comprises a C214S mutation (according to the EU numbering scheme) in its light chain and a C219S mutation (according to the EU numbering scheme) in its heavy chain.

[00354] In embodiments in which the anti-TREM2 antibodies comprise a CH1 region and hinge region from a human IgG2 antibody and an Fc region from a human IgG1 antibody, the anti-TREM2 antibodies may comprise any of the mutations in the Fc region described above to modulate the glycosylation of the antibodies. For instance, the human IgG1 Fc region of such anti-TREM2 antibodies may comprise a mutation at amino acid position N297 (according to the EU numbering scheme) in its heavy chain. In one particular embodiment, the N297 mutation is a N297G mutation. In certain embodiments, the Fc region may further comprise R292C and V302C mutations (according to the EU numbering scheme) in its heavy chain.

[00355] In certain embodiments, the anti-TREM2 antibodies of the invention comprise a CH1 region and hinge region from a human IgG2 antibody and an Fc region from a human IgG1 antibody, wherein the Fc region comprises the amino acid sequence of:

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 281).

[00356] In other embodiments, the anti-TREM2 antibodies of the invention comprise a CH1 region and hinge region from a human IgG2 antibody and an Fc region from a human IgG1 antibody, wherein the Fc region comprises the amino acid sequence of:

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 282).

[00357] Modifications of the TREM2 agonist antigen binding proteins of the invention to increase serum half-life also may desirable, for example, by incorporation of or addition of a salvage receptor binding epitope (e.g., by mutation of the appropriate region or by incorporating the epitope into a peptide tag that is then fused to the antigen binding protein at either end or in the middle, e.g., by DNA or peptide synthesis; *see, e.g.*, WO96/32478) or adding molecules such as PEG or other water soluble polymers, including polysaccharide polymers. The salvage receptor binding epitope preferably constitutes a region wherein any one or more amino acid residues from one or two loops of an Fc region are transferred to an analogous position in the antigen binding protein. Even more preferably, three or more residues from one or two loops of the Fc region are transferred. Still more preferred, the epitope is taken from the CH2 domain of the Fc region (e.g., an IgG Fc region) and transferred to the CH1, CH3, or VH region, or more than one such region, of the antigen binding protein. Alternatively, the epitope is taken from the CH2 domain of the Fc region and transferred to the CL region or VL region, or both, of the antigen binding protein. *See* International applications WO 97/34631 and WO 96/32478 for a description of Fc variants and their interaction with the salvage receptor.

Antibody Fragments

[00358] In some embodiments, the antigen binding agent can be a fragment of the antibody of the present disclosure, including portions of a full length antibody, and includes the antigen binding or variable region. Exemplary antibody fragments include Fab, Fab', $F(ab')_2$ and Fv

fragments. In some embodiments, proteolytic digestion with papain produces two identical antigen binding fragments, the Fab' fragment, each with a single antigen binding site. In some embodiments, proteolytic digestion with pepsin yields an $F(ab')_2$ fragment that has two antigen binding fragments which are capable of cross-linking antigen, and a residual pFc' fragment. In some embodiments, antibody fragments are produced directly in recombinant host-cells, for example host cells that that have a polynucleotide encoding an antigen binding agent described herein. For example, Fab, Fv and scFv antibody fragments can all be expressed in and secreted from E. coli, thus allowing the straightforward production of large amounts of these fragments. Anti-TREM2 antibody fragments can also be isolated from the antibody phage libraries as discussed above. Alternatively, Fab'-SH fragments can be directly recovered from E. coli and chemically coupled to form $F(ab')_2$ fragments (Carter et al., Bio/Technology 10:163-167 (1992)). According to another approach, $F(ab')_2$ fragments can be isolated directly from recombinant host-cell culture. Production of Fab and $F(ab')_2$ antibody fragments with increased in vivo half-lives are described in U.S. Pat. No. 5,869,046. In other embodiments, the antibody of choice is a single chain Fv fragment (scFv). See WO 93/16185; U.S. Pat. No. 5,571,894 and U.S. Pat. No. 5,587,458. Accordingly, other types of fragments can include diabodies, linear antibodies, single-chain antibodies, and multispecific antibodies formed from antibody fragments. In some embodiments, the antibody fragments are functional in that they retain the desired antigen binding properties, e.g., specific binding to TREM2, activation of TREM2 activities, and the like as described herein.

Bispecific Antibodies

[00359] In some embodiments, the TREM2 binding protein is a bispecific antibody that binds to a TREM2 protein of the present disclosure and a second antigen. In some embodiments, bispecific antibodies of the present disclosure bind to one or more amino acid residues of human TREM2 (SEQ ID NO: 1), or amino acid residues on a TREM2 protein corresponding to amino acid residues of SEQ ID NO: 1. In some embodiments, any of the TREM2 binding proteins described herein can be used to prepare the bispecific antibody.

[00360] In some embodiments, bispecific antibodies of the present disclosure recognize a first antigen and a second antigen. In some embodiments, the first antigen is human TREM2 or a naturally occurring variant thereof. In some embodiments, the second antigen is DAP12, or other proteins or ligand that interact with TREM2. In some embodiments, the second antigen is (a) an

antigen facilitating transport across the blood-brain-barrier; (b) an antigen facilitating transport across the blood-brain-barrier, for example transferrin receptor (TR), insulin receptor (HIR), insulin-like growth factor receptor (IGFR), low-density lipoprotein receptor related proteins 1 and 2 (LPR-1 and 2), diphtheria toxin receptor, CRM 197, a llama single domain antibody, TMEM 30(A), a protein transduction domain, TAT, Syn-B, penetratin, a poly-arginine peptide, an angiopep peptide, and ANG1005; (c) a disease-causing protein selected from amyloid beta, oligomeric amyloid beta, amyloid beta plaques, amyloid precursor protein or fragments thereof, Tau, IAPP, alpha-synuclein, TDP-43, FUS protein, C9orf72 (chromosome 9 open reading frame 72), c9RAN protein, prion protein, PrPSc, huntingtin, calcitonin, superoxide dismutase, ataxin, ataxin 1, ataxin 2, ataxin 3, ataxin 7, ataxin 8, ataxin 10, Lewy body, atrial natriuretic factor, islet amyloid polypeptide, insulin, apolipoprotein AI, serum amyloid A, medin, prolactin, transthyretin, lysozyme, beta 2 microglobulin, gelsolin, keratoepithelin, cystatin, immunoglobulin light chain AL, S-IBM protein, Repeat-associated non-ATG (RAN) translation products, DiPeptide repeat (DPR) peptides, glycine-alanine (GA) repeat peptides, glycine -proline (GP) repeat peptides, glycine-arginine (GR) repeat peptides, proline-alanine (PA) repeat peptides, ubiquitin, and proline-arginine (PR) repeat peptides; and (d) ligands and/or proteins expressed on immune cells, wherein the ligands and/or proteins selected from CD40, OX40, ICOS, CD28, CD137/4-1BB, CD27 , GITR, PD-L1, CTLA-4, PD-L2, PD-1, B7-H3, B7-H4, HVEM, BTLA, KIR, GAL9, TIM3, A2AR, LAG-3, and phosphatidylserine; and (e) a protein, lipid, polysaccharide, or glycolipid expressed on one or more tumor cells and any combination thereof.

[00361] Methods for making bispecific antibodies are known in the art. Traditional production of full-length bispecific antibodies is based on the coexpression of two immunoglobulin heavy-chain/light chain pairs, where the two chains have different specificities. Millstein et al., Nature, 305:537-539 (1983). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829 and in Traunecker et al., EMBO J. , 10:3655-3659 (1991).

[00362] In some embodiments, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The

fusion preferably is with an immunoglobulin heavy chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light chain binding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance.

[00363] In some embodiments, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only half of the bispecific molecules provides for an easy way of separation. This approach is disclosed in WO 94/04690. For further details of generating bispecific antibodies, see, for example, Suresh et al., Methods in Enzymology 121 : 210 (1986); and Garber, Nature Reviews Drug Discovery 13, 799-801 (2014).

[00364] In some embodiments, the bispecific antibody can be prepared as described in WO 96/27011 or U.S. Patent No. 5,731,168. In these embodiments, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant-cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. , tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chains(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. , alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

[00365] In some embodiments, bispecific antibody can be prepared Techniques for generating bispecific antibodies from antibody fragments have been described in for example, Brennan et al., Science, 1985, 229:81, which describe proteolytic cleavage of intact antibodies to generate F(ab')2 fragments, which are then reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzyme.

[00366] Various techniques for making and isolating bivalent antibody fragments directly from recombinant-cell culture have also been described. For example, bivalent heterodimers have been produced using leucine zippers. Kostelny et al., Immunol., 1992, 148(5):1547-1553. The "diabody" technology described by Hollinger et al., Proc. Nat'l Acad. Sci. USA, 1993, 90: 6444-6448, provides an alternative mechanism for making bispecific/bivalent antibody fragments. The fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific/bivalent antibody fragments by the use of single-chain Fv (sFv) dimers (see, e.g., Gruber et al., Immunol , 152:5368 (1994).

Single Chain Antibodies

[00367] In some embodiments, the TREM2 binding protein is a single chain antibody, e.g., single chain Fv (sFv or scFv) antibodies, in which a variable heavy and a variable light chain are joined together (directly or through a peptide linker) to form a continuous polypeptide. A single-chain Fv" or "sFv" antibody fragments comprise the VH and VL domains of an antibody, where these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, Vol. 113, pp. 269-315, Rosenburg and Moore, eds., Springer- Verlag, New York (1994). Any of the TREM2 binding agents described herein can be used to prepare a single chain antibody.

[00368] In some embodiments, single chain antibody can be prepared by phage display methods, where the antigen binding domain is expressed as a single polypeptide and screened for specific binding activity. Alternatively, the single chain antibody can be prepared by cloning the heavy and light chains from a cell, typically a hybridoma cell line expressing a desired antibody. Generally, a linker peptide, typically from 10 to 25 amino acids in length is used to link the heavy and light chains. The linker can be glycine, serine, and/or threonine rich to impart flexibility and solubility to the single chain antibody. Specific methods for generating single chain antibodies are described in, for example, Loffler et al., 2000, Blood 95(6):2098- 103; Worn and Pluckthun, 2001, J Mol Biol. 305, 989-1010; Pluckthun, In The Pharmacology of Monoclonal Antibodies, Vol. 113, pp. 269-315, Rosenburg and Moore, eds., Springer-Verlag, New York (1994); U.S. Patent No. 5,840,301; U.S. Patent No. 5,844,093; and U.S. Patent No. 5,892,020; all of which are incorporated herein by reference.

Multivalent antibodies

[00369] In some embodiments, the anti-TREM2 antibody is a multivalent antibody, which may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. In some embodiments, the anti-TREM2 antibodies of the present disclosure or antibody fragments thereof can be multivalent antibodies (which are other than of the IgM class) with three or more antigen binding sites (e.g. , tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid encoding the polypeptide chains of the antibody. The multivalent antibody can comprise a dimerization domain and three or more antigen binding sites. A preferred dimerization domain comprises an Fc region or a hinge region. In this scenario, the antibody will comprise an Fc region and three or more antigen binding sites amino-terminal to the Fc region. The preferred multivalent antibody herein contains three to about eight, but preferably four, antigen binding sites. The multivalent antibody contains at least one polypeptide chain (and preferably two polypeptide chains), wherein the polypeptide chain or chains comprise two or more variable domains. For instance, the polypeptide chain or chains may comprise VDl-(Xl)n-VD2-(X2)n-Fc, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is one polypeptide chain of an Fc region, XI and X2 represent an amino acid or polypeptide, and n is 0 or 1. Similarly, the polypeptide chain or chains may comprise VH-CH1 -flexible linker- VH-CH1-Fc region chain; or VH-CH1-VH-CH1-FC region chain. The multivalent antibody herein preferably further comprises at least two (and preferably four) light

chain variable domain polypeptides. The multivalent antibody herein may, for instance, comprise from about two to about eight light chain variable domain polypeptides. The light chain variable domain polypeptides contemplated here comprise a light chain variable domain and, optionally, further comprise a CL domain.

[00370] Multivalent antibodies may recognize the TREM2 antigen as well as without limitation additional antigens A beta peptide, antigen or an alpha synuclein protein antigen or, Tau protein antigen or, TDP-43 protein antigen or, prion protein antigen or, huntingtin protein antigen, or RAN, translation Products antigen, including the DiPeptide Repeats,(DPRs peptides) composed of glycine-alanine (GA), glycine -proline (GP), glycine-arginine (GR), proline-alanine (PA), or proline-arginine (PR), Insulin receptor, insulin like growth factor receptor. Transferrin receptor or any other antigen that facilitate antibody transfer across the blood brain barrier.

Polynucleotides Encoding TREM2 Antibodies

[00371] In another aspect, the present disclosure provides polynucleotides encoding the antibodies or antigen binding regions of the described herein. In particular, the polynucleotides are isolated polynucleotides. The polynucleotides may be operatively linked to one or more heterologous control sequences that control gene expression to create a recombinant polynucleotide capable of expressing the polypeptide of interest. Expression constructs containing a heterologous polynucleotide encoding the relevant polypeptide or protein can be introduced into appropriate host cells to express the corresponding polypeptide.

[00372] As will be appreciated by those in the art, due to the degeneracy of the genetic code, where the same amino acids are encoded by alternative or synonymous codons, an extremely large number of nucleic acids can be made, all of which encode the CDRs, variable regions, and heavy and light chains or other components of the antigen binding proteins described herein. Thus, having identified a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids, by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the encoded protein. In this regard, the present disclosure includes each and every possible variation of polynucleotides that encode the polypeptides disclosed herein.

[00373] An "isolated nucleic acid," which is used interchangeably herein with "isolated polynucleotide," is a nucleic acid that has been separated from adjacent genetic sequences present in the genome of the organism from which the nucleic acid was isolated, in the case of nucleic acids isolated from naturally-occurring sources. In the case of nucleic acids synthesized enzymatically from a template or chemically, such as PCR products, cDNA molecules, or oligonucleotides for example, it is understood that the nucleic acids resulting from such processes are isolated nucleic acids. An isolated nucleic acid molecule refers to a nucleic acid molecule in the form of a separate fragment or as a component of a larger nucleic acid construct. In one preferred embodiment, the nucleic acids are substantially free from contaminating endogenous material.

[00374] In some embodiments, the polynucleotide encodes a CDR L1, CDR L2 and CDR L3 of a light chain variable region described herein. In some embodiments, the polynucleotide encodes a CDR H1, CDR H2 and CDR H3 of a heavy chain variable region described herein.

[00375] In some embodiments, the polynucleotide encodes a CDR L1, CDR L2 and CDR L3 of a light chain variable region and a CDR H1, CDR H2 and CDR H3 of a heavy chain variable region described herein.

[00376] In some embodiments, the polynucleotide encodes a light chain variable region VL having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to the amino acid sequence of a variable light chain disclosed herein.

[00377] In some embodiments, the polynucleotide encodes a heavy chain variable region VH having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to the amino acid sequence of a variable heavy chain disclosed herein.

[00378] In some embodiments, the polynucleotides herein may be manipulated in a variety of ways to provide for expression of the encoded polypeptide. In some embodiments, the polynucleotide is operably linked to control sequences, including among others, transcription promoters, leader sequences, transcription enhancers, ribosome binding or entry sites, termination sequences, and polyadenylation sequences for expression of the polynucleotide and/or corresponding polypeptide. Manipulation of the isolated polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides and nucleic acid sequences utilizing recombinant DNA

methods are well known in the art. Guidance is provided in Sambrook et al., Molecular Cloning: A Laboratory Manual, 3rd Ed., Cold Spring Harbor Laboratory Press (2001); and Current Protocols in Molecular Biology, Ausubel. F. ed., Greene Pub. Associates (1998), updates to 2013.

[00379] In some embodiments, variants of the antigen binding proteins, including the variants described herein, can be prepared by site-specific mutagenesis of nucleotides in the DNA encoding the polypeptide, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the recombinant DNA in cell culture as outlined herein. However, antigen binding proteins comprising variant CDRs having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, e.g., binding to antigen. Such variants include, for example, deletions and/or insertions and/or substitutions of residues within the amino acid sequences of the antigen binding proteins. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antigen binding protein, such as changing the number or position of glycosylation sites. In some embodiments, antigen binding protein variants are prepared with the intent to modify those amino acid residues which are directly involved in epitope binding. In other embodiments, modification of residues which are not directly involved in epitope binding or residues not involved in epitope binding in any way, is desirable, for purposes discussed herein. Mutagenesis within any of the CDR regions, framework regions, and/or constant regions is contemplated. Covariance analysis techniques can be employed by the skilled artisan to design useful modifications in the amino acid sequence of the antigen binding protein. *See, e.g.*, Choulier, et al., Proteins 41:475-484, 2000; Demarest et al., J. Mol. Biol., 2004, 335:41-48; Hugo et al., Protein Engineering, 2003, 16(5):381-86; Aurora et al., US Patent Publication No. 2008/0318207 A1; Glaser et al., US Patent Publication No. 2009/0048122 A1; Urech et al., WO 2008/110348 A1; Borras et al., WO 2009/000099 A2. Such modifications determined by covariance analysis can improve potency, pharmacokinetic, pharmacodynamic, and/or manufacturability characteristics of an antigen binding protein.

[00380] In another aspect, the present invention also provides vectors comprising one or more nucleic acids or polynucleotides encoding one or more components of the antigen binding proteins

describe herein (e.g. variable regions, light chains, and heavy chains). As used herein, the term "vector" refers to any molecule or entity (e.g., nucleic acid, plasmid, bacteriophage or virus) used to transfer protein coding information into a host cell. Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors. The term "expression vector" or "expression construct" as used herein refers to a recombinant DNA molecule containing a desired coding sequence and appropriate nucleic acid control sequences necessary for the expression of the operably linked coding sequence in a particular host cell. An expression vector can include, but is not limited to, sequences that affect or control transcription, translation, and, if introns are present, affect RNA splicing of a coding region operably linked thereto. Nucleic acid sequences necessary for expression in prokaryotes include a promoter, optionally an operator sequence, a ribosome binding site and possibly other sequences. Eukaryotic cells are known to utilize promoters, enhancers, and termination and polyadenylation signals. A secretory signal peptide sequence can also, optionally, be encoded by the expression vector, operably linked to the coding sequence of interest, so that the expressed polypeptide can be secreted by the recombinant host cell, for more facile isolation of the polypeptide of interest from the cell, if desired.

[00381] The recombinant expression vector may be any vector (e.g., a plasmid or virus), which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the polynucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids. Exemplary expression vectors include, among others, vectors based on T7 or T7lac promoters (pACY: Novagen; pET); vectors based on Baculovirus promoters (e.g., pBAC); vectors based on Ef1-α and HTLV promoters (e.g., pFUSE2; Invitrogen, CA, USA); vectors based on CMV enhancer and human ferritin light chain gene promoters (e.g., pFUSE: Invitrogen, CA, USA); vectors based on CMV promoters (e.g, pFLAG: Sigma, USA); and vectors based on dihydrofolate reductase promoters (e.g., pEASE: Amgen, USA). Various vectors can be used for transient or stable expression of the polypeptides of interest.

Host Cells

[00382] In another aspect, the polynucleotide encoding the antigen binding proteins described herein (e.g. variable regions, light chains, and heavy chains) is operatively linked to one or more

control sequences for expression of the polypeptide in the host cell. Accordingly, in a further aspect, the present disclosure provides a host cell comprising one or more expression vectors encoding the components of the TREM2 agonist antigen binding proteins described herein.

[00383] Exemplary host cells include prokaryote, yeast, or higher eukaryote cells. Prokaryotic host cells include eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as Escherichia, e.g., E. coli, Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella, e.g., Salmonella typhimurium, Serratia, e.g., Serratia marcescans, and Shigella, as well as Bacillus, such as B. subtilis and B. licheniformis, Pseudomonas, and Streptomyces. Eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for recombinant polypeptides. Saccharomyces cerevisiae, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as Pichia, e.g. P. pastoris, Schizosaccharomyces pombe; Kluyveromyces, Yarrowia; Candida; Trichoderma reesia; Neurospora crassa; Schwanniomyces, such as Schwanniomyces occidentalis; and filamentous fungi, such as, e.g., Neurospora, Penicillium, Tolypocladium, and Aspergillus hosts such as A. nidulans and A. niger.

[00384] Host cells for the expression of glycosylated antigen binding proteins can be derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as Spodoptera frugiperda (caterpillar), Aedes aegypti (mosquito), Aedes albopictus (mosquito), Drosophila melanogaster (fruitfly), and Bombyx mori have been identified. A variety of viral strains for transfection of such cells are publicly available, e.g., the L-1 variant of Autographa californica NPV and the Bm-5 strain of Bombyx mori NPV.

[00385] Vertebrate host cells are also suitable hosts, and recombinant production of antigen binding proteins from such cells has become routine procedure. Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, including CHOK1 cells (ATCC CCL61), DXB-11, DG-44, and Chinese hamster ovary cells/-DHFR (CHO, Urlaub et al., Proc. Natl. Acad. Sci. USA, 1980, 77: 4216); monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human

embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, (Graham et al., J. Gen Virol. 36: 59, 1977); baby hamster kidney cells (BHK, ATCC CCL 10); mouse sertoli cells (TM4, Mather, Biol. Reprod., 1980, 23:243-251); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human hepatoma cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y Acad. Sci., 1982, 383:44-68); MRC 5 cells or FS4 cells; mammalian myeloma cells, and a number of other cell lines. In certain embodiments, cell lines may be selected through determining which cell lines have high expression levels and constitutively produce antigen binding proteins with human TREM2 binding properties. In another embodiment, a cell line from the B cell lineage that does not make its own antibody but has a capacity to make and secrete a heterologous antibody can be selected. CHO cells are preferred host cells in some embodiments for expressing the TREM2 agonist antigen binding proteins of the invention.

[00386] In various embodiments, introduction and transformation of a host cell with a polynucleotide of the present disclosure, such as an expression vector for expressing an antigen binding protein, is accomplished by methods that including transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. In some embodiments, the method selected can be guided by the type of host cell used. Suitable methods are described in, for example, Sambrook *et al.*, 2001.

Expression and Isolation

[00387] In some embodiments, the host cell comprising a polynucleotide encoding one or more components of the antigen binding proteins described herein (e.g. variable regions, light chains, and heavy chains) is used to express the antigen binding protein of interest. In some embodiments, a method for expressing the antigen binding protein comprises culturing the host cell in suitable media and conditions appropriate for expression of the protein of interest.

[00388] The type of media and culture conditions selected is based on the type of host cell. In some embodiments, exemplary media for mammalian host cells include, by way of example and not limitation, Ham's F10 (Sigma), Minimal Essential Medium (MEM, Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium (DMEM, Sigma. In some embodiments, the

media can 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 (such as Gentamycin™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. In some embodiments, culture conditions, such as temperature, pH, % CO_2, and the like, can use conditions available and known to the skilled artisan.

[00389] In some embodiments, the expressed antigen binding protein is isolate and/or purified from the host cell. In some embodiments in which the expressed protein in present in the media, the media containing the expressed protein is subject to isolation procedures. In some embodiments in which the antigen binding protein is produced intracellularly, the cells are subject to disruption, and as a first step, the particulate debris, either host cells or lysed fragments, is removed, for example, by centrifugation or ultrafiltration. Subsequently, the antigen binding protein can be isolated and further purified by various known techniques. Such isolation techniques include affinity chromatography with Protein-A Sepharose, size-exclusion chromatography, ion-exchange chromatography, high performance liquid chromatography, differential solubility, and the like (see, e.g., Fisher, Laboratory Techniques, In Biochemistry And Molecular Biology, Work and Burdon, eds., Elsevier (1980); Antibodies: A Laboratory Manual, Greenfield, E.A., ed., Cold Spring Harbor Laboratory Press, New York (2012); Coligan, et al., supra, sections 2.7.1-2.7.12 and sections 2.9.1-2.9.3; Barnes, et al., Purification of Immunoglobulin G (IgG), in Methods Mol. Biol., Vol. 10, pages 79-104, Humana Press (1992)).

[00390] In some embodiments, the isolated antibody can be further purified as measurable by: (1) weight of protein as determined using the Lowry method; (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning-cup sequencer; or (3) to homogeneity by SDS-PAGE under reducing or non-reducing conditions using Coomassie blue or, preferably, silver stain. The purified antibody can be 85% or greater, 90% or greater, 95% or greater, or at least 99% by weight as determined by the foregoing methods.

Antibody Formulations

[00391] In certain embodiments, the invention provides a composition (e.g. a pharmaceutical composition) comprising one or a plurality of the TREM2 activating antibodies and TREM2

agonist antibodies and antigen binding proteins disclosed herein together with pharmaceutically acceptable diluents, carriers, excipients, solubilizers, emulsifiers, preservatives, and/or adjuvants. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions. "Pharmaceutically-acceptable" refers to molecules, compounds, and compositions that are non-toxic to human recipients at the dosages and concentrations employed and/or do not produce allergic or adverse reactions when administered to humans. In some embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate 80, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. Methods and suitable materials for formulating molecules for therapeutic use are known in the pharmaceutical arts, and are described, for example, in Remington's Pharmaceutical Sciences, 18th Ed., (A.R. Genrmo, ed.), 1990, Mack Publishing Company.

[00392] In some embodiments, the pharmaceutical composition of the invention comprises a standard pharmaceutical carrier, such as a sterile phosphate buffered saline solution, bacteriostatic water, and the like. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.4% saline, 0.3% glycine and the like, and may include other proteins for enhanced stability, such as albumin, lipoprotein, globulin, etc., subjected to mild chemical modifications or the like.

[00393] Exemplary concentrations of the antigen binding proteins in the formulation may range from about 0.1 mg/ml to about 200 mg/ml or from about 0.1 mg/mL to about 50 mg/mL, or from about 0.5 mg/mL to about 25 mg/mL, or alternatively from about 2 mg/mL to about 10 mg/mL. An aqueous formulation of the antigen binding protein may be prepared in a pH-buffered solution, for example, at pH ranging from about 4.5 to about 6.5, or from about 4.8 to about 5.5, or alternatively about 5.0. Examples of buffers that are suitable for a pH within this range include acetate (e.g. sodium acetate), succinate (such as sodium succinate), gluconate, histidine, citrate and other organic acid buffers. The buffer concentration can be from about 1 mM to about 200 mM, or from about 10 mM to about 60 mM, depending, for example, on the buffer and the desired isotonicity of the formulation.

[00394] A tonicity agent, which may also stabilize the antigen binding protein, may be included in the formulation. Exemplary tonicity agents include polyols, such as mannitol, sucrose or trehalose. Preferably the aqueous formulation is isotonic, although hypertonic or hypotonic solutions may be suitable. Exemplary concentrations of the polyol in the formulation may range from about 1% to about 15% w/v.

[00395] A surfactant may also be added to the antigen binding protein formulation to reduce aggregation of the formulated antigen binding protein and/or minimize the formation of particulates in the formulation and/or reduce adsorption. Exemplary surfactants include nonionic surfactants such as polysorbates (e.g., polysorbate 20 or polysorbate 80) or poloxamers (e.g., poloxamer 188). Exemplary concentrations of surfactant may range from about 0.001% to about 0.5%, or from about 0.005% to about 0.2%, or alternatively from about 0.004% to about 0.01% w/v.

[00396] In one embodiment, the formulation contains the above-identified agents (i.e. antigen binding protein, buffer, polyol and surfactant) and is essentially free of one or more

preservatives, such as benzyl alcohol, phenol, m-cresol, chlorobutanol and benzethonium chloride. In another embodiment, a preservative may be included in the formulation, e.g., at concentrations ranging from about 0.1% to about 2%, or alternatively from about 0.5% to about 1%. One or more other pharmaceutically acceptable carriers, excipients or stabilizers such as those described in REMINGTON'S PHARMACEUTICAL SCIENCES, 18th Edition, (A.R. Genrmo, ed.), 1990, Mack Publishing Company, may be included in the formulation provided that they do not adversely affect the desired characteristics of the formulation.

[00397] Therapeutic formulations of the antigen binding protein are prepared for storage by mixing the antigen binding protein having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences, 18th Ed., (A.R. Genrmo, ed.), 1990, Mack Publishing Company), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers (e.g. phosphate, citrate, and other organic acids); antioxidants (e.g. ascorbic acid and methionine); preservatives (such as octadecyldimethylbenzyl ammonium chloride, hexamethonium chloride, benzalkonium chloride, benzethonium chloride, phenol, butyl or benzyl alcohol, alkyl parabens such as methyl or propyl paraben, catechol; resorcinol, cyclohexanol, 3-pentanol, and m-cresol); low molecular weight (e.g. less than about 10 residues) polypeptides; proteins (such as serum albumin, gelatin, or immunoglobulins); hydrophilic polymers (e.g. polyvinylpyrrolidone); amino acids (e.g. glycine, glutamine, asparagine, histidine, arginine, or lysine); monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, maltose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants, such as polysorbates (e.g. polysorbate 20 or polysorbate 80) or poloxamers (e.g. poloxamer 188); or polyethylene glycol (PEG).

[00398] In one embodiment, a suitable formulation of the claimed invention contains an isotonic buffer such as a phosphate, acetate, or TRIS buffer in combination with a tonicity agent, such as a polyol, sorbitol, sucrose or sodium chloride, which tonicifies and stabilizes. One example of such a tonicity agent is 5% sorbitol or sucrose. In addition, the formulation could optionally include a surfactant at 0.01% to 0.02% wt/vol, for example, to prevent aggregation or improve stability. The pH of the formulation may range from 4.5 to 6.5 or 4.5 to 5.5. Other

exemplary descriptions of pharmaceutical formulations for antigen binding proteins may be found in US Patent Publication No. 2003/0113316 and US Patent No. 6,171,586, each of which is hereby incorporated by reference in its entirety.

[00399] Suspensions and crystal forms of antigen binding proteins are also contemplated. Methods to make suspensions and crystal forms are known to one of skill in the art.

[00400] The formulations to be used for *in vivo* administration must be sterile. The compositions of the invention may be sterilized by conventional, well-known sterilization techniques. For example, sterilization is readily accomplished by filtration through sterile filtration membranes. The resulting solutions may be packaged for use or filtered under aseptic conditions and lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration.

[00401] The process of freeze-drying is often employed to stabilize polypeptides for long-term storage, particularly when the polypeptide is relatively unstable in liquid compositions. A lyophilization cycle is usually composed of three steps: freezing, primary drying, and secondary drying (*see* Williams and Polli, Journal of Parenteral Science and Technology, 1984, 38(2):48-59). In the freezing step, the solution is cooled until it is adequately frozen. Bulk water in the solution forms ice at this stage. The ice sublimes in the primary drying stage, which is conducted by reducing chamber pressure below the vapor pressure of the ice, using a vacuum. Finally, sorbed or bound water is removed at the secondary drying stage under reduced chamber pressure and an elevated shelf temperature. The process produces a material known as a lyophilized cake. Thereafter the cake can be reconstituted prior to use.

[00402] The standard reconstitution practice for lyophilized material is to add back a volume of pure water (typically equivalent to the volume removed during lyophilization), although dilute solutions of antibacterial agents are sometimes used in the production of pharmaceuticals for parenteral administration (*see* Chen, Drug Development and Industrial Pharmacy, Volume 18: 1311-1354, 1992).

[00403] Excipients have been noted in some cases to act as stabilizers for freeze-dried products (*see* Carpenter *et al.*, Volume 74: 225-239, 1991). For example, known excipients include polyols (including mannitol, sorbitol and glycerol); sugars (including glucose and sucrose); and amino acids (including alanine, glycine and glutamic acid).

[00404] In addition, polyols and sugars are also often used to protect polypeptides from freezing and drying-induced damage and to enhance the stability during storage in the dried state. In general, sugars, in particular disaccharides, are effective in both the freeze-drying process and during storage. Other classes of molecules, including mono- and di-saccharides and polymers such as PVP, have also been reported as stabilizers of lyophilized products.

[00405] For injection, the pharmaceutical formulation and/or medicament may be a powder suitable for reconstitution with an appropriate solution as described above. Examples of these include, but are not limited to, freeze dried, rotary dried or spray dried powders, amorphous powders, granules, precipitates, or particulates. For injection, the formulations may optionally contain stabilizers, pH modifiers, surfactants, bioavailability modifiers and combinations of these.

[00406] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antigen binding protein, which matrices are in the form of shaped articles, e.g., films, or microcapsule. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Patent No. 3,773,919), copolymers of L-glutamic acid and y ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the Lupron Depot™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated polypeptides remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

[00407] The formulations of the invention may be designed to be short-acting, fast-releasing, long-acting, or sustained-releasing. Thus, the pharmaceutical formulations may also be formulated for controlled release or for slow release.

[00408] Specific dosages may be adjusted depending on the disease, disorder, or condition to be treated, the age, body weight, general health conditions, sex, and diet of the subject, dose intervals, administration routes, excretion rate, and combinations of drugs.

[00409] The TREM2 agonist antigen binding proteins of the invention can be administered by any suitable means, including parenteral, subcutaneous, intraperitoneal, intrapulmonary, intrathecal, intracerebral, intracerebroventricular, and intranasal, and, if desired for local treatment, intralesional administration. Parenteral administration includes intravenous, intraarterial, intraperitoneal, intramuscular, intradermal or subcutaneous administration. In addition, the antigen binding protein is suitably administered by pulse infusion, particularly with declining doses of the antigen binding protein. Preferably, the dosing is given by injections, most preferably intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic. Other administration methods are contemplated, including topical, particularly transdermal, transmucosal, rectal, oral or local administration e.g. through a catheter placed close to the desired site. In certain embodiments, the TREM2 agonist antigen binding protein of the invention is administered intravenously or subcutaneously in a physiological solution at a dose ranging between 0.01 mg/kg to 100 mg/kg at a frequency ranging from daily to weekly to monthly (e.g. every day, every other day, every third day, or 2, 3, 4, 5, or 6 times per week), preferably a dose ranging from 0.1 to 45 mg/kg, 0.1 to 15 mg/kg or 0.1 to 10 mg/kg at a frequency of once per week, once every two weeks, or once a month.

[00410] The TREM2 agonist antigen binding proteins described herein (e.g. anti-TREM2 agonist monoclonal antibodies and binding fragments thereof) are useful for preventing, treating, or ameliorating a condition associated with TREM2 deficiency or loss of biological function of TREM2 in a patient in need thereof. As used herein, the term “treating” or “treatment” is an intervention performed with the intention of preventing the development or altering the pathology of a disorder. Accordingly, “treatment” refers to both therapeutic treatment and prophylactic or preventative measures. Patients in need of treatment include those already diagnosed with or suffering from the disorder or condition as well as those in which the disorder

or condition is to be prevented, such as patients who are at risk of developing the disorder or condition based on, for example, genetic markers. "Treatment" includes any indicia of success in the amelioration of an injury, pathology or condition, including any objective or subjective parameter such as abatement, remission, diminishing of symptoms, or making the injury, pathology or condition more tolerable to the patient, slowing in the rate of degeneration or decline, making the final point of degeneration less debilitating, or improving a patient's physical or mental well-being. The treatment or amelioration of symptoms can be based on objective or subjective parameters, including the results of a physical examination, self-reporting by a patient, cognitive tests, motor function tests, neuropsychiatric exams, and/or a psychiatric evaluation.

III. Small Molecule TREM2 Agonists

[00411] In some embodiments, the agonist of TREM2 is a small molecule agonist of TREM2.

[00412] In some embodiments, the agonist of TREM2 is a lipid ligand of TREM2. In some embodiments, the lipid ligand of TREM2 is selected from l-palmitoyl-2-(5'-oxo-valeroyl)-sn-glycero-3-phosphocholine (POVPC), 2-Arachidonoylglycerol (2-AG), 7-ketocholesterol (7-KC), 24(S)hydroxycholesterol (240HC), 25(S)hydroxycholesterol (250HC), 27- hydroxycholesterol (270HC), Acyl Carnitine (AC), alkylacylglycerophosphocholine (PAF), a-galactosylceramide (KRN7000), Bis(monoacylglycero)phosphate (BMP), Cardiolipin (CL), Ceramide, Ceramide-1 -phosphate (CIP), Cholesteryl ester (CE), Cholesterol phosphate (CP), Diacylglycerol 34: 1 (DG 34: 1), Diacylglycerol 38:4 (DG 38:4), Diacylglycerol pyrophosphate (DGPP), Dihyrdoceramide (DhCer), Dihydrosphingomyelin (DhSM), Ether phosphatidylcholine (PCe), Free cholesterol (FC), Galactosylceramide (GalCer), Galactosylsphingosine (GalSo), Ganglioside GM1, Ganglioside GM3, Glucosylsphingosine (GlcSo), Hank's Balanced Salt Solution (HBSS), Kdo2-Lipid A (KLA), Lactosylceramide (LacCer), lysoalkylacylglycerophosphocholine (LPAF), Lysophosphatidic acid (LPA), Lysophosphatidylcholine (LPC), Lysophosphatidylethanolamine (LPE), Lysophosphatidylglycerol (LPG), Lysophosphatidylinositol (LPI), Lysosphingomyelin (LSM), Lysophosphatidylserine (LPS), N-Acyl-phosphatidylethanolamine (NAPE), N-Acyl-Serine (NSer), Oxidized phosphatidylcholine (oxPC), Palmitic-acid-9-hydroxy-stearic-acid (PAHSA), Phosphatidylethanolamine (PE), Phosphatidylethanol (PEtOH), Phosphatidic acid (PA), Phosphatidylcholine (PC), Phosphatidylglycerol (PG), Phosphatidylinositol (PI),

Phosphatidylserine (PS), Sphinganine, Sphinganine-1-phosphate (SalP), Sphingomyelin (SM), Sphingosine, Sphingosine-1-phosphate (SolP), or Sulfatide, or a salt thereof.

[00413] In some embodiments, the agonist of TREM2 is a lipopolysaccharide.

[00414] In some embodiments, the agonist of TREM2 is a small molecule disclosed in PCT Application Publication WO2019/079529, which is incorporated by reference herein in its entirety. In some embodiments, the agonist of TREM2 is Tyrphostin AG 538, AC1NS458, IN1040, Butein, Okanin, AGL 2263, GB19, GB16, GB20, GB17, GB18, GB21, GB22, GB27, GB44, GB42, GB2, 4,4'-Dihydroxychalcone, or 3,4-Dihydroxybenzophenone, or a derivative or salt of any of the aforementioned.

[00415] In some embodiments, the agonist of TREM2 is a small molecule identified by a method disclosed in PCT Application Publication WO2019/079529. In some embodiments, the small molecule agonist of TREM2 is identified by applying the small molecule compound to a host cell expressing TREM2 and tyrosine kinase binding protein (TYROBP), wherein the host cell has a synthetic sequence comprising an NFAT-response element and a nucleotide sequence encoding a reporter, and measuring a signal emitted by the reporter.

IV. Other TREM2 agonists

[00416] In some embodiments, the agonist of TREM2 is heat shock protein 60 (HSP60).

[00417] In some embodiments, the agonist of TREM2 is apopoliprotein E (ApoE).

V. Neurofilament biomarkers

[00418] In some embodiments, the method of the invention further comprises measuring the level of neurofilaments and/or neurofilament degradation products in a sample collected from the patient.

[00419] In some embodiments, the sample is a whole blood sample. In some embodiments, the sample is a serum sample. In some embodiments, the sample is a plasma sample. In some embodiments, the sample is a cerebrospinal fluid (CSF) sample.

[00420] In some embodiments, the method comprises measuring the levels of neurofilament proteins in the central nervous system of the patient. In some embodiments, the method comprises measuring the levels of neurofilament light chain protein in the central nervous system of the patient. In some embodiments, the method comprises measuring the levels of neurofilament light

chain protein in the serum of the patient. In some embodiments, the method comprises measuring the levels of neurofilament light chain protein in the plasma of the patient. In some embodiments, the method comprises measuring the levels of neurofilament heavy chain protein in the central nervous system of the patient. In some embodiments, the method comprises measuring the levels of neurofilament heavy chain protein in the serum of the patient. In some embodiments, the method comprises measuring the levels of neurofilament heavy chain protein in the plasma of the patient.

[00421] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with CSF1R dysfunction in a human patient, the method comprising:

(a) measuring the level of neurofilaments and/or neurofilament degradation products in a sample collected from the patient;

(b) determining whether the patient has a disease or disorder caused by and/or associated with CSF1R dysfunction or is a carrier of a CSF1R mutation based on the measured levels of neurofilaments and/or neurofilament degradation products in the sample; and

(c) if the patient is determined to have a disease or disorder caused by and/or associated with CSF1R dysfunction or is a carrier of a CSF1R mutation, administering to the patient an effective amount of an agonist of TREM2.

[00422] In some embodiments, the patient is determined to have a disease or disorder caused by and/or associated with CSF1R dysfunction or is a carrier of a CSF1R mutation if the levels of neurofilament degradation products in the sample are elevated. As used herein, the term "elevated" refers to a level of neurofilament degradation products higher than observed in a sample collected from a patient with normal CSF1R function. In some embodiments, an elevated level of neurofilament degradation products refers to a neurofilament degradation product level that is more than 2 times higher than normal levels, more than 3 times higher than normal levels, more than 4 times higher than normal levels, more than 5 times higher than normal levels, more than 10 times higher than normal levels, more than 20 times higher than normal levels, more than 30 times higher than normal levels, more than 40 times higher than normal levels, more than 50 times higher than normal levels, or more than 100 times higher than normal levels. In some embodiments, the elevated neurofilament degradation product is neurofilament light chain protein.

[00423] In some embodiments, the patient is determined to have a disease or disorder caused by and/or associated with CSF1R dysfunction or is a carrier of a CSF1R mutation if the central

levels of neurofilament in the sample are lower than the central levels of neurofilament observed in a sample collected from a patient with normal CSF1R function. In some embodiments, the central level of neurofilament is less than 90% of normal central neurofilament levels, less than 80% of normal central neurofilament levels, less than 70% of normal central neurofilament levels, less than 60% of normal central neurofilament levels, or less than 50% of normal central neurofilament levels.

[00424] In another aspect, the present invention provides a method of identifying a patient suffering from a disease or disorder caused by and/or associated with CSF1R dysfunction, or a carrier of a CSF1R mutation, that would benefit from treatment with an agonist of TREM2, the method comprising:

(a) collecting a first sample from the patient;

(b) measuring the level of neurofilaments and/or neurofilament degradation products in the first sample collected from the patient;

(c) administering to the patient an agonist of TREM2;

(d) collecting a second sample from the patient; and

(e) measuring the level of neurofilaments and/or neurofilament degradation products in the second sample collected from the patient;

wherein the difference in the level of neurofilaments and/or neurofilament degradation products between the first sample and second sample is predictive of treatment response.

[00425] In some embodiments, a decrease in neurofilament degradation product levels from the first sample to the second sample indicates that treatment of the disease or disorder with the TREM2 agonist is effective. In some embodiments, the first sample and second sample are plasma samples, serum samples or CSF samples.

[00426] In some embodiments, an increase or no change in neurofilament degradation product levels from the first sample to the second sample indicates that treatment of the disease or disorder with the TREM2 agonist is ineffective. In some embodiments, the first sample and second sample are plasma samples, serum samples or CSF samples.

[00427] In some embodiments, an increase in central neurofilament levels from the first sample to the second sample indicates that treatment of the disease or disorder with the TREM2 agonist is effective.

[00428] In some embodiments, a decrease or no change in central neurofilament levels from the first sample to the second sample indicates that treatment of the disease or disorder with the TREM2 agonist is ineffective.

[00429] In another aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with CSF1R dysfunction in a human patient, the method comprising:

(a) collecting a first sample from the patient;

(b) measuring the level of neurofilaments and/or neurofilament degradation products in the first sample collected from the patient;

(c) administering to the patient an agonist of TREM2 at a first dosage;

(d) collecting a second sample from the patient;

(e) measuring the level of neurofilaments and/or neurofilament degradation products in the second sample collected from the patient;

(f) modifying the initial dosage of the agonist of TREM2 based on the level of neurofilaments and/or neurofilament degradation products in the sample collected from the patient to determine a modified dosage; and

(g) administering to the patient the agonist of TREM2 at the modified dosage.

[00430] In some embodiments, if there is a decrease in neurofilament degradation product levels from the first sample to the second sample, the first dosage does not require modification, and the modified dosage should contain the same or lower dosage of TREM2 agonist than the first dosage. In some embodiments, the first sample and second sample are plasma samples, serum samples or CSF samples. In some embodiments, the neurofilament degradation product is neurofilament light chain protein.

[00431] In some embodiments, if there is an increase or no change in neurofilament degradation product levels from the first sample to the second sample, the modified dosage should contain a higher dosage of TREM2 agonist than the second dosage. In some embodiments, the first sample and second sample are plasma samples, serum samples or CSF samples. In some embodiments, the neurofilament degradation product is neurofilament light chain protein.

[00432] In some embodiments, if there is an increase in central neurofilament levels from the first sample to the second sample, the first dosage does not require modification, and the modified dosage should contain the same or lower dosage of TREM2 agonist than the first dosage.

[00433] In some embodiments, if there is a decrease or no change in central neurofilament levels from the first sample to the second sample, the modified dosage should contain a higher dosage of TREM2 agonist than the second dosage.

[00434] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with a CSF1R dysfunction in a human patient, wherein the patient has an elevated level of neurofilament degradation product, the method comprising administering to the patient an effective amount of an agonist of TREM2. In some embodiments, the disease or disorder is ALSP. In some embodiments, the neurofilament degradation product is neurofilament light chain protein.

Pharmaceutically Acceptable Compositions

[00435] In certain embodiments, a TREM2 activating antibody or small molecule disclosed herein is formulated as a composition for administration to a patient in need of such composition.

[00436] The term "pharmaceutically acceptable carrier, adjuvant, or vehicle" refers to a non-toxic carrier, adjuvant, or vehicle that does not destroy the pharmacological activity of the compound with which it is formulated. Pharmaceutically acceptable carriers, adjuvants or vehicles that may be used in the compositions of this invention include, but are not limited to, ion exchangers, alumina, aluminum stearate, lecithin, serum proteins, such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, water, salts or electrolytes, such as protamine sulfate, disodium hydrogen phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, cellulose-based substances, polyethylene glycol, sodium carboxymethylcellulose, polyacrylates, waxes, polyethylene-polyoxypropylene-block polymers, polyethylene glycol and wool fat.

[00437] A "pharmaceutically acceptable derivative" means any non-toxic salt, ester, salt of an ester or other derivative of a compound of this invention that, upon administration to a recipient, is capable of providing, either directly or indirectly, a compound of this invention or an inhibitorily active metabolite or residue thereof.

[00438] Compositions of the present invention may be administered orally, parenterally, by inhalation spray, topically, rectally, nasally, buccally, vaginally or via an implanted reservoir.

The term "parenteral" as used herein includes subcutaneous, intravenous, intramuscular, intra-articular, intra-synovial, intrasternal, intrathecal, intrahepatic, intralesional and intracranial injection or infusion techniques. In some embodiments, the compositions are administered orally, intraperitoneally or intravenously. Sterile injectable forms of the compositions of this invention may be aqueous or oleaginous suspension. These suspensions may be formulated according to techniques known in the art using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium.

[00439] For this purpose, any bland fixed oil may be employed including synthetic mono- or di-glycerides. Fatty acids, such as oleic acid and its glyceride derivatives are useful in the preparation of injectables, as are natural pharmaceutically-acceptable oils, such as olive oil or castor oil, especially in their polyoxyethylated versions. These oil solutions or suspensions may also contain a long-chain alcohol diluent or dispersant, such as carboxymethyl cellulose or similar dispersing agents that are commonly used in the formulation of pharmaceutically acceptable dosage forms including emulsions and suspensions. Other commonly used surfactants, such as Tweens, Spans and other emulsifying agents or bioavailability enhancers which are commonly used in the manufacture of pharmaceutically acceptable solid, liquid, or other dosage forms may also be used for the purposes of formulation.

[00440] Pharmaceutically acceptable compositions of this invention may be orally administered in any orally acceptable dosage form including, but not limited to, capsules, tablets, aqueous suspensions or solutions. In the case of tablets for oral use, carriers commonly used include lactose and corn starch. Lubricating agents, such as magnesium stearate, are also typically added. For oral administration in a capsule form, useful diluents include lactose and dried cornstarch. When aqueous suspensions are required for oral use, the active ingredient is combined with emulsifying and suspending agents. If desired, certain sweetening, flavoring or coloring agents may also be added.

[00441] Alternatively, pharmaceutically acceptable compositions of this invention may be administered in the form of suppositories for rectal administration. These can be prepared by

mixing the agent with a suitable non-irritating excipient that is solid at room temperature but liquid at rectal temperature and therefore will melt in the rectum to release the drug. Such materials include cocoa butter, beeswax and polyethylene glycols.

[00442] Pharmaceutically acceptable compositions of this invention may also be administered topically, especially when the target of treatment includes areas or organs readily accessible by topical application, including diseases of the eye, the skin, or the lower intestinal tract. Suitable topical formulations are readily prepared for each of these areas or organs.

[00443] Topical application for the lower intestinal tract can be effected in a rectal suppository formulation (see above) or in a suitable enema formulation. Topically-transdermal patches may also be used.

[00444] For topical applications, provided pharmaceutically acceptable compositions may be formulated in a suitable ointment containing the active component suspended or dissolved in one or more carriers. Carriers for topical administration of compounds of this invention include, but are not limited to, mineral oil, liquid petrolatum, white petrolatum, propylene glycol, polyoxyethylene, polyoxypropylene compound, emulsifying wax and water. Alternatively, provided pharmaceutically acceptable compositions can be formulated in a suitable lotion or cream containing the active components suspended or dissolved in one or more pharmaceutically acceptable carriers. Suitable carriers include, but are not limited to, mineral oil, sorbitan monostearate, polysorbate 60, cetyl esters wax, cetearyl alcohol, 2-octyldodecanol, benzyl alcohol and water.

[00445] For ophthalmic use, provided pharmaceutically acceptable compositions may be formulated as micronized suspensions in isotonic, pH adjusted sterile saline, or as solutions in isotonic, pH adjusted sterile saline, either with or without a preservative such as benzylalkonium chloride. Alternatively, for ophthalmic uses, the pharmaceutically acceptable compositions may be formulated in an ointment such as petrolatum.

[00446] Pharmaceutically acceptable compositions of this invention may also be administered by nasal aerosol or inhalation. Such compositions are prepared according to techniques well-known in the art of pharmaceutical formulation and may be prepared as solutions in saline, employing benzyl alcohol or other suitable preservatives, absorption promoters to enhance bioavailability, fluorocarbons, and/or other conventional solubilizing or dispersing agents.

[00447] In some embodiments, pharmaceutically acceptable compositions of this invention are formulated for oral administration. Such formulations may be administered with or without food. In some embodiments, pharmaceutically acceptable compositions of this invention are administered without food. In other embodiments, pharmaceutically acceptable compositions of this invention are administered with food.

[00448] In other embodiments, pharmaceutically acceptable compositions of this invention are formulated for intravenous (IV) administration.

[00449] The amount of compounds of the present invention that may be combined with the carrier materials to produce a composition in a single dosage form will vary depending upon the host treated, the particular mode of administration. Preferably, provided compositions should be formulated so that a dosage of between 0.01 - 100 mg/kg body weight/day of the inhibitor can be administered to a patient receiving these compositions.

[00450] It should also be understood that a specific dosage and treatment regimen for any particular patient will depend upon a variety of factors, including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, rate of excretion, drug combination, and the judgment of the treating physician and the severity of the particular disease being treated. The amount of a compound of the present invention in the composition will also depend upon the particular compound in the composition.

Uses of Compounds and Pharmaceutically Acceptable Compositions

[00451] Compounds and compositions described herein are generally useful for the treatment of ALSP in the various methods disclosed herein.

[00452] The activity of a compound utilized in the present invention may be assayed *in vitro*, *in vivo* or in a cell line. *In vitro* assays include assays that determine modulation or binding to a protein. Detailed conditions for assaying a compound are set forth in the Examples below.

[00453] As used herein, the terms "treatment," "treat," and "treating" refer to reversing, alleviating, delaying the onset of, or inhibiting the progress of a disease or disorder, or one or more symptoms thereof, as described herein. In some embodiments, treatment may be administered after one or more symptoms have developed. In other embodiments, treatment may be administered in the absence of symptoms. For example, treatment may be administered to a susceptible individual prior to the onset of symptoms (e.g., in light of a history of

symptoms and/or in light of genetic or other susceptibility factors). Treatment may also be continued after symptoms have resolved, for example to prevent or delay their recurrence.

[00454] The compounds and compositions, according to the method of the present invention, may be administered using any amount and any route of administration effective for treating or lessening the severity of a disclosed disease or condition, or associated condition or symptom. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of the disease or condition, the particular agent, its mode of administration, and the like. Compounds of the invention are preferably formulated in dosage unit form for ease of administration and uniformity of dosage. The expression "dosage unit form" as used herein refers to a physically discrete unit of agent appropriate for the patient to be treated. It will be understood, however, that the total daily usage of the compounds and compositions of the present invention will be decided by the attending physician within the scope of sound medical judgment. The specific effective dose level for any particular patient or organism will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific compound employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific compound employed; the duration of the treatment; drugs used in combination or coincidental with the specific compound employed, and like factors well known in the medical arts. The term "patient", as used herein, means an animal, in some embodiments a mammal, or in certain other embodiments a human.

[00455] Pharmaceutically acceptable compositions of this invention can be administered to humans and other animals orally, sublingually, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, or drops), intraocularly (such as eye drops), bucally, as an oral or nasal spray, or the like, depending on the severity of the disease or condition being treated. In certain embodiments, the compounds of the invention may be administered orally or parenterally at dosage levels of about 0.01 mg/kg to about 50 mg/kg or from about 1 mg/kg to about 25 mg/kg, of subject body weight per day, one or more times a day, to obtain the desired therapeutic effect.

[00456] Liquid dosage forms for oral administration include, but are not limited to, pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups and

elixirs. In addition to the active compounds, the liquid dosage forms may contain inert diluents commonly used in the art such as, for example, water or other solvents, solubilizing agents and emulsifiers such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, dimethylformamide, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor, and sesame oils), glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof. Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, and perfuming agents.

[00457] Injectable preparations, for example, sterile injectable aqueous or oleaginous suspensions may be formulated according to the known art using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution, suspension or emulsion in a nontoxic parenterally acceptable diluent or solvent, for example, as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, U.S.P. and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid are used in the preparation of injectables.

[00458] Injectable formulations can be sterilized, for example, by filtration through a bacterial-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable medium prior to use.

[00459] In order to prolong the effect of a compound of the present invention, it is often desirable to slow the absorption of the compound from subcutaneous or intramuscular injection. This may be accomplished by the use of a liquid suspension of crystalline or amorphous material with poor water solubility. The rate of absorption of the compound then depends upon its rate of dissolution that, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally administered compound form is accomplished by dissolving or suspending the compound in an oil vehicle. Injectable depot forms are made by forming microencapsule matrices of the compound in biodegradable

polymers such as polylactide-polyglycolide. Depending upon the ratio of compound to polymer and the nature of the particular polymer employed, the rate of compound release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are also prepared by entrapping the compound in liposomes or microemulsions that are compatible with body tissues.

[00460] Compositions for rectal or vaginal administration are preferably suppositories which can be prepared by mixing the compounds of this invention with suitable non-irritating excipients or carriers such as cocoa butter, polyethylene glycol or a suppository wax which are solid at ambient temperature but liquid at body temperature and therefore melt in the rectum or vaginal cavity and release the active compound.

[00461] Solid dosage forms for oral administration include capsules, tablets, pills, powders, and granules. In such solid dosage forms, the active compound is mixed with at least one inert, pharmaceutically acceptable excipient or carrier such as sodium citrate or dicalcium phosphate and/or a) fillers or extenders such as starches, lactose, sucrose, glucose, mannitol, and silicic acid, b) binders such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinylpyrrolidinone, sucrose, and acacia, c) humectants such as glycerol, d) disintegrating agents such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate, e) solution retarding agents such as paraffin, f) absorption accelerators such as quaternary ammonium compounds, g) wetting agents such as, for example, cetyl alcohol and glycerol monostearate, h) absorbents such as kaolin and bentonite clay, and i) lubricants such as talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, and mixtures thereof. In the case of capsules, tablets and pills, the dosage form may also comprise buffering agents.

[00462] Solid compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugar as well as high molecular weight polyethylene glycols and the like. The solid dosage forms of tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings and other coatings well known in the pharmaceutical formulating art. They may optionally contain opacifying agents and can also be of a composition that they release the active ingredient(s) only, or in a certain part of the intestinal tract, optionally, in a delayed manner. Examples of embedding compositions that can be used include polymeric substances and

waxes. Solid compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugar as well as high molecular weight polethylene glycols and the like.

[00463] The active compounds can also be in micro-encapsulated form with one or more excipients as noted above. The solid dosage forms of tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings, release controlling coatings and other coatings well known in the pharmaceutical formulating art. In such solid dosage forms the active compound may be admixed with at least one inert diluent such as sucrose, lactose or starch. Such dosage forms may also comprise, as is normal practice, additional substances other than inert diluents, e.g., tableting lubricants and other tableting aids such a magnesium stearate and microcrystalline cellulose. In the case of capsules, tablets and pills, the dosage forms may also comprise buffering agents. They may optionally contain opacifying agents and can also be of a composition that they release the active ingredient(s) only, or in a certain part of the intestinal tract, optionally, in a delayed manner. Examples of embedding compositions that can be used include polymeric substances and waxes.

[00464] Dosage forms for topical or transdermal administration of a compound of this invention include ointments, pastes, creams, lotions, gels, powders, solutions, sprays, inhalants or patches. The active component is admixed under sterile conditions with a pharmaceutically acceptable carrier and any needed preservatives or buffers as may be required. Ophthalmic formulation, ear drops, and eye drops are also contemplated as being within the scope of this invention. Additionally, the present invention contemplates the use of transdermal patches, which have the added advantage of providing controlled delivery of a compound to the body. Such dosage forms can be made by dissolving or dispensing the compound in the proper medium. Absorption enhancers can also be used to increase the flux of the compound across the skin. The rate can be controlled by either providing a rate controlling membrane or by dispersing the compound in a polymer matrix or gel.

[00465] Depending upon the particular condition, or disease, to be treated, additional therapeutic agents that are normally administered to treat that condition, may also be present in the compositions of this invention. As used herein, additional therapeutic agents that are normally administered to treat a particular disease, or condition, are known as "appropriate for the disease, or condition, being treated."

[00466] All features of each of the aspects of the disclosure apply to all other aspects mutatis mutandis. Each of the references referred to herein, including but not limited to patents, patent applications and journal articles, is incorporated by reference herein as though fully set forth in its entirety.

[00467] In order that the disclosure described herein may be more fully understood, the following examples are set forth. It should be understood that these examples are for illustrative purposes only and are not to be construed as limiting this disclosure in any manner.

EXAMPLES

General Procedures

Preparation of human monocytes

[00468] Add EDTA to a whole blood sample taken from a human subject, to a final EDTA concentration of 3 mM. Dilute the whole blood 1 : 1 with isolation buffer (PBS, calcium and magnesium free; supplemented with 2% FBS + 3mM EDTA). Layer 35 ml of diluted blood on top of 15 ml of a Ficoll® -Paque Plus gradient medium with a density of 1.077 g/ml in 50 ml centrifuge tubes. When layering the diluted blood, care should be taken so as not to disturb the gradient. Centrifuge at 400 x g for 30 min at room temperature with no break. Using a Pasteur pipette, remove the white layer containing peripheral blood mononuclear cells (PBMCs) that forms after centrifugation. Transfer the white layer material to a clean 50 ml centrifuge tube (maximum 10 ml PBMCs per tube). Add 3x volume of isolation buffer and mix gently by inverting to wash the PBMCs.

[00469] Centrifuge at 300 x g for 10 min at room temperature (brake on) to pellet the PBMCs and remove supernatant gently so as to minimize loss of any cells. Each pellet is resuspended in 1 ml of isolation buffer, pooled together, if multiple PBMC samples are used, and the PBMC cells are counted.

[00470] **Negative Selection Method** - Use an EasySep™ human negative selection monocyte isolation kit to isolate monocytes. Follow the manufacturer provided instructions for isolating the monocytes. Briefly, add a 'human monocyte isolation cocktail', included with the EasySep™ kit consisting of an Fc receptor blocking antibody and a combination of monoclonal antibodies that recognize specific cell surface markers, to the human PBMC sample. Add the optional 'platelet removal cocktail', included with the EasySep™ kit, to the sample. Incubate for 10 min. Add the

magnetic particles included with the EasySep™ kit. Incubate for an additional 10 min. Place the tube inside the EasySep™ magnet. The non-monocytes are pulled to the side of the tube, and the remaining human monocytes can be decanted and used for multiple experiments as follows.

[00471] **Positive Selection Method** – Add PBMCs to a mixture containing Miltenyi Biotec® CD14 magnetic microbeads. Add the mixture to a magnetic column according to manufacturer provided instructions, washing away non-CD14+ cells, leaving only CD14+ PBMCs bound to the microbeads. Remove the column from the magnet and flush CD14+ cells with manufacturer recommended buffer solution.

Antibody Ab-3

[00472] Antibody Ab-3 is a murinized version of a human TREM2 agonist antibody, first described as an engineered variant of antibody 13E7 in PCT Application Publication WO2018/195506A1. Ab-3 has an HC according to SEQ ID NO:2779, an LC according to SEQ ID NO:2780 (as shown in **Table 21**), and exemplifies an anti-TREM2 antibody having the CDRs according to SEQ ID NOS:10, 23, 81, 330, 331, and 372-374.

Table 21. Murinized Anti-TREM2 Antibody Ab-3 Sequences

Sequence Description	**Amino Acid Sequence**
Ab-3 HC SEQ ID NO: 2779	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPG KGLEWMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSL KASDTAMYFCARRRQGIFGDALDFWGQGTLVTVSSAKTTPPS VYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSG VHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTC VVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFGSTFRSVS ELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQ VYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAEN YKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGL HNHHTEKSLSHSPGK
Ab-3 LC SEQ ID NO: 2780	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQA PRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCL QDNNFPPTFGQGTKVDIKRADAAPTVSIFPPSSEQLTSGGASVV

	CFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

Example 1: The effects of antibody TREM2 agonists on signaling and survival in monocyte-derived human macrophages that have impaired CSF1R receptor signaling due to an insufficient dosage of M-CSF.

A. Surface-coated TREM2 agonist antibody – luminescence cell viability assay

[00473] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well plate that has been pre-coated with a titration (0.001 μg/ml to 100 μg/ml in ten-fold increments) of a TREM2 agonist antibody or an isotype control overnight at 4°C. Antibody-coated plates are washed with PBS twice, and cells are plated in media with a low concentration of macrophage colony-stimulating factor (M-CSF; Gibco, Cat# PHC9501) or a normal concentration of M-CSF. The appropriate low and normal concentrations levels are determined experimentally by testing various levels of M-CSF that yield maximal survival of the cultured macrophages (normal) and hindered survival (low). Exemplary concentrations are 5 ng/ml M-CSF for the low concentration wells and 10 ng/ml for the normal concentration wells. After 5 days, cellular ATP levels are measured via luminescence detection to indicate cell viability using a CellTiter-Glo® Luminescent Cell Viability Assay (Promega Catalog Number G7571). The effects of the TREM2 agonist antibody vs control on the viable cell count of macrophages cultured in the presence of low or normal levels of M-CSF are compared.

B. Solvated TREM2 agonist antibody – luminescence cell viability assay

[00474] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with a low concentration of M-CSF (Gibco, Cat# PHC9501) or a normal concentration of M-CSF. The appropriate low and normal concentrations levels are determined experimentally by testing various levels of M-CSF that yield maximal survival of the cultured macrophages (normal) and hindered survival (low). Exemplary concentrations are 5 ng/ml M-CSF for the low concentration wells and 10 ng/ml for the normal concentration wells. At the start of plating, Trem2 agonist antibody or an isotype control is added to each cell at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. After 5 days, cellular ATP levels are

measured via luminescence detection to indicate cell viability using a CellTiter-Glo® Luminescent Cell Viability Assay (Promega Catalog Number G7571). The effects of the TREM2 agonist antibody vs control on the viable cell count of macrophages cultured in the presence of low or normal levels of M-CSF are compared.

C. Solvated TREM2 agonist antibody – cell viability determined by automated microscopy

[00475] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with a low concentration of M-CSF (Gibco, Cat# PHC9501) or a normal concentration of M-CSF. The appropriate low and normal concentrations levels are determined experimentally by testing various levels of M-CSF that yield maximal survival of the cultured macrophages (normal) and hindered survival (low). Exemplary concentrations are 5 ng/ml M-CSF for the low concentration wells and 10 ng/ml for the normal concentration wells. At the start of plating, TREM2 agonist antibody or an isotype control is added to each cell at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. Each day, cells are counted by automated microscopy (for instance using a Scintica® C100 automated cell counter), or by flow cytometry analysis on cell stained for viability with propidium iodide, or by any equivalent method, and the effect of treatment with the TREM2 agonist antibody on viable cell numbers is measured. The effects of the TREM2 agonist antibody vs control on viable cell numbers of macrophages cultured in the presence of low or normal levels of M-CSF are compared.

D. Solvated TREM2 agonist antibody – phospho-SYK assay

[00476] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells were plated in media with a low concentration of M-CSF (Gibco, Cat# PHC9501) or a normal concentration of M-CSF. The appropriate low and normal concentrations levels are determined experimentally by testing various levels of M-CSF that yield maximal survival of the cultured macrophages (normal) and hindered survival (low). Exemplary concentrations are 5 ng/ml M-CSF for the low concentration wells and 10 ng/ml for the normal concentration wells. At the start of plating, TREM2 agonist antibody or an isotype control were added to each cell at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. After 5 days, cells are washed, lysed with M-PER™ reagent (Thermo Scientific) and aliquots of the lysate were analyzed for levels of phospho-SYK using the AlphaLisa® platform, and the reagent kit

AlphaLISA® SureFire Ultra p-Syk (Tyr525/526) (Perkin Elmer, part number ALSU-PSYK-A-HV). The effects of TREM2 agonist antibody vs control on phosphorylation levels of SYK, as a measure of signaling, in macrophages cultured in the low or normal levels of M-CSF are compared.

[00477] The above protocols *A-D* are first carried out with donated human monocytes of no known disease-associated genotype, and repeated with monocytes from ALSP patients carrying a mutation in one allele of the CSF1R gene (CSF1R +/- haploinsufficient monocytes). For experiments using monocytes from ALSP patients, only normal amounts of M-CSF are used, as CSF1R function is already impaired.

[00478] The above protocols can be adapted to test the effects of any TREM2 agonist antibodies on macrophage cell viability and signaling, including, but not limited to TREM2 agonist antibodies disclosed herein.

E. Effects of CSF1 Withdrawal on Survival and Morphology in Human Monocyte Derived Macrophages

[00479] PBMCs were isolated from fresh, whole blood from human donors. CD14+ monocytes were isolated using positive magnetic selection (Miltenyi). Cells were plated in UpCell® low-adhesion plates and incubated in culture media with 50 ng/mL CSF1 for 48 hours. After 48 hours, cells were non-enzymatically harvested and plated at 25,000 cells per well in cell culture plates coated with 0.4, 2.0, or 10 µg/mL of either Ab-3 or a matching isotype control, and incubated in a humidified incubator at 37C, 5% CO_2 for 72 hours. Caspase-3/7 Green reporter dye was included in the some wells to determine the number of apoptotic events over time. During incubation, cells were monitored every two hours using an Incucyte S3® analyzer (2 fields of view per well, imaged at 10x). Confluence levels were determined using the Incucyte® software, and normalized to CSF1 at 50 ng/mL, which was considered as normal culture conditions. Caspase 3/7 positive counts per field of view were calculated using Incucyte® software. Significance was determined by Ordinary One-Way ANOVA, using multiple comparisons in Graphpad Prism.

[00480] Ab-3 was tested at three different CSF1 concentrations for its ability to inhibit CSF1 withdrawal-induced reduction in confluence in human monocyte-derived macrophages (hMDMs) derived from two different donors. As seen in **FIG. 1** (showing macrophages taken from "donor 16") and **FIG. 2** (showing macrophages taken from "donor 26"), withdrawal of

CSF1 from the media resulted in a significant decrease in confluence ("CSF1 0 ng/mL"). Treatment of cells with Ab-3 increased confluence levels to that of high CSF1 treated cells ("CSF1 50 ng/mL"), while treatment with isotype matched IgG (having no agonism of hTREM2) at the same concentrations had no significant effect on confluence. These results demonstrate that in hMDM from both donors, reduction of CSF1R signaling decreased confluence, and this confluence decrease was rescued by Ab-3-mediated agonism of TREM2.

[00481] Ab-3 was also tested at three different CSF1 concentrations for its ability to inhibit CSF1 withdrawal-induced apoptosis in hMDMs derived from the two different donors. As seen in **FIG. 3** (showing macrophages taken from "donor 16") and **FIG. 4** (showing macrophages taken from "donor 26"), complete withdrawal of CSF1 from the media resulted in a significant increase in Caspase 3/7 staining ("CSF1 0 ng/mL"). Treatment of cells with Ab-3 reduced Caspase 3/7 levels to that of high CSF1 treated cells ("CSF1 50 ng/mL"), while treatment with isotype matched IgG at the same concentrations had no significant effect on levels of Caspase 3/7. These results demonstrate that in hMDM from both donors, reduction of CSF1R signaling increased apoptosis, and this increase in apoptosis was rescued by Ab-3-mediated agonism of TREM2.

Example 2: The effects of antibody TREM2 agonists on signaling and survival in monocyte-derived human macrophages that have impaired CSF1R receptor signaling through the use of a chemical inhibitor of CSF1R.

A. Surface-coated TREM2 agonist antibody – luminescence cell viability assay

[00482] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well plate that has been pre-coated with a titration (0.001µg/ml to 100 µg/ml in ten-fold increments) of TREM2 agonist antibody or an isotype control overnight at 4°C. Antibody-coated plates are washed with PBS twice, and cells are plated in media with experimentally determined normal levels of M-CSF (e.g. 10 ng/ml M-CSF) and in the presence or absence of CSF1R inhibitor PLX5622 (Medchem express). After 5 days, cellular ATP levels are measured via luminescence detection to indicate cell viability using a CellTiter-Glo® Luminescent Cell Viability Assay (Promega Catalog Number G7571). The effects of the TREM2 agonist antibody vs control on viable cell count of macrophages cultured in the presence or absence of PLX5622 are compared.

B. Solvated TREM2 agonist antibody – luminescence cell viability assay

[00483] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with experimentally determined normal levels of M-CSF (e.g. 10 ng/ml M-CSF). At the start of plating, the CSF1R inhibitor PLX5622 (Medchem express) is added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. TREM2 agonist antibody or an isotype control is also added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. After 5 days, cellular ATP levels are measured via luminescence detection to indicate cell viability using a CellTiter-Glo® Luminescent Cell Viability Assay (Promega Catalog Number G7571). The effects of the TREM2 agonist antibody vs control on viable cell count of macrophages cultured in the presence or absence of PLX5622 are compared.

C. Solvated TREM2 agonist antibody – cell viability determined by automated microscopy

[00484] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with experimentally determined normal levels of M-CSF (e.g. 10 ng/ml M-CSF). At the start of plating, the CSF1R inhibitor PLX5622 (Medchem express) is added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. TREM2 agonist antibody or an isotype control is also added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. Every day, cells are counted by automated microscopy, and the effect of treatment with TREM2 agonist antibody on cell numbers is measured. The effects of the TREM2 agonist antibody vs control on viable cell counts of macrophages cultured in the presence or absence of PLX5622 are compared.

D. Solvated TREM2 agonist antibody – phospho-SYK assay

[00485] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with experimentally determined normal levels of M-CSF (e.g. 10 ng/ml M-CSF). At the start of plating, the CSF1R inhibitor PLX5622 (Medchem express) is added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. TREM2 agonist antibody or an isotype control is also added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. After 5 days, cells are washed, lysed with M-PER™ reagent (Thermo Scientific) and aliquots of the lysate were analyzed for levels of phospho-SYK using the

AlphaLisa® platform, and the reagent kit AlphaLISA® SureFire Ultra p-Syk (Tyr525/526) (Perkin Elmer, part number ALSU-PSYK-A-HV). The effects of TREM2 agonist antibody vs control on phosphorylation levels of SYK, as a measure of signaling, in macrophages cultured in the presence or absence of PLX5622 are compared.

[00486] The above protocols *A-D* are first carried out with donated human monocytes of no known disease-associated genotype, and repeated with monocytes from ALSP patients carrying a mutation in one allele of the CSF1R gene (CSF1R +/- haploinsufficient monocytes) for comparison. In experiments using monocytes from ALSP patients, CSF1R inhibitor PLX5622 is not used, as CSF1R signaling is already inhibited.

[00487] The above protocols can be adapted to test the effects of any TREM2 agonist antibodies on macrophage cell viability and signaling, including, but not limited to TREM2 agonist antibodies disclosed herein.

[00488] *E. Effects of CSF1 Receptor Inhibition on Morphology in Human Monocyte Derived Macrophages*

[00489] PBMCs were isolated from fresh, whole blood from human donors. CD14+ monocytes were isolated using positive magnetic selection (Miltenyi). Cells were plated in UpCell® low-adhesion plates and incubated in culture media with 50 ng/mL CSF1 for 48 hours. After 48 hours, cells were non-enzymatically harvested and plated at 25,000 cells per well in cell culture plates coated with 10 µg/mL of either Ab-3 or a matching isotype control. PLX5622 was immediately added to the cultures to 1 µM, and plates were incubated in a humidified incubator at 37C, 5% CO_2 for an additional 96 hours. During incubation, cells were monitored every two hours using an Incucyte S3® analyzer (2 fields of view per well, imaged at 10x). Confluence was measured using built in S3 software, while area and eccentricity (cell shape) were measured using the built in "Cell By Cell" analysis software. Significance was determined by Student's T-test, two-tailed in Graphpad Prism.

[00490] Ab-3 was tested at 10 µg/mL for its ability to inhibit the effects of PLX5622-induced CSF1R inhibition on morphology. As seen in **FIG. 5**, inhibition of CSF1R by PLX5622 resulted in a significant reduction in confluence ("PLX5622 1 µM") relative to vehicle alone. Treatment of cells with Ab-3 resulted in restoration of confluence to levels similar to that of vehicle alone, while treatment with isotype matched IgG at the same concentration had no significant effect. In addition, a cell-by-cell assessment was carried out to quantify cell shape, specifically

determining the percentage of the cell population that is rounded (amoeboid) as compared to cells that are "high area, high eccentricity" (ramified). As shown in **FIG. 6**, inhibition of CSF1R by PLX5622 resulted in a significant reduction in cells with "high area, high eccentricity" ("PLX5622 1 μM") relative to vehicle alone. Treatment of cells with Ab-3 resulted in restoration of "high area, high eccentricity" to levels higher than that of vehicle alone, while treatment with isotype matched IgG at the same concentration had no significant effect.

[00491] In addition, it was found that changes in confluence were not due to cell count in donors with no PLX5622-dependent apoptosis, but were instead due to changes in morphology. This effect is shown in **FIG. 7**. The Incucyte S3 includes a "Cell By Cell" module that can quantify cell shape, specifically what percentage of the cell population are rounded (amoeboid) as compared to cells that are "high area, high eccentricity" (ramified). Inhibition of CSF1R by PLX5622 resulted in a significant reduction in cells with "high area, high eccentricity" ("PLX5622 1 μM") relative to vehicle alone. Treatment of cells with Ab-3 resulted in restoration of "high area, high eccentricity" to levels higher than that of vehicle alone, while treatment with isotype matched IgG at the same concentration had no significant effect.

[00492] These results demonstrate that reduction of CSF1R signaling by PLX5622 reduced cellular confluence, and this effect was rescued by agonism of TREM2 signaling by Ab-3.

Example 3: The effects of small molecule TREM2 agonists on signaling and survival in monocyte-derived human macrophages that have impaired CSF1R receptor signaling due to an insufficient dosage of M-CSF.

A. Luminescence cell viability assay

[00493] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with a low concentration of M-CSF (Gibco, Cat# PHC9501) or a normal concentration of M-CSF. The appropriate low and normal concentrations levels are determined experimentally by testing various levels of M-CSF that yield maximal survival of the cultured macrophages (normal) and hindered survival (low). Exemplary concentrations are 5 ng/ml M-CSF for the low concentration wells and 10 ng/ml for the normal concentration wells. At the start of plating, a TREM2 small molecule agonist or DMSO control is added to each cell at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. After 5 days, cellular ATP

levels are measured via luminescence detection to indicate cell viability using a CellTiter-Glo® Luminescent Cell Viability Assay (Promega Catalog Number G7571). The effects of the small molecule TREM2 agonist vs DMSO control on viable cell count of macrophages cultured in the presence of low or normal levels of M-CSF are compared.

B. Cell viability determined by automated microscopy

[00494] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with a low concentration of M-CSF (Gibco, Cat# PHC9501) or a normal concentration of M-CSF. The appropriate low and normal concentrations levels are determined experimentally by testing various levels of M-CSF that yield maximal survival of the cultured macrophages (normal) and hindered survival (low). Exemplary concentrations are 5 ng/ml M-CSF for the low concentration wells and 10 ng/ml for the normal concentration wells. At the start of plating, a TREM2 small molecule agonist or DMSO control is added to each cell at concentrations ranging from 0.01nM to 10 μM in 3-fold increments. Every day, cells are counted by automated microscopy, and the effects of treatment on cell numbers was measured. The effects of the small molecule TREM2 agonist vs DMSO control on macrophages cultured in the presence of low or normal levels of M-CSF are compared.

C. Phospho-SYK assay

[00495] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in standard a 96-well, or a 384-well cell culture plate. Cells are plated in media with a low concentration of M-CSF (Gibco, Cat# PHC9501) or a normal concentration of M-CSF. The appropriate low and normal concentrations levels are determined experimentally by testing various levels of M-CSF that yield maximal survival of the cultured macrophages (normal) and hindered survival (low). Exemplary concentrations are 5 ng/ml M-CSF for the low concentration wells and 10 ng/ml for the normal concentration wells. At the start of plating, a TREM2 small molecule agonist or DMSO control is added to each cell at concentrations ranging from 0.01nM to 10 μM in 3-fold increments. After 5 days, cells are washed, lysed with M-PER™ reagent (Thermo Scientific) and aliquots of the lysate were analyzed for levels of phospho-SYK using the AlphaLisa® platform, and the reagent kit AlphaLISA® SureFire Ultra p-Syk (Tyr525/526) (Perkin Elmer, part number ALSU-PSYK-A-HV). The effects of the small molecule TREM2 agonist vs DMSO control on phosphorylation

levels of SYK, as a measure of signaling, macrophages cultured in the low or normal levels of M-CSF were compared.

[00496] The above protocols *A-C* are first carried out with donated human monocytes of no known disease-associated genotype, and repeated with monocytes from ALSP patients carrying a mutation in one allele of the CSF1R gene (CSF1R +/- haploinsufficient monocytes). For experiments using monocytes from ALSP patients, only normal amounts of M-CSF are used, as CSF1R function is already impaired.

[00497] The above protocols *A-C* can be repeated to test the effects of other any small molecule TREM2 agonist on macrophage cell viability and signaling, including, but not limited to small molecule TREM2 agonists disclosed herein.

Example 4: The effects of small molecule TREM2 agonists on signaling and survival in monocyte-derived human macrophages that have impaired CSF1R receptor signaling through the use of a chemical inhibitor of CSF1R.

A. Luminescence cell viability assay

[00498] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with experimentally determined normal levels of M-CSF (e.g. 10 ng/ml M-CSF). At the start of plating, the CSF1R inhibitor PLX5622 (Medchem express) is added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. A small molecule TREM2 agonist or DMSO control is also added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. After 5 days, cellular ATP levels are measured via luminescence detection to indicate cell viability using a CellTiter-Glo® Luminescent Cell Viability Assay (Promega Catalog Number G7571). The effects of a small molecule TREM2 agonist vs DMSO control on macrophages cultured in the presence of PLX5622 were compared.

B. Cell viability determined by automated microscopy

[00499] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with experimentally determined normal levels of M-CSF (e.g. 10 ng/ml M-CSF). At the start of plating, the CSF1R inhibitor PLX5622 (Medchem express) is added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. A small molecule TREM2

agonist or DMSO control is also added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. Every day, cells are counted by automated microscopy, and the effects of treatment on cell numbers is measured. The effects of the small molecule TREM2 agonist vs DMSO control on macrophages cultured in the presence or absence of PLX5622 are compared.

C. Phospho-SYK assay

[00500] Monocytes isolated from human blood by magnetic separation are washed, resuspended in culture media and plated in a 96-well, or a 384-well cell culture plate. Cells are plated in media with experimentally determined normal levels of M-CSF (e.g. 10 ng/ml M-CSF). At the start of plating, the CSF1R inhibitor PLX5622 (Medchem express) is added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. A small molecule TREM2 agonist or DMSO control is also added to the wells at concentrations ranging from 0.01 nM to 10 μM in 3-fold increments. After 5 days, cells are washed, lysed with M-PER™ reagent (Thermo Scientific) and aliquots of the lysate were analyzed for levels of phospho-SYK using the AlphaLisa® platform, and the reagent kit AlphaLISA® SureFire Ultra p-Syk (Tyr525/526) (Perkin Elmer, part number ALSU-PSYK-A-HV). The effects of the small molecule TREM2 agonist vs DMSO control on phosphorylation levels of SYK, as a measure of signaling, macrophages cultured in the presence or absence of PLX5622 were compared.

[00501] The above protocols *A-C* are first carried out with donated human monocytes of no known disease-associated genotype, and repeated with monocytes from ALSP patients carrying a mutation in one allele of the CSF1R gene (CSF1R +/- haploinsufficient monocytes)for comparison. In experiments using monocytes from ALSP patients, CSF1R inhibitor PLX5622 is not used, as CSF1R signaling is already inhibited.

[00502] The above protocols *A-C* can be repeated to test the effects of other any small molecule TREM2 agonist on macrophage cell viability and signaling, including, but not limited to small molecule TREM2 agonists disclosed herein.

Example 5. The effects of a TREM2 agonist on numbers, survival, proliferation and signaling in a hTREM2 KI mouse model treated with a small molecule CSF1R inhibitor.

[00503] Male transgenic mice containing a knockout at the mouse TREM2 locus, and with the human TREM2 (hTREM2) gene inserted, are treated with a CSF1R small molecule inhibitor.

For long term dosing to impair microglia, the compound PLX5622 is formulated in AIN-76A standard chow by Research Diets Inc. at 1200 ppm (PLX5622).

A. Microglia population numbers

[00504] After 10 weeks of treatment with PLX5622, mice are dosed with IP injections of TREM2 agonist or control (vehicle when TREM2 agonist antibodies are used, DMSO when TREM2 small molecule agonists are used) for a week, where dosing occurs every 3d. At the end of this treatment week, animals are terminated and the number of microglia present in multiple brain regions is analyzed. Treatment with PLX5622 results in loss of microglia in the brains of treated mice; treatment with TREM2 agonist restores microglia numbers. For all studies, brains are removed, and hemispheres separated along the midline. Brain halves are drop-fixed in 4% paraformaldehyde (Thermo Fisher Scientific, Waltham, MA) for immunohistochemical analysis. Fixed half brains are sliced at 40 μm using a Leica SM2000R freezing microtome. The flash-frozen hemispheres are microdissected into cortical, hippocampal, and thalamic/striatal regions and then ground with a mortar and pestle to yield a fine powder. Total microglia and plaque counts/volumes are obtained by imaging comparable sections of tissue from each animal at the ×10, ×20, or ×63 objective, at multiple z-planes, followed by automated analyses using Bitplane Imaris 7.5 spots or surfaces modules, respectively. Results are recorded as the total number of microglia in different brain regions. The effects of the TREM2 agonist vs control treatment on numbers of microglia in brain regions are compared.

B. Gene expression

[00505] Treatment with PLX5622 results in altered gene expression in the microglia of treated mice, reflecting impaired trophic survival pathways. After 10w of treatment with PLX5622, mice are dosed with TREM2 agonist (5-60 mpk oral doses daily) or control (vehicle for antibody TREM2 agonists, DMSO for small molecule TREM2 agonists) for a week. At the end of this week, animals are terminated, and the animal brains are processed as follows. Debris and myelin are removed using a modified cold Percoll® gradient: Cell pellets are resuspended in 10 mL (total) of ice cold 40% Percoll® (Sigma) diluted in HBSS and then spun for 30 min at 500 g with full acceleration and braking. Using this approach, the microglia pellet at the bottom of the 15mL tube and the Percoll® and myelin are then removed by vacuum suction. The cell pellet is washed with 10 mL of ice cold HBSS and spun again for 5 min at 300 g at 4 °C. All samples were then resuspended in 500 ml of ice cold FACS buffer (0.5% BSA, 1mM EDTA, in 1x PBS, Sterile

Filtered) containing Cd11b (PE), CD45 (APC-Cy7), and Cx3cr1 (APC) antibodies (from Biolegend®) at a 1:200 dilution for 30 min on ice. Samples are then washed in 10 mL of ice cold FACS buffer and spun down for 5 min at 300 g and then resuspended in 500 ml of ice cold FACS buffer. Pre-chilled 96 well plates (Eppendorf) are precoated with FACS buffer for 1 hour on ice and then all but 5 ml of FACS buffer is removed from each well. Plates are kept on ice until the respective sample is ready to sort. 12,000-15,000 microglia are then sorted on a BD FACSAria II using the 70 micron nozzle with purity mode into individual wells with a sort speed of approximately 10,000 events per second. Each sample takes approximately 5-10 min to sort. After sorting one sample the plate is immediately put back on ice. The resulting volume in each well is approximately 20 ml depending on the number of cells sorted. FACS purified microglia are sequenced using the Chromium™ single cell gene expression platform (10x Genomics). Approximately 10,000-13,000 microglia from each sample are directly loaded into each sample well following manufacturer instructions and combined into droplets with barcoded beads using the Chromium™ controller. Manufacturer specifications are followed for generation of the barcoded libraries and then the samples are sequenced to an average depth of 40,000-60,000 reads on an Illumina Nextseq® 500 sequencer.

[00506] Sequenced samples are processed using the Cell Ranger 1.2 pipeline and aligned to the GRCm38 (mm10) mouse reference genome. For each sample a digital gene expression matrix (DGE) is generated containing the raw UMI counts for each cell in a given sample. DGEs from each sample are then merged and processed using the independent component analysis (ICA) based platform. Cell with fewer than 650 detected genes/cell and genes that are expressed by fewer than 20 cells (0.025% of all cells in the dataset) are removed before identification of variable genes in the dataset, cell centering and scaling, and generation of independent components (ICs). For the total dataset analysis two rounds of ICA are performed. In the first round, 50 ICs are generated. The goal of the first round of clustering analysis is to identify (and remove) contaminating cell types using well-established markers for neurons and other brain cell types. Following this stage, a second round of ICA is performed using 40 ICs on microglia and immune cells. ICs corresponding to batch or replicate effects are removed from analysis, and the cells are then clustered based on their values for the remaining ICs. A clustering resolution parameter value of 0.8 is used. For each analysis ICs are curated and assigned to one of the following categories: ICs for which high-scoring cells express markers of other cell types (“doublets”); ICs for which fewer

than 5 cells have high cell loading scores ("outliers"); noisy ICs or ICs that correlate with batch or individual sample replicate ("artifacts"); or ICs to be used for subsequent clustering analysis ("real"). Genes that define each cluster of microglia are those that exceed a minimum threshold of 1.5 fold change and a P value less than 1E-4 and are adjusted using Benjamini–Hochberg false discovery rate (FDR) correction. After initial processing gene expression is compared between different treatments and subjected to pathway analysis and microglia cells are categorized based on cell-cycle/proliferation state and state of polarization/differentiation. The effects of the TREM2 agonist vs control treatment on total gene expression of microglia, and on activity of gene pathways involved in survival and proliferation, in brain regions are compared.

Example 6. Neurofilament light chain as a biomarker for tracking ALSP treatment efficacy

[00507] Monitoring of serum from patients with ALSP for levels of neurofilament light chain (NfL) in order to select patients for treatment, and to monitor the efficacy of treatment will be done as follows. Serum is collected from patients at various time points as required for the use. Serum is stored in sample aliquots at -80 °C. When ready for analysis, samples are thawed on ice. Measurement of NfL is determined using an assay run on a Simoa® HD-1 instrument (QUANTERIX) using a 2-step Assay Neat 2.0 protocol; 100 µl of sample or calibrator (diluent: Tris-buffered saline [TBS], 0.1% Tween 20, 1% milk powder, 400 µg/ml Heteroblock [Omega Biologicals, Bozeman, MT]), 25 µl conjugated beads (diluent: TBS, 0.1% Tween 20, 1% milk powder, 300ug/ml Heteroblock), and 20 µl of mAB 2:1 (0.1 µg/ml; diluent: TBS, 0.1% Tween 20, 1% milk powder, 300ug/ml Heteroblock) are incubated for 47 cadences (1 cadence = 45 seconds). After washing, 100 µl of streptavidin-conjugated b-galactosidase (150pM; Quanterix) is added, followed by a 7-cadence incubation and a wash. Prior to reading, 25 µl resorufin b-D-galactopyranoside (QUANTERIX) is added. Calibrators (neat) and samples (serum: 1:4 dilution) are measured in duplicates. Bovine lyophilized NfL is obtained from UmanDiagnostics. Calibrators ranged from 0 to 2,000 pg/ml for serum and from 0 to 10,000 pg/ml for CSF measurements. Batch prepared calibrators are stored at -80°C. Final NfL levels measured by the above method are used to help both select patients to treat with an agonist of TREM2 and guide response to treatment with an agonist of TREM2.

Example 7. In Vivo Model of Cuprizone-Induced Demyelination

[00508] R47H hTREM2$^{+/+}$ KI mice (on mTREM2 $^{-/-}$ KO background) are utilized in a study using the cuprizone model to study the effects of dosing with a TREM2 agonist antibody. Mice are maintained under controlled conditions (19–22 °C and in a 12-h light/dark cycle with unrestricted access to food and water). The objective of this study is to evaluate the effects of two doses of Cuprizone (Cpz) on brain Iba1 and dMBP expression in TREM2 R47H KI mice vs. corresponding wild-type (WT) mice, and to test the effects of additional dosing with aTREM2 agonist (antibody or small molecule) on the Iba1 and dMBP measurements.

[00509] Reversible demyelination in mouse brain areas are induced by twice-daily oral gavages of Cpz for 5 weeks (35 days). The daily Cpz dose are 300 mg/kg, administered in two separate gavages (morning and evening), starting on D0. To avoid premature terminations/deaths due to excessively induced model, the Cpz challenge in this study are commenced to the mice while at 9-12 weeks of age, weighing > 20 g. If any of the mice upon D0 weighed less than 20 g, it would be more prone to premature death or termination due to excess weight loss – a major model-related symptom. Therefore, mice with BW under the critical weight are assigned to the Vehicle groups.

[00510] After the last Cpz dosing day (D34), the mice are terminally anesthetized and perfusion-fixed, followed by collecting of the brain to prepare cryo-blocks. Three series of sections (8 sections/ serise) are cut, and immunohistochemistry with anti-Iba1 and anti-degraded Myelin Basic Protein antibody (anti-dMBP) are performed, to assess the intensity of inflammation and demyelination (respectively) in the corpus callosum of Cpz exposed mice.

[00511] 8-24w old mice are dosed PO BID by oral gavage with cuprizone for 5 weeks (WK 5) or for 5 weeks followed by 3 days (WK5+3D), or 7 days (WK5+7D), with no cuprizone. TREM2 agonist is administered once weekly, starting at four days before the first dose of cuprizone, by IP, at a dose of 100 mpk.

[00512] Treatment arms are as follows:

1. WT + Vehicle (n=6)
2. WT + CPZ + Vehicle, termination 4d after stopping cpz (n=12)
3. WT + CPZ + Vehicle, termination 7d after stopping cpz (n=12)
4. KI + CPZ + Vehicle, termination 4d after stopping cpz (n=12)
5. KI + CPZ + Vehicle, termination 7d after stopping cpz (n=12)
6. KI + CPZ + TREM2 Agonist Treated, termination 4d after stopping cpz (n=12)
7. KI + CPZ + TREM2 Agonist Treated, termination 7d after stopping cpz (n=12)

[00513] At the end of the experiment for each arm described above, mice are perfused with 4% paraformaldehyde. Mouse brains are removed and post-fixed in 4% PFA for 24 h, followed by immersion in 30% sucrose for 48 h, then embedded in Optimal Cutting Temperature (OCT). 5-μm sections are placed on glass slides and stained with solochrome cyanine to confirm the presence of a lesion. Sections are stained with the following primary antibodies: Rb anti-dMBP (Millipore, ab5864, 1:2000), and Rb anti-IBA1 (Wako, 019-19741, 1:600). AlexaFluor- conjugated secondary antibodies (Invitrogen, 1:1000) were used. Images are acquired with a Nikon Eclipse 90*i* fluorescent and bright field microscope equipped with 10 × and 20 × zoom objectives and analyzed with Metamorph 7.7 software. dMBP is analyzed as the percentage area of positive staining (number of positive pixels/mm2) within the region of interest.

[00514] Immunohistochemical (IHC) analysis is performed to count the number of IBA1 positive cells for each treatment. Additionally, amounts of dMBP are quantitated for each treatment arm and compared.

Example 8. Profiling of ALSP Patient PBMCs

[00515] It has been shown in a small study of 4 patients with ALSP that peripherally derived monocytes had elevated expression levels of CCR2, CX3CR1, CD62L, CD80 and CD86 compared to healthy control subjects. Furthermore, ALSP patient peripheral blood monocytes (PBMCs) stimulated with lipopolysaccharide (LPS) produced higher amounts of TNFa than healthy controls and significantly lower amounts of IL-10 as measured by flow cytometry using intracellular staining (Hamatani et al. Neurobiology of Disease, 2019, 140, 104867). The experiments disclosed below test the effect of TREM2 agonist treatment on the expression levels of the aforementioned proteins in the PBMCs of ALSP patients.

Sample collection & Gating

[00516] Peripheral blood mononuclear cells (PBMCs) are collected as described by Okada et al., J. Autoimmun., 88 (2018), 103-113. For surface molecule examination, untouched monocytes are enriched from PBMCs using minimal labeling of unwanted cells by magnetic cell separation (Pan Monocyte Isolation Kit, human; Miltenyi Biotec, Auburn, CA, USA) and stained with anti-human CD14 (clone 63D3), CD16 (clone 3G8), CD64 (clone 10.1), CD80 (clone 2D10), CD86 (clone IT2.2), CD62L (clone DREG-56), CX3CR1 (clone 2A9–1), and CCR2 (clone K036C2) antibodies conjugated to peridinin chlorophyll protein– cyanine 5.5 (PerCP/Cy5.5), phycoerythrin

(PE), allophycocyanin (APC), fluorescein isothiocyanate (FITC), Pacific Blue, APC-cyanine7 (Cy7), PE/Cy7, and APC, respectively (all purchased from BioLegend, San Diego, CA, USA) according to the manufacturer's protocol. Data is acquired using a FACS Canto II flow cytometer (BD Biosciences, San Jose, CA, USA) and analyzed with FlowJo software (TreeStar, Ashland, OR, USA). Mean fluorescence intensity (MFI) is calculated for quantification of protein expression.

[00517] Monocytes are gated according to forward scatter, side scatter, and expression of CD14 and CD16 after exclusion of doublets. After incubation in the presence of each stimulus described below, CD14-positive cells are analyzed after gating in the forward scatter/side scatter plot, because CD16 expression is reduced after incubation.

Response to M-CSF/GM-CSF +/-TREM2 agonist

[00518] To examine responses of healthy donor compared to ALSP patient PB derived monocytes, cells are exposed to macrophage colony-stimulating factor (M-CSF) and granulocyte-macrophage colony-stimulating factor (GM-CSF) with and without a TREM2 agonist. Monocytes are cultured in 96-well U-bottom plates at a concentration of 8×10^4/well for 6 days in 200 µl/well Macrophage-SFM (Thermo Fisher Scientific, Tokyo, Japan) with 3-fold serial dilutions of a TREM2 agonist mAb from 100nM to 0.1nM or antibody dilution buffer supplemented with 50 units/ml penicillin G and 50 µg/ml streptomycin (Penstrep; Thermo Fisher Scientific) and containing either 100 ng/ml human recombinant M-CSF (BioLegend) or 10 ng/ml human recombinant GM-CSF at 37 °C in 5% CO_2. On day 3, half of the medium is replaced with fresh medium containing each CSF and a corresponding concentration of TREM2 agonist or buffer, and after 6 days of incubation, surface molecules (mentioned above) are analyzed with flow cytometry.

Response to LPS +/-TREM2 agonist

[00519] PBMCs are cultured at a density of 2×10^5/well in Macrophage- SFM (Thermo Fisher Scientific) in 96-well U-bottom plates with 3-fold serial dilutions of a TREM2 agonist (for instance a TREM2 agonist mAb from 100nM to 0.1nM) or a dilution buffer. Various time points are tested such as 4 hours, 18 hours (overnight), and 48 hours TREM2 agonist treatment or buffer, followed by stimulation for 4 h with 10 µg/ml lipopolysaccharide (LPS) (Enzo Life Sciences, Farmingdale, NY, USA) and Brefeldin A solution (eBioscience, Hatfield, UK) at 37 °C in 5% CO_2. Stimulated PBMCs are harvested, washed, and stained with anti-human CD14 PerCP/Cy5.5 (clone 63D3) antibody (BioLegend). For intracellular staining, cells are washed again, fixed, permeabilized, and

stained with anti-human antibodies. Anti-human antibodies included anti-IL-10 Alexa Fluor (AF) 647 (JES3-9D7) antibody, anti-tumor necrosis factor (TNF) α AF488 (Mab11) antibody, anti-IL-6 PE/Cy7 (MQ2-13A5) antibody, anti-transforming growth factor (TGF) β Brilliant Violet 421 (TW4-2F8) antibody (all purchased from BioLegend), and anti-IL-12p70 PE (20C2) antibody (BD). Additional intracellular cytokine staining is also explored following a similar protocol. Extracellular cytokines and chemokines are measured by collecting supernatant following the 24 hours of LPS treatment and running MSD multiplex panels according to the manufacturer's specifications.

ALSP Patient Derived PBMC Gene Expression Response to a TREM2 Agonist

[00520] PBMCs are cultured at a density of 2×10^5/well in Macrophage-SFM (Thermo Fisher Scientific) in 96-well U-bottom plates with 3-fold serial dilutions of a TREM2 agonist (for instance a TREM2 agonist mAb from 100nM to 0.1nM) or a dilution buffer. Various time points are tested such as 4 hours, 18 hours (overnight), and 48 hours following TREM2 agonist treatment or buffer and RNA is isolated. Gene expression of ABCD1, ABCD2, ABCD3, Ch25h and other metabolic and inflammatory genes is performed using qRT-PCR.

TREM2 Agonist Effect on ALSP Patient Derived PBMC Phagocytosis

[00521] Phagocytosis analysis is performed according to the manufacturer's instructions. PBMCs are incubated with 20nM, 2nM and 0.2nM of TREM2 agonist or dilution buffer for 2 hours or 18 hours. Then, PBMCs are incubated with FITC-labeled bare latex beads or beads coated with rabbit immunoglobulin G (IgG) (Phagocytosis Assay Kit FITC; Cayman Chemical, Ann Arbor, MI, USA) for 2 h. Cells are stained with anti-human CD14 PerCP/Cy5.5 (clone 63D3) (BioLegend), and the percentage of CD14-positive cells that ingested beads is determined as FITC-positive cells.

CLAIMS

We claim:

1. A method of treating a disease or disorder caused by and/or associated with colony-stimulating factor 1 receptor (CSF1R) dysfunction in a human patient, the method comprising administering to the patient an effective amount of an agonist of triggering receptor expressed on myeloid cells 2 (TREM2).

2. The method of claim 1, wherein the disease or disorder is selected from adult-onset leukoencephalopathy with axonal spheroids and pigmented glia (ALSP), hereditary diffuse leukoencephalopathy with axonal spheroids (HDLS), pigmentary orthochromatic leukodystrophy (POLD), pediatric-onset leukoencephalopathy, congenital absence of microglia, or brain abnormalities neurodegeneration and dysosteosclerosis (BANDDOS).

3. The method of claim 1, wherein the disease or disorder is selected from Nasu-Hakola disease, Alzheimer's disease, frontotemporal dementia, multiple sclerosis, Guillain-Barre syndrome, amyotrophic lateral sclerosis (ALS), Parkinson's disease, traumatic brain injury, spinal cord injury, systemic lupus erythematosus, rheumatoid arthritis, prion disease, stroke, osteoporosis, osteopetrosis, osteosclerosis, skeletal dysplasia, dysosteoplasia, Pyle disease, cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy, cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy, cerebroretinal vasculopathy, or metachromatic leukodystrophy; wherein the patient exhibits CSF1R dysfunction, and/or has a mutation in a gene affecting the function of CSF1R.

4. The method of claim 1, wherein the disease or disorder is ALSP.

5. The method of claim 1, wherein the patient possesses a heterozygous loss of function mutation in the kinase domain of the CSF1R.

6. The method of claim 1, wherein the administration of the agonist of TREM2 increases microglia function in the patient.

7. The method of claim 1, wherein the agonist of TREM2 activates TREM2/DAP12 signaling in myeloid cells.

8. The method of claim 1, wherein the agonist of TREM2 activates, induces, promotes, stimulates, or otherwise increases one or more TREM2 activities selected from:

(a) TREM2 binding to DAP12; DAP12 binding to TREM2; TREM2 phosphorylation; DAP12 phosphorylation;

(b) PI3K activation;

(c) increased levels of soluble TREM2 (sTREM2);

(d) increased levels of soluble CSF1R (sCSF1R);

(e) increased expression of one or more anti-inflammatory mediators selected from the group consisting of IL-12p70, IL-6, and IL-10;

(f) reduced expression of one or more pro-inflammatory mediators selected from the group consisting of IFN-a4, IFN-b, IL-6, IL-12 p70, IL-1β, TNF, TNF-α, IL-10, IL-8, CRP, TGF-beta members of the chemokine protein families, IL-20 family members, IL-33, LIF, IFN-gamma, OSM, CNTF, TGF-beta, GM-CSF, IL-11, IL-12, IL-17, IL-18, and CRP;

(g) increased expression of one or more chemokines selected from the group consisting of CCL2, CCL4, CXCL10, CCL3 and CST7;

(h) reduced expression of TNF-α, IL-6, or both; extracellular signal-regulated kinase (ERK) phosphorylation; increased expression of C-C chemokine receptor 7 (CCR7);

(i) induction of microglial cell chemotaxis toward CCL19 and CCL21 expressing cells;

(j) an increase, normalization, or both of the ability of bone marrow-derived dendritic cells to induce antigen-specific T-cell proliferation; induction of osteoclast production;

(k) increased rate of osteoclastogenesis, or both; increasing the survival and/or function of one or more of dendritic cells, macrophages, microglial cells, M1 macrophages and/or microglial cells, activated M1 macrophages and/or microglial cells, M2 macrophages and/or microglial cells, monocytes, osteoclasts, Langerhans cells of skin, and Kupffer cells;

(l) induction of one or more types of clearance selected from the group consisting of apoptotic neuron clearance, nerve tissue debris clearance, non-nerve tissue debris clearance, bacteria or other foreign body clearance, disease-causing protein clearance, disease-causing

peptide clearance, and disease-causing nucleic acid clearance;

(m) induction of phagocytosis of one or more of apoptotic neurons, nerve tissue debris, non-nerve tissue debris, bacteria, other foreign bodies, disease-causing proteins, disease-causing peptides, or disease-causing nucleic acids; normalization of disrupted TREM2/DAP12-dependent gene expression;

(n) recruitment of Syk, ZAP70, or both to the TREM2/DAP12 complex; Syk phosphorylation; increased expression of CD83 and/or CD86 on dendritic cells, macrophages, monocytes, and/or microglia;

(o) reduced secretion of one or more inflammatory cytokines selected from the group consisting of TNF-α, IL-10, IL-6, MCP-1, IFN-a4, IFN-b, IL-1β, IL-8, CRP, TGF-beta members of the chemokine protein families, IL-20 family members, IL-33, LIF, IFN-gamma, OSM, CNTF, TGF-beta, GM-CSF, IL-11, IL-12, IL-17, IL-18, and CRP;

(p) reduced expression of one or more inflammatory receptors; increasing phagocytosis by macrophages, dendritic cells, monocytes, and/or microglia under conditions of reduced levels of MCSF;

(q) decreasing phagocytosis by macrophages, dendritic cells, monocytes, and/or microglia in the presence of normal levels of MCSF; increasing activity of one or more TREM2-dependent genes;

(r) increased expression of one or more of IL-4, CCL8, FasL, CSF1, CSF2, FIZZ1, CD206, Arg1, Ym1, IGF-1, Chi3l3, Fzd1, and IL-34;

(s) decreased expression of one or more of IL-12 p40, IL-27, CSF3, CCR5, ABCD1 and CH25H; or

(t) any combination thereof.

9. The method of any one of claims 1-8, wherein the agonist of TREM2 is an antigen binding protein or an antibody, or an antigen-binding fragment thereof.

10. The method of claim 9, wherein the agonist of TREM2 is a monoclonal antibody.

11. The method of claim 9, wherein the agonist of TREM2 is a humanized antibody.

12. The method of claim 9, wherein the agonist of TREM2 is a human antibody.

13. The method of any one of claims 7-12, wherein the agonist of TREM2 is an antibody that specifically binds to the polypeptide of SEQ ID NO: 1.

14. The method of claim 13, wherein the antibody binds specifically to a polypeptide of amino acid residues 19-174 of SEQ ID NO:1.

15. The method of claim 13, wherein the antibody binds specifically to a polypeptide of amino acid residue 19-140 of SEQ ID NO:1.

16. The method of any one of claims 7-15, wherein the agonist of TREM2 is an antibody comprising a light chain variable region having a CDRL1, CDRL2, and CDRL3 selected from **Table 1A** and **3E**, and a heavy chain variable region having a CDRH1, CDRH2, and CDRH3 selected from **Table 1B** and **3E**.

17. The method of claim 16, wherein the TREM2 agonist is an antibody having a CDRL1 comprising a sequence selected from SEQ ID NOs: 5-18; a CDRL2 comprising a sequence selected from SEQ ID NOs: 19-30; a CDRL3 comprising a sequence selected from SEQ ID NOs: 31-45; a CDRH1 comprising a sequence selected from SEQ ID NOs: 77-86; a CDRH2 comprising a sequence selected from SEQ ID NOs: 87-94; and a CDRH3 comprising a sequence selected from SEQ ID NOs: 95-109.

18. The method of claim 16, wherein the TREM2 agonist is an antibody comprising:

(a) a CDRL1, CDRL2, and CDRL3 comprising the sequence of SEQ ID NOs: 8, 22, and 35, respectively, and a CDRH1, CDRH2, and CDRH3 comprising the sequence of SEQ ID NOs: 77, 368, and 98, respectively;

(b) a CDRL1, CDRL2, and CDRL3 comprising the sequence of SEQ ID NOs: 16, 369, and 370, respectively, and a CDRH1, CDRH2, and CDRH3 comprising the sequence of SEQ ID NOs: 85, 371, and 107, respectively;

(c) a CDRL1, CDRL2, and CDRL3 comprising the sequence of SEQ ID NOs: 10, 23, and

372, respectively, and a CDRH1, CDRH2, and CDRH3 comprising the sequence of SEQ ID NOs: 81, 373, and 374, respectively; or

(d) a CDRL1, CDRL2, and CDRL3 comprising the sequence of SEQ ID NOs: 17, 29, and 44, respectively, and a CDRH1, CDRH2, and CDRH3 comprising the sequence of SEQ ID NOs: 86, 94, and 375, respectively.

19. The method of any one of claims 9-15, wherein the agonist of TREM2 is an antibody comprising a light chain variable region selected from **Table 1A** or **3E**, and a heavy chain variable region selected from **Table 1B** and **3E**.

20. The method of claim 19, wherein the TREM2 agonist antigen binding protein comprises a light chain variable region comprising a sequence selected from SEQ ID NOs: 46-63 and a heavy chain variable region comprising a sequence selected from SEQ ID NOs: 110-126.

21. The method of claim 19, wherein the TREM2 agonist antigen binding protein comprises

(a) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 326 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 327;

(b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 328 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 329;

(c) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 330 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 331; or

(d) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 332 and a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 333.

22. The method of claim 1, wherein the agonist of TREM2 is a small molecule agonist of TREM2.

23. The method of claim 22, wherein the agonist of TREM2 is a lipid ligand of TREM2.

24. The method of claim 23, wherein the agonist of TREM2 is selected from l-palmitoyl-2-(5'-oxo-valeroyl)-sn-glycero-3-phosphocholine (POVPC), 2-Arachidonoylglycerol (2-AG), 7-

ketocholesterol (7-KC), 24(S)hydroxycholesterol (240HC), 25(S)hydroxycholesterol (250HC), 27- hydroxycholesterol (270HC), Acyl Carnitine (AC), alkylacylglycerophosphocholine (PAF), a-galactosylceramide (KRN7000), Bis(monoacylglycero)phosphate (BMP), Cardiolipin (CL), Ceramide, Ceramide-1 -phosphate (CIP), Cholesteryl ester (CE), Cholesterol phosphate (CP), Diacylglycerol 34: 1 (DG 34: 1), Diacylglycerol 38:4 (DG 38:4), Diacylglycerol pyrophosphate (DGPP), Dihyrdoceramide (DhCer), Dihydrosphingomyelin (DhSM), Ether phosphatidylcholine (PCe), Free cholesterol (FC), Galactosylceramide (GalCer), Galactosylsphingosine (GalSo), Ganglioside GM1, Ganglioside GM3, Glucosylsphingosine (GlcSo), Hank's Balanced Salt Solution (HBSS), Kdo2-Lipid A (KLA), Lactosylceramide (LacCer), lysoalkylacylglycerophosphocholine (LPAF), Lysophosphatidic acid (LPA), Lysophosphatidylcholine (LPC), Lysophosphatidylethanolamine (LPE), Lysophosphatidylglycerol (LPG), Lysophosphatidylinositol (LPI), Lysosphingomyelin (LSM), Lysophosphatidylserine (LPS), N-Acyl-phosphatidylethanolamine (NAPE), N-Acyl- Serine (NSer), Oxidized phosphatidylcholine (oxPC), Palmitic-acid-9-hydroxy-stearic-acid (PAHSA), Phosphatidylethanolamine (PE), Phosphatidylethanol (PEtOH), Phosphatidic acid (PA), Phosphatidylcholine (PC), Phosphatidylglycerol (PG), Phosphatidylinositol (PI), Phosphatidylserine (PS), Sphinganine, Sphinganine-1-phosphate (SalP), Sphingomyelin (SM), Sphingosine, Sphingosine-1-phosphate (SolP), or Sulfatide, or a salt thereof.

25. The method of claim 23, wherein the agonist of TREM2 is a lipopolysaccharide.

26. The method of claim 22, wherein the agonist of TREM2 is selected from Tyrphostin AG 538, AC1NS458, IN1040, Butein, Okanin, AGL 2263, GB19, GB16, GB20, GB17, GB18, GB21, GB22, GB27, GB44, GB42, GB2, 4,4'-Dihydroxychalcone, or 3,4-Dihydroxybenzophenone, or a salt thereof.

27. The method of claim 1, wherein the agonist of TREM2 is heat shock protein 60 (HPS60).

28. The method of claim 1, wherein the agonist of TREM2 is apopoliprotein E (ApoE).