TREATMENT OF DISEASES RELATED TO ATP-BINDING CASSETTE TRANSPORTER 1 DYSFUNCTION USING TREM2 AGONISTS

SEQUENCE LISTING

[0001] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on November 30, 2021, is named 403433_006WO_SL.txt and is 2,755,371 bytes in size.

TECHNICAL FIELD OF THE INVENTION

[0002] The present invention relates to compounds and methods of use thereof for treating diseases and disorders caused by ATP-binding cassette transporter 1 (ABCD1) dysfunction.

BACKGROUND OF THE INVENTION

[0003] Microglia are brain-resident macrophages with many homeostatic and injury responsive roles, including trophic and phagocytic functions. Microglia are highly dependent on peroxidation for maintaining normal function. The ATP-binding cassette transporter 1 (ABCD1) gene encodes a key peroxisomal protein responsible for transport of activated very long chain fatty acids (VLCFA) into the peroxisome for further degradation and beta-oxidation for energy production. Therefore, mutations in the ABCD1 gene can lead to microglial dysfunction and damage due to accumulation of VLCFA, resulting in neurological and adrenal gland diseases and disorders. X-linked adrenoleukodystrophy (X-ALD) is one such condition associated with ABCD1 mutations, characterized by cerebral and spinal cord white matter degeneration with demyelination and adrenal insufficiency, which lead to progressive cognitive and motor dysfunction and ultimately death. To date, there are no known treatments for diseases and disorders caused by ABCD1 dysfunction, 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 ABCD1 loss of function mutations.

SUMMARY OF THE INVENTION

[0004] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with a dysfunction in ABCD1 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 ABCD1 is x-ALD.

DETAILED DESCRIPTION OF CERTAIN EMBODIMENTS

TREM2, ABCD1 and X-ALD

[0005] 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 innate immune receptor that binds many endogenous substrates, 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.

[0006] 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). One of the key TREM2 functions is regulating myeloid cell number. Knocking down expression of TREM2 in primary microglia using translation blockers leads to reduced cell number (Zheng, et al., Neurobiol. Aging, 2016; 42: 132-141). Evidence suggests that in various contexts, TREM2 is important for myeloid cell survival, proliferation and chemotaxis, all of which could lead to disease-associated increases in myeloid cell number including microglia (Jay, et al., Mol Neurodegener. 2017;12(1):56).

[0007] A well-characterized function of TREM2 is to enhance phagocytosis. TREM2 is expressed in a subset of myeloid cells within the CNS that have high phagocytic capacity (Bisht et al., Glia. 2016; 64: 826–839). Across numerous in vitro studies, loss of TREM2 results in reduced phagocytosis of a variety of substrates, including apoptotic neurons or neuronal cell lines (Takahashi et al., Exp Med. 2005;

201(4):647-657.; Hsieh et al., J Neurochem. 2009; 109(4): 1144-1156). Conversely, TREM2 activation or overexpression enhanced uptake of these substrates (Takahashi et al., J Exp Med. 2005; 201(4):647-657; Takahashi *et al.*, PLoS Med. 2007; 4(4):e124; Jiang et al., Neuropsychopharmacology. 2014; 39(13): 2949-2962.). TREM2 is important for clearance of myelin debris in experimental autoimmune encephalomyelitis (EAE) (Takahashi *et al.*, PLoS Med. 2007; 4(4):e124) and peri-infarct tissue in mice following middle coronary artery occlusion (MCAO) (Kawabori *et al.*, J Neurosci. 2015; 35(8): 3384-3396).

[0008] TREM2 has been classically described as being anti-inflammatory and several in vitro and in vivo studies are supportive of an anti-inflammatory role for TREM2 in certain contexts (Yin *et al.*, Traffic. 2016; 17(12): 1286-1296). Knocking down TREM2 in cell lines increases levels of proinflammatory mediators such as iNOS, TNFα, IL1β and IL6 (Yin *et al.*, Traffic. 2016; 17(12): 1286-1296) in response to apoptotic neuronal membrane debris (Takahashi *et al.*, J Exp Med. 2005; 201(4):647-657.), TLR ligands (Turnbull *et al.*, J Immunol. 2006; 177(6):3520-3524.), including LPS (Gawish et al., FASEB J. 2015 Apr; 29(4):1247-1257.; Gao et al., Mol Med Rep. 2013 Mar; 7(3):921-926.; Takahashi *et al.*, PLoS Med. 2007; 4(4):e124.) and Aβ42 (Jiang et al., Neuropsychopharmacology. 2014; 39(13): 2949-2962.). Moreover, overexpressing TREM2 in cell lines or amyloid (Jiang et al., Neuropsychopharmacology. 2014; 39(13): 2949-2962.) and tau mouse models of AD (Jiang et al., Neuropharmacology. 2016; 105:196-206.) reduced levels of these pro-inflammatory transcripts. Together, these studies suggest that in some contexts, TREM2 can attenuate inflammatory responses.

[0009] TREM2 has been linked to several serious 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). 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). 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).

[0010] The ABCD1 gene provides instructions for producing the adrenoleukodystrophy protein (ALDP). ABCD1 (ALDP) maps to Xq28. ABCD1 is a member of the ATP-binding cassette (ABC) transporter superfamily. The superfamily contains membrane proteins that translocate a wide variety of substrates across extra- and intracellular membranes, including metabolic products, lipids and sterols, and drugs.

ALDP is located in the membranes of cell structures called peroxisomes. Peroxisomes are small sacs within cells that process many types of molecules. ALDP brings a group of fats called very long-chain fatty acids (VLCFAs) into peroxisomes, where they are broken down. As ABCD1 is highly expressed in microglia, it is possible that microglial dysfunction and their close interaction with other cell types actively participates in neurodegenerative processes (Gong *et al*., Annals of Neurology. 2017; 82(5):813-827.). It has been shown that severe microglia loss and damage is an early feature in patients with cerebral form of X-linked ALD (cALD) carrying ABCD1 mutations (Bergner *et al*., Glia. 2019; 67: 1196–1209). It has also been shown that ABCD1-deficiency leads to an impaired plasticity of myeloid lineage cells that is reflected in incomplete establishment of anti-inflammatory responses, thus possibly contributing to the devastating rapidly progressive demyelination in cerebral adrenoleukodystrophy (Weinhor *et al*., BRAIN 2018: 141; 2329–2342). It has also been shown in a recent report of 83 young males with cALD that patients harboring the *APOE4* allele, a known ligand of TREM2, have an increased burden of cerebral disease involvement as determined by Loes score, gadolinium intensity score (GIS), and neurologic function score (NFS) (Orchard *et al.,* Nature Scientific Reports 2019 9:7858). These findings emphasize microglia/ monocytes/ macrophages as crucial therapeutic targets for preventing or stopping myelin destruction in patients with X-linked adrenoleukodystrophy.

[0011] 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 the ABCD1 gene. 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 ABCD1 function leading to sustained activation, proliferation, chemotaxis of microglia, maintenance of anti-inflammatory environment and reduced astrocytosis caused by a decrease in ABCD1 and accumulation of VLCFAs. The present invention relates to the unexpected discovery that activation of TREM2 can rescue microglia harboring the ABCD1 mutation and challenged with an increase in VLCFA, and that this effect may be also observed in patients suffering from loss of functional microglia due to ABCD1 mutation. This discovery has not been previously taught or suggested in the available art.

[0012] To date, no prior study has shown that TREM2 agonism can rescue the loss of microglia in cells where mutations in the ABCD1 and a VLCFA increase is present. No prior study has taught or suggested that reversal of the loss of microglia due to an ABCD1 mutation through TREM2 agonism can be used to treat a disease or disorder caused by and/or associated with an ABCD1 mutation.

[0013] X-linked adrenoleukodystrophy (x-ALD) is an X chromosome-linked central nervous system disease caused by an ABCD1 mutation that manifests in the form of variable developmental behavioral, cognitive, motor and sensory function changes in patients suffering from the disease. Three main phenotypes are seen in affected males: (1) The childhood cerebral form manifests most commonly between ages four and eight years. It initially resembles attention-deficit disorder or hyperactivity; progressive impairment of cognition, behavior, vision, hearing, and motor function follow the initial symptoms and often lead to total disability within six months to two years and death within 5 years. (2) Adrenomyeloneuropathy (AMN) manifests most commonly between the second and fourth decades as progressive stiffness and weakness of the legs, sphincter disturbances, sexual dysfunction, and often, impaired adrenocortical function; all symptoms are progressive over decades. (3) "Addison disease only" presents with primary adrenocortical insufficiency between age two years and adulthood and most commonly by age 7.5 years, without evidence of neurologic abnormality. The cerebral childhood form of x-ALD also know as cerebral ALD (cALD) is characterized by patchy cerebral white matter abnormalities visible by magnetic resonance imaging. However, the clinical symptoms and MRI changes are not specific to cALD and are common for other neurological conditions, including Adult-onset leukoencephalopathy with axonal spheroids and pigmented glia (ALSP), Nasu-Hakola disease (NHD) and other leukodystrophies, making diagnosis and treatment of cALD very difficult.

[0014] Studies have discovered that x-ALD is a genetic disorder in which male patients that carry a loss of function mutation in the peroxisomal transporter gene ABCD1, leading to VLCFA increase and activation of inflammatory processes leading to demyelination and axonal degeneration. In one aspect, the present invention relates to the surprising discovery that activation of the TREM2 pathway can rescue the loss of microglia in patients carrying ABCD1 mutations, preventing microglia apoptosis, thereby treating ABCD1-related conditions, such as, but not limited to, x-ALD.

[0015] 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 ABCD1 dysfunction, such as x-ALD. Neurofilament light chain (NfL) is highly elevated in the plasma, serum and CSF of patients with x-ALD, (van Ballegoij, *et al.*, Ann Clin Transl Neurol, 7: 2127-2136.). cALD 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.). Patients with cALD have quantitatively fewer

microglia than healthy individuals in multiple regions of the brain (Bergner *et al.*, Glia. 2019;67(6):1196-1209). 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 ABCD1 dysfunction, such as x-ALD, 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 x-ALD 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.

Definitions

[0016] 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.

[0017] "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.

[0018] "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.

[0019] "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.

[0020] "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.

[0021] "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.

[0022] "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.

[0023] "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.

[0024] "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.

[0025] "Antigen" refers to a substance, such as, without limitation, a particular peptide, protein, nucleic acid, or carbohydrate which can bind to a specific antibody.

[0026] "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).

[0027] "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.

[0028] "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)).

[0029] "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.

[0030] "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).

[0031] "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.

[0032] "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.

[0033] "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.

[0034] "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.

[0035] "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.

[0036] "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.

[0037] "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).

[0038] "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).

[0039] "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.

[0040] "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.

[0041] "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.

[0042] "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., 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.

[0043] 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.

[0044] 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.

[0045] "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.

[0046] "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.

[0047] "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.

[0048] "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.

[0049] "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.

[0050] "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.

[0051] "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}).

[0052] "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))

[0053] 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).

[0054] "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.

[0055] "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.

[0056] "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.

[0057] "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.

[0058] "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.

[0059] "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.

[0060] "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.

[0061] 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).

[0062] 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.

[0063] 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.

[0064] 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.

[0065] 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.

[0066] 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

[0067] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with an ABCD1 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.

[0068] In one aspect, the present invention provides a method of treating a disease or disorder caused by and/or associated with an ABCD1 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.

[0069] 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-4, 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-12 p40, 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 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; increased levels of one or more of CSF1, CSF2 and IL-34; or any combination thereof. 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 an ABCD1 dysfunction.

[0070] In another aspect, the invention provides a TREM2 agonist for use in treating a disease or disorder caused by and/or associated with an ABCD1 dysfunction in a human patient.

I. Diseases and Disorders

[0071] The methods of the present invention can be used to treat any disease or disorder related to a dysfunction in ABCD1. In some embodiments, the patient is selected for treatment based on a diagnosis that includes the presence of a mutation in an ABCD1 gene affecting the function of ABCD1. In some embodiments, the mutation in the ABCD1 gene is a mutation that causes a decrease in ABCD1 activity or a cessation of ABCD1 activity.In some embodiments, the disease or disorder is caused by a heterozygous ABCD1 mutation. In some embodiments, the disease or disorder is caused by a homozygous ABCD1 mutation. In some embodiments,

[0072] the disease or disorder is caused by a splice mutation in the ABCD1 gene. In some embodiments, the disease or disorder is caused by a missense mutation in the ABCD1 gene.

[0073] 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 ABCD1. In some embodiments, the disease or disorder is a disease or disorder resulting from a decrease or cessation in the activity of ABCD1. ABCD1 related activities that are changed in the disease or disorder include, but are not limited to peroxisomal import of fatty acids and/or fatty acyl-CoAs and production of adrenoleukodystrophy protein (ALDP).

[0074] In some embodiments, the disease or disorder is caused by a loss-of-function mutation in ABCD1. In some embodiments, the loss-of-function mutation results in a complete cessation of ABCD1 function. In some embodiments, the loss-of-function mutation results in a partial loss of ABCD1 function, or a decrease in ABCD1 activity. In some embodiments, the disease or disorder is caused by a homozygous mutation in ABCD1.

[0075] 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 an ABCD1 dysfunction.

[0076] In some embodiments, the disease or disorder is an immunological disorder. In some embodiments, the disease or disorder is an immunological disorder caused by and/or associated with an ABCD1 dysfunction.

[0077] In some embodiments, the disease or disorder is selected from X-linked adrenoleukodystrophy (x-ALD), Globoid cell leukodystrophy (also known as Krabbe disease), Metachromatic leukodystrophy (MLD), Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), Alexander disease, fragile X-associated tremor ataxia syndrome (FXTAS), adult-onset autosomal dominant leukodystrophy (ADLD), and X-linked Charcot–Marie–Tooth disease (CMTX).

[0078] In some embodiments, the disease or disorder is selected from X-linked adrenoleukodystrophy (x-ALD), Globoid cell leukodystrophy (also known as Krabbe disease), Metachromatic leukodystrophy (MLD), Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), Vanishing white matter disease (VWM), Alexander disease, fragile X-associated tremor ataxia syndrome (FXTAS), adult-onset autosomal dominant leukodystrophy (ADLD), and X-linked Charcot–Marie–Tooth disease (CMTX), wherein any of the aforementioned diseases or disorders are present in a patient exhibiting ABCD1 dysfunction, or having a mutation in a gene affecting the function of ABCD1.

[0079] In some embodiments, the disease or disorder is X-linked adrenoleukodystrophy (x-ALD). In some embodiments, the x-ALD is a cerebral form of X-linked ALD (cALD).

[0080] In some embodiments, the disease or disorder is Addison disease wherein the patient has been found to have a mutation in one or more ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is Addison disease, wherein the patient has a loss-of-function mutation in ABCD1.

[0081] In some embodiments, the disease or disorder is a white matter disease wherein the patient has been found to have a mutation in one or more ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is a white matter disease, wherein the patient has a loss-of-function mutation in ABCD1.

[0082] In some embodiments, the disease or disorder is vanishing white matter disease wherein the patient has been found to have a mutation in one or more ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is vanishing white matter disease, wherein the patient has a loss-of-function mutation in ABCD1.

[0083] 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), or Parkinson's disease, wherein any of the aforementioned diseases or disorders are present in a patient exhibiting ABCD1 dysfunction, or having a mutation in a gene affecting the function of ABCD1.

[0084] 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 ABCD1 genes affecting ABCD1 function. 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 ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is Alzheimer's disease, wherein the patient has a loss-of-function mutation in ABCD1.

[0085] 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 ABCD1 genes affecting ABCD1 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 ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is Nasu-Hakola disease, wherein the patient has a loss-of-function mutation in ABCD1.

[0086] 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 ABCD1 genes affecting ABCD1 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 ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is Parkinson's disease, wherein the patient has a loss-of-function mutation in ABCD1.

[0087] In some embodiments, the disease or disorder is multiple sclerosis wherein the patient has been found to have a mutation in one or more ABCD1 genes affecting ABCD1 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 ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is multiple sclerosis, wherein the patient has a loss-of-function mutation in ABCD1.

[0088] In some embodiments, the disease or disorder is ALS wherein the patient has been found to have a mutation in one or more ABCD1 genes affecting ABCD1 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 ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is ALS, wherein the patient has a loss-of-function mutation in ABCD1.

[0089] 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 ABCD1 genes affecting ABCD1 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 ABCD1 genes affecting ABCD1 function. In some embodiments, the disease or disorder is Guillain-Barre syndrome, wherein the patient has a loss-of-function mutation in ABCD1.

[0090] In some embodiments, the patient also possesses a mutation in one or more of NOTCH3, HTRA1, TREX1, ARSA, EIF2B1, EIF2B2, EIF2B3, EIF2B4, and EIF2B5.

[0091] 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, adrenal insufficiency, vision impairment, hearing impairment, sexual dysfunction, impaired adrenocortical function, attention-deficit, hyperactivity, and incontinence.

[0092] In one aspect, the present invention provides a method of treating x-ALD 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.

[0093] In one aspect, the present invention provides a method of treating x-ALD 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 x-ALD. In some embodiments, the agonist of TREM2 is an antibody or a small molecule.

[0094] In another aspect, the invention provides a TREM2 agonist for the manufacture of a medicament for the treatment of a disease or disorder related to an ABCD1 dysfunction. In another aspect, the invention provides a TREM2 agonist for the manufacture of a medicament for the treatment of x-ALD.

[0095] In another aspect, the invention provides a TREM2 agonist for use in treating a disease or disorder related to an ABCD1 dysfunction in a human patient. In another aspect, the invention provides a TREM2 agonist for use in treating x-ALD in a human patient.

Huntington's Disease

[0096] In one aspect, the present invention provides a method of treating Huntington's disease 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 Huntington's disease. In some embodiments, the agonist of TREM2 is an antibody or a small molecule. In some embodiments, the agonist of TREM2 is an antibody or a small molecule disclosed elsewhere herein. In some embodiments, the agonist of TREM2 is an antibody disclosed elsewhere herein. In some embodiments, the agonist of TREM2 is a small molecule disclosed elsewhere herein. In another aspect, the invention provides a TREM2 agonist for the manufacture of a medicament for the treatment of Huntington's disease. In another aspect, the invention provides a TREM2 agonist for use in treating Huntington's disease in a human patient.

II. Antibodies

[0097] 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.

[0098] 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).

[0099] In some embodiments, the TREM2 antibody specifically bind to human TREM2 human TREM2 residues 19-174. In some embodiments, the TREM2 antibody specifically bind to IgV region of human TREM2, for example human TREM2 residues 19-140.

[00100] 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), 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.

[00101] 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 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.

[00102] In some embodiments, the antibody, or an antigen-binding fragment thereof, specifically binds TREM2 and prevents the degradation or cleavage of TREM2.

[00103] 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.

[00104] 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.

[00105] 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.

[00106] In some embodiments, a TREM2 activating antibody comprise 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.

Sequence Information

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

[00107] 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.

[00108] 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 A1** and **A2** below, along with exemplary light chain and variable regions.

TABLE A1: 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	SFELTQPPSVSVSPGQTASITCSGDKLGDKYVCWYQQKPGQSPMLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL (SEQ ID NO:48)	SGDKLGDKYVC (SEQ ID NO:6)	QDTKRPS (SEQ ID NO:21)	QAWDSSTVV (SEQ ID NO:33)
26F2	LV-04	SYELTQPPSVSVSPGQTASITCSGDKLGDKYVCWYQQKPGQSPVLVIFQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL (SEQ ID NO:49)	SGDKLGDKYVC (SEQ ID NO:6)	QDSKRPS (SEQ ID NO:20)	QAWDSSTVV (SEQ ID NO:33)

Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
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	DIVMTQSPDSLAVSLGERATITCKSSHNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHQYYSTPCSFGQGTKLEIK (SEQ ID NO:53)	KSSHNVLYSSNNKNYLA (SEQ ID NO:9)	WASTRES (SEQ ID NO:22)	HQYYSTPCS (SEQ ID NO:36)
10E3	LV-09	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLIYGASTRATGIPARFSVSGSGTEFTLTISSLQSEDFAFYYCLQDNNWPPTFGPGTKVDIK (SEQ ID NO:54)	RASQSVSSNLA (SEQ ID NO:10)	GASTRAT (SEQ ID NO:23)	LQDNNWPPT (SEQ ID NO:37)
13E7 14C12	LV-10	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLIYGASTRATGIPARFSVSGSGTEFTLTISSLQSEDFAVYYCLQDNNWPPTFGPGTKVDIK (SEQ ID NO:55)	RASQSVSSNLA (SEQ ID NO:10)	GASTRAT (SEQ ID NO:23)	LQDNNWPPT (SEQ ID NO:37)
25F12	LV-11	EKVMTQSPATLSVSPGERATLSCRASQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK (SEQ ID NO:56)	RASQSVNNNLA (SEQ ID NO:11)	GASTRAT (SEQ ID NO:23)	QQYNNWPRT (SEQ ID NO:38)
32E3	LV-12	EFVLTQSPGTLSLSPGERATLSCRASQIISSNYLAWYQQKPGQAPRLLIYSASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFDSSPITFGRGTRLDIK (SEQ ID NO:57)	RASQIISSNYLA (SEQ ID NO:12)	SASSRAT (SEQ ID NO:24)	QQFDSSPIT (SEQ ID NO:39)
24F4	LV-13	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR	RASQSVSSSYLA	GASSRAT	QQYDTSPFT

Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
		FSGSGSGTDFTLTISRLEPEDFALYYCQQYD TSPFTFGPGTKVDIK (SEQ ID NO:58)	(SEQ ID NO:13)	(SEQ ID NO:25)	(SEQ ID NO:40)
16B8	LV-14	DIQMTQSPSSVSASVGDRVTVTCRASQDIN SWLAWYQQKPGKAPKLLIYAASSLQTGVP SRFSGSGSGTDFTLTISSLQPEDFATYSCQQS NSFPITFGQGTRLEIK (SEQ ID NO:59)	RASQDI NSWLA (SEQ ID NO:14)	AASSLQ T (SEQ ID NO:26)	QQSNSF PIT (SEQ ID NO:41)
4C5	LV-15	DIQMTQSPSSVSASVGDRVTITCRASQGISN WLAWYQQKPGKAPKLLIYAASSLQVGVPL RFSGSGSGTDFTLTISSLQPEDFATYYCQQA DSFPRNFGQGTKLEIK (SEQ ID NO:60)	RASQGI SNWLA (SEQ ID NO:15)	AASSLQ V (SEQ ID NO:27)	QQADSF PRN (SEQ ID NO:42)
6E7	LV-16	DIQMTQSPSSVSASVGDRVTITCRASQGISS WLAWYQQKPGKAPKLLIYAASSLQNGVPS RFSGSGSGTDFTLTISSLQPEDFATYFCQQA DSFPRTFGQGTKLEIK (SEQ ID NO:61)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ N (SEQ ID NO:28)	QQADSF PRT (SEQ ID NO:43)
5E3	LV-17	DIQMTQSPSSLSASVGDRVTITCRASQGISN YLAWFQQKPGKAPKSLIYAASSLQSGVPSK FSGSGSGTDFTLTISSLQPEDFATYYCQQYS TYPFTFGPGTKVDIK (SEQ ID NO:62)	RASQGI SNYLA (SEQ ID NO:17)	AASSLQ S (SEQ ID NO:29)	QQYSTY PFT (SEQ ID NO:44)
4G10	LV-18	DIQMTQSPSSLSASVGDRVTITCRASQGIRN DLGWYQQKPGNAPKRLIYAASSLPSGVPSR FSGSGSGPEFTLTISSLQPEDFATYYCLQHN SYPWTFGQGTKVEIT (SEQ ID NO:63)	RASQGI RNDLG (SEQ ID NO:18)	AASSLPS (SEQ ID NO:30)	LQHNSY PWT (SEQ ID NO:45)

TABLE A2: 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	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAIGGGGVST YCADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAKFYIAVAGSHFDYWGQGTLV TVSS (SEQ ID NO:110)	SYAMS (SEQ ID NO:77)	AIGGGG VSTYCA DSVKG (SEQ ID NO:87)	FYIAVA GSHFDY (SEQ ID NO:95)
26A10	HV-02	EVQLVESGGALVQRGGSLRLSCAASRFTFS SFGMSWVRQAPGKGLEWVSYISSSSFTIYY ADSVKGRFTISRDNAKNSFYLQMNSLRDED TAVYYCAREGGLTMVRGVSSYGLDVWGQ GTTVTVSS (SEQ ID NO:111)	SFGMS (SEQ ID NO:78)	YISSSSF TIYYAD SVKG (SEQ ID NO:88)	EGGLTM VRGVSS YGLDV (SEQ ID NO:96)
26C10	HV-03	EVQLVESGGALVQPGGSLRLSCAASGFTFS SFGMSWVRQAPGKGLEWVSYISSSSFTIYY ADSVKGRFTISRDNAKNSFYLQMNSLRDED	SFGMS (SEQ ID NO:78)	YISSSSF TIYYAD SVKG	EGGITM VRGVSS YGMDV

Ab ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
		TAVYFCVREGGITMVRGVSSYGMDVWGQ GTTVTVSS (SEQ ID NO:112)		(SEQ ID NO:88)	(SEQ ID NO:97)
26F2	HV-04	EVQLVESGGALVQPGGSLRLSCAASGFTFS SFGMSWVRQAPGKGLEWISYISSSSFTIYYA DSVKGRFTISRDNAKNSFYLQMNSLRDEDT AVYFCAREGGITMVRGVSSYGMDVWGQG TTVTVSS (SEQ ID NO:113)	SFGMS (SEQ ID NO:78)	YISSSSF TIYYAD SVKG (SEQ ID NO:88)	EGGITM VRGVSS YGMDV (SEQ ID NO:97)
33B12	HV-05	EVQLVESGGALVQPGGSLRLSCAASGFTFS SFGMSWVRQAPGKGLEWVSYISKSSFTIYY ADSVKGRFTISRDNAKNSFYLQMNSLRDED TAVYYCAREGGLTMVRGVSSYGLDVWGQ GTTVTVSS (SEQ ID NO:114)	SFGMS (SEQ ID NO:78)	YISKSSF TIYYAD SVKG (SEQ ID NO:89)	EGGLTM VRGVSS YGLDV (SEQ ID NO:96)
24G6	HV-06	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAKAYTPMAFFDYWGQGTLVTV SS (SEQ ID NO:115)	SYAMS (SEQ ID NO:77)	AISGSGG STYYAD SVKG (SEQ ID NO:90)	AYTPMA FFDY (SEQ ID NO:98)
24A10	HV-07	EVQVLESGGGLVQPGGSLRLSCAASGFTFS NYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAKGGWELFYWGQGTLVTVSS (SEQ ID NO:116)	NYAMS (SEQ ID NO:79)	AISGSGG STYYAD SVKG (SEQ ID NO:90)	GGWELF Y (SEQ ID NO:99)
10E3	HV-08	EVQLVQSGAEVKKPGESLMISCKGSGYSFT NYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASD TAMYFCARRRQGIWGDALDIWGQGTLVTV SS (SEQ ID NO:117)	NYWIG (SEQ ID NO:80)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	RRQGIW GDALDI (SEQ ID NO:100)
13E7 14C12	HV-09	EVQLVQSGAEVKKPGESLMISCKGSGYSFT SYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASD TAMYFCARRRQGIWGDALDFWGQGTLVT VSS (SEQ ID NO:118)	SYWIG (SEQ ID NO:81)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	RRQGIW GDALDF (SEQ ID NO:101)
25F12	HV-10	QVQLQQWGAGLLKPSETLSLTCAVYGGSF SSYYWSWIRQPPGKGLEWIGEINHSGNTNY NPSLKSRVTISVDTSKNQFSLKLSSVTAADT AVYYCAREGYYDILTGYHDAFDIWDQGTM VTVFS (SEQ ID NO:119)	SYYWS (SEQ ID NO:82)	EINHSG NTNYNP SLKS (SEQ ID NO:92)	EGYYDI LTGYHD AFDI (SEQ ID NO:102)
32E3	HV-11	EVQLVQSGAEVKKPGESLKISCKGSGYSFT SYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSTLKASD	SYWIG (SEQ ID NO:81)	IIYPGDS DTRYSP SFQG	HDIIPAA PGAFDI (SEQ ID NO:103)

Ab ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
		TAIYYCARHDIIPAAPGAFDIWGQGTMVTV SS (SEQ ID NO:120)		(SEQ ID NO:91)	
24F4	HV-12	EVQLVQSGAEVKKPGESLKISCKGSGYTFT SYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISVDKSSSTAYLQWSSLKAS DTAIYYCTRQAIAVTGLGGFDPWGQGTLV TVSS (SEQ ID NO:121)	SYWIG (SEQ ID NO:81)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	QAIAVT GLGGFD P (SEQ ID NO:104)
16B8	HV-13	QVQLVQSGAEVKKPGASVKVSCKASGYTF TNYGISWVRQAPGQGLEWMGWISAYNGN TNYAQKLQGRVTMTTDTSTSTVYMELRSL RSDDTAVYYCARRGYSYGSFDYWGQGTL VTVSS (SEQ ID NO:122)	NYGIS (SEQ ID NO:83)	WISAYN GNTNYA QKLQG (SEQ ID NO:93)	RGYSYG SFDY (SEQ ID NO:105)
4C5	HV-14	EVQLVQSGAEVKKPGESLKISCKGSGHSFT NYWIAWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASD TAVYFCARQRTFYYDSSGYFDYWGQGTLV TVSS (SEQ ID NO:123)	NYWIA (SEQ ID NO:84)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	QRTFYY DSSGYF DY (SEQ ID NO:106)
6E7	HV-15	EVQLVQSGAEVKKPGESLKISCKGSGYSFT SYWIAWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASD TAMYFCARQRTFYYDSSDYFDYWGQGTL VTVSS (SEQ ID NO:124)	SYWIA (SEQ ID NO:85)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	QRTFYY DSSDYF DY (SEQ ID NO:107)
5E3	HV-16	QVQLVQSGAEVKKPGASVKVSCKASGYTF TGYYIHWVRQAPGLGLEWMGWINPYSGG TTSAQKFQGRVTMTRDTSISSAYMELSRLR SDDTAVYYCARDGGYLALYGTDVWGQGT TVTVSS (SEQ ID NO:125)	GYYIH (SEQ ID NO:86)	WINPYS GGTTSA QKFQG (SEQ ID NO:94)	DGGYLA LYGTDV (SEQ ID NO:108)
4G10	HV-17	EVQLVQSGAEVKKPGESLKISCKGSGYSFP SYWIAWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAFLKWSSLKASD TAMYFCARQGIEVTGTGGLDVWGQGTTVT VSS (SEQ ID NO:126)	SYWIA (SEQ ID NO:85)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	QGIEVT GTGGLD V (SEQ ID NO:109)

[00109] As noted above, a TREM2 agonist antigen binding protein may comprise one or more of the CDRs presented in **TABLE A1** (light chain CDRs; i.e. CDRLs) and **TABLE A2** (heavy chain CDRs, i.e. CDRHs).

[00110] 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.

[00111] 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 A1** and **A2**, each having at least 80%, 85%, 90% or 95% sequence identity to a CDR sequence listed in **TABLES A1** and **A2**. In some embodiments, the TREM2 agonist antigen binding protein includes 1, 2, 3, 4, 5, or 6 of the CDRs listed in **TABLES A1** and **A2**, each differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables.

[00112] 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.

[00113] 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.

[00114] 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.

[00115] 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.

[00116] 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;

(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.

[00117] 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 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.

[00118] 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 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 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.

[00119] 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 A1**, 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 A2**, and functional fragments, derivatives, muteins and variants of these light chain and heavy chain variable regions.

[00120] In some embodiments, each of the light chain variable regions listed in **TABLE A1**may be combined with any of the heavy chain variable regions listed in **TABLE A2** 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).

[00121] 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).

[00122] 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 A1**, 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 A1**). 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 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.

[00123] 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 A2**, 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 A2**). 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.

[00124] 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 A3-A4** below.

[00125] 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.

[00126] 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 A3-A4** below.

[00127] 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.

[00128] 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 A3-A4** 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, 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 A3**, **A4**, **A4**, **A5**, **A6**, **A7**, and **A8**. 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 94% identical, or at least 95% identical to a sequence selected from SEQ ID NOS:124, 180-190, and 307-312.

[00129] 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.

[00130] 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.

[00131] 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.

[00132] 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.

[00133] 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 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.

[00134] 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 A3: 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

Position in 10E3 VL Sequence or VH sequence	Region	Hot Spot	Parent Amino Acid	Amino Acid Substitutions
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
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 A4: 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 A5: 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)				
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 A6: 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 A7: 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
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 A8: 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

[00135] 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 A10**, **A11**, **A12**, **A13**, and **A14**, below.

[00136] 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 A9**.

TABLE A9: 6E7 Antibody Affinity Modulation Variants

	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

	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
V31		D57E					0.61*			0.73
V32		P62N					0.82*			0.89
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

	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
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	
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	

	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
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
V93				S31G			0.35*			1.05
V94					S52A		0.31*			0.87

[00137] 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.

[00138] 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 A7** and **A8**, 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 A10** and **A11**, respectively. The corresponding sequences for the 6E7 antibody are listed for comparison.

TABLE A10: Light Chain Variable Region Amino Acid Sequences for Improved Affinity TREM2 Antibodies

Variant Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
6E7	LV-16	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQNGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC QQADSFPRTFGQGTKLEIK (SEQ ID NO:61)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ N (SEQ ID NO:28)	QQADS FPRT (SEQ ID NO:43)
V3	LV-101	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSRQNGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC QQADRFPRTFGQGTKLEIK (SEQ ID NO:153)	RASQGI SSWLA (SEQ ID NO:16)	AASSRQ N (SEQ ID NO:143)	QQADR FPRT (SEQ ID NO:148)
V24	LV-102	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQKGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC QQADSFPHTFGQGTKLEIK (SEQ ID NO:154)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ K (SEQ ID NO:144)	QQADS FPHT (SEQ ID NO:149)
V27	LV-103	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQRGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC QQADSFPRTFGQGTKLEIK (SEQ ID NO:155)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ R (SEQ ID NO:145)	QQADS FPRT (SEQ ID NO:43)
V40	LV-104	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQLGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC QQADRFPRTFGQGTKLEIK (SEQ ID NO:156)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ L (SEQ ID NO:146)	QQADR FPRT (SEQ ID NO:148)
V48	LV-105	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQTGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC QQADSLPRTFGQGTKLEIK (SEQ ID NO:157)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ T (SEQ ID NO:26)	QQADS LPRT (SEQ ID NO:150)
V49 V73	LV-106	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSRQNGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC QQADSYPRTFGQGTKLEIK (SEQ ID NO:158)	RASQGI SSWLA (SEQ ID NO:16)	AASSRQ N (SEQ ID NO:143)	QQADS YPRT (SEQ ID NO:151)
V52	LV-107	DIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQRGV PSRFSGSGSGTDFTLTISSLQPEDFATYFC	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ R (SEQ ID NO:145)	QQADR FPRT (SEQ ID NO:148)

Variant Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
		QQADRFPRTFGQGTKLEIK (SEQ ID NO:159)			
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 A11: 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 (SEQ ID NO:124)	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPGDSDTRYSPSFQG (SEQ ID NO:91)	QRTFYYDSSDYFDY (SEQ ID NO:107)
V3	HV-101	EVQLVQSGAEVKKPGESLKISCKGSGYSFASYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQDQVTISADKSISTAYLQWSSLKASDTAMYFCARGRTFYY	YSFA (SEQ ID NO:164)	SYWIA (SEQ ID NO:85)	IIYPGDSDTRYSPSFQD (SEQ ID NO:170)	GRTFYYDSSDYFDY (SEQ ID NO:176)

Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 Border	CDRH1	CDRH2	CDRH3
		DSSDYFDYWGQGTLVTVSS (SEQ ID NO:180)				
V24	HV-102	EVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIAWVRQMP GKGLEWMGIIYPGDSDVRYSP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARSRTFYYD SSDYFDYWGQGTLVTVSS (SEQ ID NO:181)	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPGDS DVRYSP SFQG (SEQ ID NO:171)	SRTFYY DSSDYF DY (SEQ ID NO:177)
V27	HV-103	EVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIAWVRQMP GKGLEWMGIIYPGDSDTRYAP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCVRSRTFYYD SSDYFDYWGQGTLVTVSS (SEQ ID NO:182)	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPGDS DTRYAP SFQG (SEQ ID NO:172)	SRTFYY DSSDYF DY (SEQ ID NO:177)
V40	HV-104	EVQLVQSGAEVKKPGESLKIS CKGSGYSFGSYWIAWVRQMP GKGLEWMGIIYPGDSDVRYSP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARQRTFYY DSSDYSDYWGQGTLVTVSS (SEQ ID NO:183)	YSFG (SEQ ID NO:165)	SYWIA (SEQ ID NO:85)	IIYPGDS DVRYSP SFQG (SEQ ID NO:171)	QRTFYY DSSDYS DY (SEQ ID NO:178)
V48	HV-105	EVQLVQSGAEVKKPGESLKIS CKGSGYSFGSYWIAWVRQMP GKGLEWMGIIYPGDSDVRYSP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARMRTFYY DSSDYFDYWGQGTLVTVSS (SEQ ID NO:184)	YSFG (SEQ ID NO:165)	SYWIA (SEQ ID NO:85)	IIYPGDS DVRYSP SFQG (SEQ ID NO:171)	MRTFYY DSSDYF DY (SEQ ID NO:179)

Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 Border	CDRH1	CDRH2	CDRH3
V49	HV-106	EVQLVQSGAEVKKPGESLKIS CKGSGYSFNSYWIAWVRQMP GKGLEWMGTIYPGDSDTRLSP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARSRTFYYD SSDYFDYWGQGTLVTVSS (SEQ ID NO:185)	YSFN (SEQ ID NO:166)	SYWIA (SEQ ID NO:85)	TIYPGDS DTRLSPS FQG (SEQ ID NO:173)	SRTFYY DSSDYF DY (SEQ ID NO:177)
V52	HV-107	EVQLVQSGAEVKKPGESLKIS CKGSGYSFESYWIAWVRQMP GKGLEWMGIIYPGDSDTRYSP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARGRTFYY DSSDYFDYWGQGTLVTVSS (SEQ ID NO:186)	YSFE (SEQ ID NO:167)	SYWIA (SEQ ID NO:85)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	GRTFYY DSSDYF DY (SEQ ID NO:176)
V60	HV-108	EVQLVQSGAEVKKPGESLKIS CKGSGYHFTSYWIAWVRQMP GKGLEWMGIIYPGDSDVRYSP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARQRTFYY DSSDYSDYWGQGTLVTVSS (SEQ ID NO:187)	YHFT (SEQ ID NO:168)	SYWIA (SEQ ID NO:85)	IIYPGDS DVRYSP SFQG (SEQ ID NO:171)	QRTFYY DSSDYS DY (SEQ ID NO:178)
V73	HV-109	EVQLVQSGAEVKKPGESLKIS CKGSGYSFGSYWIAWVRQMP GKGLEWMGIIYPGDSDTRYSP GFQGQVTISADKSISTAYLQW SSLKASDTAMYFCARGRTFYY DSSDYFDYWGQGTLVTVSS (SEQ ID NO:188)	YSFG (SEQ ID NO:165)	SYWIA (SEQ ID NO:85)	IIYPGDS DTRYSP GFQG (SEQ ID NO:174)	GRTFYY DSSDYF DY (SEQ ID NO:176)

Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 Border	CDRH1	CDRH2	CDRH3
V76	HV-110	EVQLVQSGAEVKKPGESLKIS CKGSGYSFGSYWIAWVRQMP GKGLEWMGIIYPGDSDTRYSP EFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARQRTFYY DSSDYSDYWGQGTLVTVSS (SEQ ID NO:189)	YSFG (SEQ ID NO:165)	SYWIA (SEQ ID NO:85)	IIYPGDS DTRYSP EFQG (SEQ ID NO:175)	QRTFYY DSSDYS DY (SEQ ID NO:178)
V84	HV-111	EVQLVQSGAEVKKPGESLKIS CKGSGYGFTSYWIAWVRQMP GKGLEWMGIIYPGDSDTRYSP SFQGQVTISADKSISTAYLQWS SLKASDTAMYFCARQRTFYY DSSDYSDYWGQGTLVTVSS (SEQ ID NO:190)	YGFT (SEQ ID NO:169)	SYWIA (SEQ ID NO:85)	IIYPGDS DTRYSP SFQG (SEQ ID NO:91)	QRTFYY DSSDYS DY (SEQ ID NO:178)

[00139] 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 A10** (light chain CDRs; i.e. CDRLs) and **TABLE A11** (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 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.

[00140] 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.

[00141] 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.

[00142] 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 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.

[00143] 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.

[00144] 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 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.

[00145] 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 A10**, 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 A11**, 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 **TABLE A10** and **A11**. 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.

[00146] Each of the light chain variable regions listed in **TABLE A10** may be combined with any of the heavy chain variable regions listed in **TABLE A11** 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 A12: 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	DIQMTQSPSSVSASVGDRVTITCRASQGI SSWLAWYQQKPGKAPKLLIYAASSLQN GVPSRFSGSGSGTDFTLTISSLQPEDFATY FCQQADSFPRTFGQGTKLEIK (SEQ ID NO:61)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ N (SEQ ID NO:28)	QQADS FPRT (SEQ ID NO:43)
V9 V30 V33 V44 V68	LV-16	DIQMTQSPSSVSASVGDRVTITCRASQGI SSWLAWYQQKPGKAPKLLIYAASSLQN GVPSRFSGSGSGTDFTLTISSLQPEDFATY FCQQADSFPRTFGQGTKLEIK (SEQ ID NO:61)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ N (SEQ ID NO:28)	QQADS FPRT (SEQ ID NO:43)
V10	LV-201	DIQMTQSPSSVSASVGDRVTITCRASQGI SSWLAWYQQKPGKAPKLLIYSASSLQN GVPSRFSGSGSGTDFTLTISSLQPEDFATY FCQQADSFPRTFGQGTKLEIK (SEQ ID NO:295)	RASQGI SSWLA (SEQ ID NO:16)	SASSLQ N (SEQ ID NO:292)	QQADS FPRT (SEQ ID NO:43)

Variant Ab ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
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)
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 A13: 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	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQ	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPGDSDTRYSPSFQG	QRGFYYDSSDYFDY

Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 border	CDRH1	CDRH2	CDRH3
		VTISADKSISTAYLQWSSLKASD TAMYFCARQRGFYYDSSDYFDY WGQGTLVTVSS (SEQ ID NO:307)			(SEQ ID NO:91)	(SEQ ID NO:304)
V10 V23 V57 V70 V83	HV-15	EVQLVQSGAEVKKPGESLKISCK GSGYSFTSYWIAWVRQMPGKG LEWMGIIYPGDSDTRYSPSFQGQ VTISADKSISTAYLQWSSLKASD TAMYFCARQRTFYYDSSDYFDY WGQGTLVTVSS (SEQ ID NO:124)	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPGD SDTRYS PSFQG (SEQ ID NO:91)	QRTFYY DSSDYF DY (SEQ ID NO:107)
V30	HV-202	EVQLVQSGAEVKKPGESLKISCK GSGSSFTSYWIAWVRQMPGKGL EWMGIIYPGDSDTRYSPSFQGQV TISADKSISTAYLQWSSLKASDT AMYFCARQRTFYYDSSDYFDY WGQGTLVTVSS (SEQ ID NO:308)	SSFT (SEQ ID NO:301)	SYWIA (SEQ ID NO:85)	IIYPGD SDTRYS PSFQG (SEQ ID NO:91)	QRTFYY DSSDYF DY (SEQ ID NO:107)
V33	HV-203	EVQLVQSGAEVKKPGESLKISCK GSGYSFTSYWIAWVRQMPGKG LEWMGIIYPGDSDTRYSPSFQGQ VTISADKSISTAYLQWSSLKASD TAMYFCARQRTFYGDSSDYFDY WGQGTLVTVSS (SEQ ID NO:309)	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPGD SDTRYS PSFQG (SEQ ID NO:91)	QRTFYG DSSDYF DY (SEQ ID NO:305)
V44	HV-204	EVQLVQSGAEVKKPGESLKISCK GSGYSFTSYWIAWVRQMPGKG LEWMGIIYPSDSDTRYSPSFQGQ VTISADKSISTAYLQWSSLKASD TAMYFCARQRTFYYDSSDYFDY WGQGTLVTVSS (SEQ ID NO:310)	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPSDS DTRYSP SFQG (SEQ ID NO:303)	QRTFYY DSSDYF DY (SEQ ID NO:107)
V68	HV-205	EVQLVQSGAEVKKPGESLKISCK GSGYSFTSYWIAWVRQMPGKG LEWMGIIYPGDSDTRYSPSFQGQ VTISADKSISTAYLQWSSLKASD TAMYFCARQRTFRYDSSDYFDY WGQGTLVTVSS (SEQ ID NO:311)	YSFT (SEQ ID NO:163)	SYWIA (SEQ ID NO:85)	IIYPGD SDTRYS PSFQG (SEQ ID NO:91)	QRTFRY DSSDYF DY (SEQ ID NO:306)

Variant Ab ID.	VH Group	VH Amino Acid Sequence	FR1/ CDRH1 border	CDRH1	CDRH2	CDRH3
V90	HV-206	EVQLVQSGAEVKKPGESLKISCK GSGYSFTSEWIAWVRQMPGKGL EWMGIIYPGDSDTRYSPSFQGQV TISADKSISTAYLQWSSLKASDT AMYFCARQRTFYYDSSDYFDY WGQGTLVTVSS (SEQ ID NO:312)	YSFT (SEQ ID NO:163)	SEWIA (SEQ ID NO:302)	IIYPGD SDTRYS PSFQG (SEQ ID NO:91)	QRTFYY DSSDYF DY (SEQ ID NO:107)

[00147] 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 A12** (light chain CDRs; i.e. CDRLs) and **TABLE A13** (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: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.

[00148] 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.

[00149] 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.

[00150] 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.

[00151] 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.

[00152] 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 A12**, 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 A13**, 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 A12** and **A13**. 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.

[00153] In some embodiments, each of the light chain variable regions listed in **TABLE A12** may be combined with any of the heavy chain variable regions listed in **TABLE A13** 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).

[00154] In some embodiments, the TREM2 agonist antigen binding proteins comprise one or more CDRs of the anti-TREM2 antibody variants set forth in **TABLE A14**. 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 A14**.

TABLE A14: Exemplary Variable Region Amino Acid Sequences of Engineered Antibodies

Ab ID.	LC variable region	CDRL1	CDRL2	CDRL3
24G6 (SST28347 and SST204812)	DIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKHFLAWYQQKPGQPPKLLIYWASTR ESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQQYYSTPLTFGGGTKVEIK (SEQ ID NO:326)	KSSQSV LYSSNN KHFLA (SEQ ID NO:8)	WASTR ES (SEQ ID NO:22)	QQYYS TPLT (SEQ ID NO:35)
6E7 (SST29857)	DIQMTQSPSSVSASVGDRVTITCRASQGISS WLAWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYFCQQA DAFPRTFGQGTKLEIK (SEQ ID NO:328)	RASQGI SSWLA (SEQ ID NO:16)	AASSLQ S (SEQ ID NO:369)	QQADA FPRT (SEQ ID NO:370)
13E7 (SST202443)	EIVMTQSPATLSVSPGERATLSCRASQSVSS NLAWFQQKPGQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQPEDFAVYYCLQDN NFPPTFGQGTKVDIK (SEQ ID NO:330)	RASQS VSSNLA (SEQ ID NO:10)	GASTR AT (SEQ ID NO:23)	LQDNN FPPT (SEQ ID NO:372)
5E3 (SST29825)	DIQMTQSPSSLSASVGDRVTITCRASQGISN YLAWYQQKPGKAPKSLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQYS TYPFTFGQGTKVDIK (SEQ ID NO:332)	RASQGI SNYLA (SEQ ID NO:17)	AASSLQ S (SEQ ID NO:29)	QQYST YPFT (SEQ ID NO:44)
Ab ID.	**HC variable region**	**CDRH1**	**CDRH2**	**CDRH3**
24G6 (SST28347 and SST204812)	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGSTY YAESVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAKAYTPMAFFDYWGQGTLVTV SS (SEQ ID NO:327)	SYAMS (SEQ ID NO:77)	AISGSG GSTYY AESVK G (SEQ ID NO:368)	AYTPM AFFDY (SEQ ID NO:98)
6E7 (SST29857)	EVQLVQSGAEVKKPGESLKISCKGSGYSFT SYWIAWVRQMPGKGLEWMGIIYPGDADA RYSPSFQGQVTISADKSISTAYLQWSSLKAS DTAMYFCARQRTFYYDSSDYFDYWGQGT LVTVSS (SEQ ID NO:329)	SYWIA (SEQ ID NO:85)	IIYPGD ADARY SPSFQG (SEQ ID NO:371)	QRTFY YDSSD YFDY (SEQ ID NO:107)
13E7 (SST202443)	EVQLVQSGAEVKKPGESLKISCKGSGYSFT SYWIGWVRQMPGKGLEWMGIIYPGDADA RYSPSFQGQVTISADKSISTAYLQWSSLKAS DTAMYFCARRRQGIFGDALDFWGQGTLVT VSS (SEQ ID NO:331)	SYWIG (SEQ ID NO:81)	IIYPGD ADARY SPSFQG (SEQ ID NO:373)	RRQGIF GDALD F (SEQ ID NO:374)
	QVQLVQSGAEVKKPGASVKVSCKASGYTF TGYYIHWVRQAPGQGLEWMGWINPYSGG TTSAQKFQGRVTMTRDTSTSSAYMELSRLR SDDTAVYYCARDAGYLALYGTDVWGQGT LVTVSS (SEQ ID NO:333)	GYYIH (SEQ ID NO:86)	WINPYS GGTTS AQKFQ G (SEQ ID NO:94)	DAGYL ALYGT DV (SEQ ID NO:375)

[00155] 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.

[00156] 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.

[00157] 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.

[00158] 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.

[00159] 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.

[00160] 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.

[00161] 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.

[00162] 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.

[00163] In some embodiments, each of the light chain variable regions disclosed in **TABLES A1, A10, A12, and A14** and each of the heavy chain variable regions disclosed in **TABLES A2, A11, A13,** and **3E** may be attached to the light chain constant regions **(TABLE EN1)** and heavy chain constant regions **(EN2)** 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.

[00164] 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 A15**.

TABLE A15: Light Chain and Heavy Chain Amino Acid Sequences of Exemplary Antibodies

Ab ID.		Sequence
24G6 (SST28347)	LC	MDMRVPAQLLGLLLLWLRGARCDIVMTQSPDSLAVSLGERATIN CKSSQSVLYSSNNKHFLAWYQQKPGQPPKLLIYWASTRESGVPD

Ab ID.		Sequence
		RFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC (SEQ ID NO:334)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLLESGGGLVQPGGSLRLS CAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYAESVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAYTPMAFFDY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:335)
24G6 (SST204812)	LC	MDMRVPAQLLGLLLLWLRGARCDIVMTQSPDSLAVSLGERATIN CKSSQSVLYSSNNKHFLAWYQQKPGQPPKLLIYWASTRESGVPD RFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC (SEQ ID NO:334)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLLESGGGLVQPGGSLRLS CAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYAESVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAYTPMAFFDY WGQGTLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:336)
6E7 (SST29857)	LC	MDMRVPAQLLGLLLLWLRGARCDIQMTQSPSSVSASVGDRVTIT CRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYFCQQADAFPRTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC (SEQ ID NO:337)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIAWVRQMPGKGLEWMGIIYPGDADARYSPSF QGQVTISADKSISTAYLQWSSLKASDTAMYFCARQRTFYYDSSD YFDYWGQGTLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN

Ab ID.		Sequence
		FGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:338)
13E7 (SST202443)	LC	MDMRVPAQLLGLLLLWLRGARCEIVMTQSPATLSVSPGERATLS CRASQSVSSNLAWFQQKPGQAPRLLIYGASTRATGIPARFSGSGS GTEFTLTISSLQPEDFAVYYCLQDNNFPPTFGQGTKVDIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC (SEQ ID NO:339)
	HC	MDMRVPAQLLGLLLLWLRGARCEVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDADARYSPSF QGQVTISADKSISTAYLQWSSLKASDTAMYFCARRRQGIFGDAL DFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:340)
5E3 (SST29825)	LC	MDMRVPAQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTIT CRASQGISNYLAWYQQKPGKAPKSLIYAASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQYSTYPFTFGQGTKVDIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC (SEQ ID NO:341)
	HC	MDMRVPAQLLGLLLLWLRGARCQVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYIHWVRQAPGQGLEWMGWINPYSGGTTSAQK FQGRVTMTRDTSTSSAYMELSRLRSDDTAVYYCARDAGYLALY GTDVWGQGTLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:342)
24G6-1 (SST28347-1)	LC	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKHFLAWYQQ KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVA

Ab ID.		Sequence
		VYYCQQYYSTPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2768)
	HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKG LEWVSAISGSGGSTYYAESVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAKAYTPMAFFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:2769)
24G6-1 (SST28347-1)	LC	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKHFLAWYQQ KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQYYSTPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2768)
	HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKG LEWVSAISGSGGSTYYAESVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAKAYTPMAFFDYWGQGTLVTVSSASTKGPSVFPLAPS SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCC VECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP G (SEQ ID NO:2770)
6E7-1 (SST29857-1)	LC	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQ ADAFPRTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2771)
	HC	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKG LEWMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKAS DTAMYFCARQRTFYYDSSDYFDYWGQGTLVTVSSASTKGPSVFP LAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVE

Ab ID.		Sequence
		RKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO:2772)
13E7-1 (SST202443-1)	LC	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPR LLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQD NNFPPTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2773)
	HC	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKG LEWMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKAS DTAMYFCARRRQGIFGDALDFWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO:2774)
5E3-1 (SST29825-1)	LC	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPK SLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQY STYPFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2775)
	HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQ GLEWMGWINPYSGGTTSAQKFQGRVTMTRDTSTSSAYMELSRL RSDDTAVYYCARDAGYLALYGTDVWGQGTLVTVSSASTKGPSV FPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKT VERKCCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPG (SEQ ID NO:2776)
13E7 Variant	LC	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPR LLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQD NNFPPTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN

Ab ID.		Sequence
		NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2777)
	HC	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKG LEWMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKAS DTAMYFCARRRQGIFGDALDFWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:2778)

[00165] 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 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.

[00166] 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 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.

[00167] 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 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.

[00168] 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.

[00169] Unless indicated otherwise by reference to a specific sequence 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.

[00170] 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 A1**, **A10**, **A12, and A14**, and a heavy chain variable region disclosed in **TABLES A2, A11, A13, and A14**. 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.

[00171] 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.

[00172] 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.

[00173] 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.

[00174] 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.

[00175] 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.

[00176] 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 A15.**.

TABLE A16: Exemplary Anti-TREM2 Antibody Variable Region Nucleic Acid Sequences

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
Light chain variable regions		
12G10	LV-01	CAGGCTGTGCCGACTCAGCCGTCTTCCCTCTCTGCATCTCCTGGAGT ATTAGCCAGTCTCACCTGCACCTTACGCAGTGGCATCAATGTTGGTA CCTACAGGATATACTGGTACCAGCAGAAGCCAGGGAGTCCTCCCCA GTATCTCCTGAGGTACAAATCAGACTCAGATAAGCAGCAGGGCTCT GGAGTCCCCAGCCGCTTCTCTGGATCCAAGGATGCTTCGGCCAATGC AGGGATTTTACTCATCTCTGGGCTCCAGTCTGAGGATGAGGCTGACT ATTACTGTATGATTTGGTACAGCAGTGCTGTGGTATTCGGCGGAGGG ACCAAACTGACCGTCCTA (SEQ ID NO:208)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
26A10	LV-02	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACA GACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGAGATAAGTAT GTTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGCTGGTCAT CTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTG GCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCA GGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGTAAC ACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA (SEQ ID NO:209)
26C10	LV-03	TCCTTTGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACA GACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAGTAT GTTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATGTTGGTCAT CTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAACGATTCTCTG GCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCA GGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGC ACTGTGGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTA (SEQ ID NO:210)
26F2	LV-04	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACA GACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAGTAT GTTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGTTGGTCAT CTTTCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTG GCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCA GGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGC ACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA (SEQ ID NO:211)
33B12	LV-05	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACA GACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAGTAT GTTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGTTGGTCAT CTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTG GCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCA GGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGTAGC ACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA (SEQ ID NO:212)
24C12	LV-06	GGCATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGG CGAGAGGGCCACCATCAACTGCAAGTCCAGCCGGAGTGTTTTGTAC AGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAGAAACCAG GACAGCCTCCTAAGGTGCTCATTTACTGGGCATCTACCCGGGAATCC GGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATAAC TGTCAGCAATATTATATTACTCCGATCACCTTCGGCCAAGGGACACG ACTGGAGATTAAA (SEQ ID NO:213)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
24G6	LV-07	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGG CGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATAC AGCTCCAACAATAAGCACTTCTTAGCTTGGTACCAGCAGAAACCAG GACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAGTCC GGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCATTTTATTAC TGTCAGCAATATTATAGTACTCCGCTCACTTTCGGCGGAGGGACCAA GGTGGAGATCAAA (SEQ ID NO:214)
24A10	LV-08	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGG CGAGAGGGCCACCATCACCTGCAAGTCCAGCCACAATGTTTTATACA GCTCCAACAATAAGAACTACTTAGCTTGGTATCAGCAGAAACCAGG ACAGCCTCCTAAACTGCTCATTTACTGGGCATCTACCCGGGAATCCG GGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACT CTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTG TCACCAATATTATAGTACTCCGTGCAGTTTTGGCCAGGGGACCAAGC TGGAGATCAAA (SEQ ID NO:215)
10E3	LV-09	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGC AACTTAGCCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCTTCCACCAGGGCCACTGGTATTCCAGCCAGGTTCA GTGTCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTG CAGTCTGAAGATTTTGCATTTTATTACTGTCTGCAGGATAATAATTG GCCTCCCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA (SEQ ID NO:216)
13E7	LV-10	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGC AACTTAGCCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCTTCCACCAGGGCCACTGGTATTCCAGCCAGGTTCA GTGTCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTG CAGTCTGAAGATTTTGCAGTTTATTACTGTCTGCAGGATAATAATTG GCCTCCCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA (SEQ ID NO:217)
25F12	LV-11	GAAAAAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAACAAC AACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCA GTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTG CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTG GCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA (SEQ ID NO:218)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
32E3	LV-12	GAATTTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCGGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGATTATTAGCAGC AACTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC TCCTCATCTATAGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTTTGATA GCTCACCGATCACCTTCGGCCGAGGGACACGACTGGACATTAAA (SEQ ID NO:219)
24F4	LV-13	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGC AGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG ACTGGAGCCTGAAGATTTTGCACTGTATTACTGTCAGCAGTATGATA CCTCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA (SEQ ID NO:220)
16B8	LV-14	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCGTCACTTGTCGGGCGAGTCAGGATATTAACAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCTCTTTGCAAACTGGGGTCCCTTCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTCTTGTCAACAGTCTAACAGTT TCCCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA (SEQ ID NO:221)
4C5	LV-15	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAAC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAGTTGGGGTCCCATTAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTGACAGTT TCCCTCGCAATTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:222)
6E7 V9 V30 V33 V44 V68	LV-16	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:223)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
5E3	LV-17	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGCATTAGCAAT TATTTAGCCTGGTTTCAGCAGAAACCAGGGAAAGCCCCTAAATCCCT GATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAAGTTCA GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAGTACTTA CCCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA (SEQ ID NO:224)
4G10	LV-18	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATAAGAAAT GATTTAGGCTGGTATCAGCAGAAACCAGGGAATGCCCCTAAGCGCC TGATCTATGCTGCATCCAGTTTGCCAAGTGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGCCAGAATTCACTCTCACAATCAGCAGTCT GCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTT ACCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCACA (SEQ ID NO:225)
V3	LV-101	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTAGGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGGT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:226)
V24	LV-102	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAAGGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCATACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:227)
V27	LV-103	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAACGTGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:228)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
V40	LV-104	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAACTTGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACCGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:229)
V48	LV-105	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAACGGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TGCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:230)
V49	LV-106	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTCGGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT ATCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:231)
V52	LV-107	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAGGGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACCGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:232)
V60	LV-108	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAGGGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTGGGCAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:233)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
V73	LV-106	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTCGTCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT ATCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:234)
V76	LV-109	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAAGGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGAGAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:235)
V84	LV-110	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGGTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCGCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:236)
V10	LV-201	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATTCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:313)
V23	LV-202	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCTTACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:314)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
V57	LV-203	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTGCGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:315)
V70	LV-204	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCAGGGAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:316)
V83	LV-205	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGC TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGTGAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:317)
V90	LV-206	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGA TGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCC TGATCTATGCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTGACAGTT TCCCTCGCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO:318)
Heavy chain variable regions		
12G10 24C12	HV-01	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGC TATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGT GGGTCTCAGCTATTGGTGGTGGTGGTGTTAGCACATACTGCGCAGAC TCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAATTTTATATAGCAGTGGCTGGTTCTCACTTTG

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
		ACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO:237)
26A10	HV-02	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCGGGGGG GGTCCCTGAGACTCTCCTGTGCAGCCTCTAGATTCACCTTCAGTAGC TTTGGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGT GGGTTTCATACATTAGTAGTAGTAGTTTTACCATATATTACGCAGAC TCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAATTC ATTCTATCTGCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTG TATTACTGTGCGAGAGAGGGGGGTCTTACTATGGTTCGGGGAGTCTC TTCCTACGGTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT CCTCA (SEQ ID NO:238)
26C10	HV-03	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGC TTTGGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGT GGGTTTCATACATTAGTAGTAGTAGTTTTACCATATACTACGCAGAC TCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAATTC GTTCTATCTGCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTG TATTTCTGTGTGAGAGAGGGGGGTATAACTATGGTTCGGGGAGTCTC TTCCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT CCTCA (SEQ ID NO:239)
26F2	HV-04	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGC TTTGGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGT GGATTTCATACATTAGTAGTAGTAGTTTTACCATATACTACGCAGAC TCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAATTC ATTCTATCTGCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTG TATTTCTGTGCGAGAGAGGGGGGTATTACTATGGTTCGGGGAGTCTC TTCCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT CCTCA (SEQ ID NO:240)
33B12	HV-05	GAGGTGCAACTGGTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGC TTTGGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCCTGGAGT GGGTTTCATACATTAGTAAAAGTAGTTTTACCATATACTACGCAGAC TCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAATTC ATTCTATCTGCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTG TATTACTGTGCGAGAGAGGGGGGTCTTACTATGGTTCGGGGAGTCTC TTCCTACGGTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT CCTCA (SEQ ID NO:241)
24G6	HV-06	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGC TATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAGT

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
		GGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGAC TCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAGGCGTATACACCTATGGCATTCTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO:242)
24A10	HV-07	GAGGTGCAGGTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAAC TATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGT GGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGAC TCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAAGGAGGGTGGGAGCTATTTTACTGGGGCCAG GGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO:243)
10E3	HV-08	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGATGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAAC TACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGAGACTCTGATACCAGATACAGCCC GTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCAT GTATTTCTGTGCGAGACGGAGACAGGGGATCTGGGGTGATGCTCTTG ATATCTGGGGCCAAGGGACATTGGTCACCGTCTCTTCA (SEQ ID NO:244)
13E7	HV-09	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGATGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGC TACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGAGACTCTGATACCAGATACAGCCC GTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCAT GTATTTCTGTGCGAGACGGAGACAGGGGATCTGGGGTGATGCTCTTG ATTTCTGGGGCCAAGGGACATTGGTCACCGTCTCTTCA (SEQ ID NO:245)
25F12	HV-10	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTAGT TACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGT GGATTGGGGAAATCAATCATAGTGGAAACACCAACTACAACCCGTC CCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAG TTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTA TTACTGTGCGAGAGAGGGGTATTACGATATCTTGACTGGTTATCATG ATGCTTTTGATATTTGGGACCAAGGGACAATGGTCACCGTNTTTTCA (SEQ ID NO:246)

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
32E3	HV-11	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGC TACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTGCAGTGGAGCACCCTGAAGGCCTCGGACACCGCCATA TATTACTGTGCGCGACATGACATTATACCAGCAGCCCCTGGTGCTTT TGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA (SEQ ID NO:247)
24F4	HV-12	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACACCTTTACCAGC TACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGTCGACAAGTCCAGCAGCAC CGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATA TATTACTGTACGAGACAGGCCATAGCAGTGACTGGTTTGGGGGGTTT CGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO:248)
16B8	HV-13	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAAC TATGGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGT GGATGGGATGGATCAGCGCTTACAATGGTAACACAAACTATGCACA GAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGT ACAGTCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCG TGTATTACTGTGCGAGACGGGGATACAGCTATGGTTCCTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO:249)
4C5	HV-14	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAAGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGACACAGTTTTACCAAC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCGTG TATTTCTGTGCGAGACAAAGGACGTTTTACTATGATAGTAGTGGTTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO:250)
6E7	HV-15	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
		TATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA (SEQ ID NO:251)
5E3	HV-16	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGGC TACTATATACACTGGGTGCGACAGGCCCCTGGACTAGGGCTTGAGTG GATGGGATGGATCAACCCTTACAGTGGTGGCACAACCTCTGCACAG AAGTTTCAGGGCAGGGTCACCATGACCAGGGACACGTCCATCAGCT CAGCCTACATGGAACTGAGCAGGCTGAGATCTGACGACACGGCCGT GTATTACTGTGCGAGAGATGGAGGCTACCTGGCCCTCTACGGTACGG ACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA (SEQ ID NO:252)
4G10	HV-17	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTCCCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTTTTTGAAGTGGAGTAGCCTGAAGGCCTCGGACACCGCCATGT ATTTCTGTGCGCGACAGGGTATAGAAGTGACTGGTACGGGAGGTTT GGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA (SEQ ID NO:253)
V3	HV-101	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGCGAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGATCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGAGGGAGGACGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:254)
V24	HV-102	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC TACTGGATTGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATGTGAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGATCTAGGACGTTTTATTATGATAGTAGTGATTAT TTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:255)
V27	HV-103	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
		TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACGCTCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGTGAGAAGTAGGACGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:256)
V40	HV-104	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGGAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATGTTAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATTA TTCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:257)
V48	HV-105	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGTAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATGTGAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGAATGAGGACGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:258)
V49	HV-106	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTAATAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGACGATCTATCCTGGTGACTCTGATACCAGACTGAGCCC GTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCAT GTATTTCTGTGCGAGAAGTAGGACGTTTTATTATGATAGTAGTGATT ATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:259)
V52	HV-107	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGAGAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGAGGGAGGACGTTTTATTATGATAGTAGTGATTA

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
		TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:260)
V60	HV-108	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACCATTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATGTGAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATTA TAGTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:261)
V73	HV-109	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGTAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG GGGTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCAT GTATTTCTGTGCGAGAGGGAGGACGTTTTATTATGATAGTAGTGATT ATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:262)
V76	HV-110	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTGGGAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG GAGTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCAT GTATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATT ATAGTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:263)
V84	HV-111	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACGGGTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACAGTGATACCAGATACAGCCC GTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCAT GTATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATT ATTCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:264)
V9	HV-201	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
		GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGGGGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:319)
V10 V23 V57 V70 V83	HV-15	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:320)
V30	HV-202	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATCGAGTTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:321)
V33	HV-203	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTTATGGGGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:322)
V44	HV-204	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTAGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATTA

Ab ID.	VL or VH Group Designation	Nucleic Acid Sequence
		TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:323)
V68	HV-205	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC TACTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTAGGTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:324)
V90	HV-206	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGTTTTACCAGC GAGTGGATCGCCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGT GGATGGGGATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCG TCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCAC CGCCTACCTACAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATG TATTTCTGTGCGAGACAAAGGACGTTTTATTATGATAGTAGTGATTA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTCCTCA (SEQ ID NO:325)

[00177] 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.

[00178] In some embodiments, the polynucleotide encodes the full length light chain and full length heavy chain. Exemplary polynucleotide sequences are provided in **TABLE A15**.

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

[00179] 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.

[00180] 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.

[00181] In some embodiments, the TREM2 antigen bind protein comprises a light chain variable region and a heavy chain variable region of monoclonal antibody 29E3.

[00182] 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.

[00183] 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

[00184] 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.

[00185] 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.

[00186] 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 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.

[00187] 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.

[00188] 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 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.

[00189] 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.

[00190] 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.

[00191] 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.

[00192] 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 C1-C2**.

TABLE C1: 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 C2: 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 C3: Kabat CDR sequences

Antibody Name	CDR H1	CDR H2	CDR H3	CDR Ll	CDR L2	CDR L3
Ab1	FTFSSYAMS (SEQ ID NO:377)	VISGSGGSTYYAD SVKG (SEQ ID NO:399)	AKGTPTLLFQH (SEQ ID NO:424)	RASQSVSSNLA (SEQ ID NO:494)	GASTRAT (SEQ ID NO:512)	QQLPYWPPT (SEQ ID NO:527)
Ab2	FTFSSSAMS (SEQ ID NO:378)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	AKVPSYDYWSGYS NYYYYMDV (SEQ ID NO:425)	RASQSVGSNLA (SEQ ID NO:495)	GASTRAT (SEQ ID NO:512)	QQYFFYPPT (SEQ ID NO:528)
Ab3	GTFSSYAIS (SEQ ID NO:379)	GIIPIFGTANYAQK FQG (SEQ ID NO:401)	AREQYHVGMDV (SEQ ID NO:426)	QASQDISNYLN (SEQ ID NO:496)	DASNLAT (SEQ ID NO:513)	QQPFNFPYT (SEQ ID NO:529)
Ab4	GTFSSYAIS (SEQ ID NO:379)	GIIPIFGTASYAQK FQG (SEQ ID NO:402)	ARGVDSIMDY (SEQ ID NO:427)	RASQSVSSNLA (SEQ ID NO:494)	SASTRAT (SEQ ID NO:514)	QQDHDYPFT (SEQ ID NO:530)
Ab5	YTFTSYYIH (SEQ ID NO:380)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARAPQESPYVFDI (SEQ ID NO:428)	RASQSVSSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQYFSSPFT (SEQ ID NO:531)
Ab6	YTFTSYYMH (SEQ ID NO:381)	IINPGGGSTSYAQK FQG (SEQ ID NO:404)	ARGSPTYGYLYDP (SEQ ID NO:429)	RASQSVSSYLA (SEQ ID NO:498)	DASKRAT (SEQ ID NO:516)	QQRVNLPPT (SEQ ID NO:532)
Ab7	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTTYAQK FQG (SEQ ID NO:405)	ARTSSKERDY (SEQ ID NO:430)	RASQSVSSYLA (SEQ ID NO:498)	DASKRAT (SEQ ID NO:516)	QQRISYPIT (SEQ ID NO:533)

Ab8	GSISSSSYYWG (SEQ ID NO:382)	SISYSGSTYYNPSLKS (SEQ ID NO:406)	ARGPYRLLLGMDV (SEQ ID NO:431)	RASQSISSYLN (SEQ ID NO:499)	GASSLQS (SEQ ID NO:517)	QQIDDTPIT (SEQ ID NO:534)
Ab9	YSFTSYWIG (SEQ ID NO:383)	IIYPGDSDTTYSPSFQG (SEQ ID NO:407)	ARLHISGEVNWFDP (SEQ ID NO:432)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQFSYWPWT (SEQ ID NO:535)
Ab10	YSFTSNWIG (SEQ ID NO:384)	IIYPGDSDTRYSPSFQG (SEQ ID NO:408)	AREAGYDYGELAFDI (SEQ ID NO:433)	RASQSVSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQHDSSPPT (SEQ ID NO:536)
Ab11	YSFTTYWIG (SEQ ID NO:385)	IIYPGDSDTRYSPSFQG (SEQ ID NO:408)	ARAGHYDGGHLGM DV (SEQ ID NO:434)	RASQSVSSDYLA (SEQ ID NO:500)	GASSRAT (SEQ ID NO:515)	QQDYSYPWT (SEQ ID NO:537)
Ab12	YSFTSYWIG (SEQ ID NO:383)	IIYPGDSDTRYSPSFQG (SEQ ID NO:408)	ARLGHYSGTVSSYGMDV (SEQ ID NO:435)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQEYAVPYT (SEQ ID NO:538)
Ab13	YTFTSYGIS (SEQ ID NO:386)	WISAYNGNTNYAQKLQG (SEQ ID NO:409)	ARGPSHYYDLA (SEQ ID NO:436)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQVSNYPIT (SEQ ID NO:539)
Ab14	GSISSGGYYWS (SEQ ID NO:387)	NIYYSGSTVYNPSLKS (SEQ ID NO:410)	ARGLYGYGVLDV (SEQ ID NO:437)	QASQDISNYLN (SEQ ID NO:496)	DASNLET (SEQ ID NO:520)	QQVDNIPPT (SEQ ID NO:540)
Ab15	GSISSGGYYWS (SEQ ID NO:387)	NIYYSGSTVYNPSLKS (SEQ ID NO:410)	ARGLYGYGVLDV (SEQ ID NO:437)	QASQDISNYLN (SEQ ID NO:496)	DASNLET (SEQ ID NO:520)	QQFDTYPT (SEQ ID NO:541)

Ab16	GSISSNSYYWG (SEQ ID NO:388)	SIYYSGSTYYNPS LKS (SEQ ID NO:411)	ARGVLGYGVFDY (SEQ ID NO:438)	QASQDISNYLN (SEQ ID NO:496)	DASNLET (SEQ ID NO:520)	QQFLNFPT (SEQ ID NO:542)
Ab17	GSISSNSYYWG (SEQ ID NO:388)	SIYYSGSTYYNPSL KS (SEQ ID NO:411)	ARGVLGYGVFDY (SEQ ID NO:438)	QASQDISNYLN (SEQ ID NO:496)	DASNLET (SEQ ID NO:520)	QQFFNFPT (SEQ ID NO:543)
Ab18	GSISSYYWS (SEQ ID NO:389)	SIYYSGSTNYNPSL KS (SEQ ID NO:412)	ARDGGGEYPSGTP FDI (SEQ ID NO:439)	QASQDISNYLN (SEQ ID NO:496)	DASNLET (SEQ ID NO:520)	QQFIDLPFT (SEQ ID NO:544)
Ab19	GSISSYYWS (SEQ ID NO:389)	SIYYSGSTNYNPSL KS (SEQ ID NO:412)	ARDGGGEYPSGTP FDI (SEQ ID NO:439)	QASQDISNYLN (SEQ ID NO:496)	DASNLET (SEQ ID NO:520)	QQYYDLPFT (SEQ ID NO:545)
Ab20	GSISSYYWS (SEQ ID NO:389)	SIYYSGSTNYNPSL KS (SEQ ID NO:412)	ARSGMASFFDY (SEQ ID NO:440)	RASQSVSSDYLA (SEQ ID NO:500)	GASSRAT (SEQ ID NO:515)	QQFSSHPFT (SEQ ID NO:546)
Ab22	YSFTTYWIG (SEQ ID NO:385)	IIYPGDSDTRYSPS FQG (SEQ ID NO:408)	ARAGHYDGGHLG MDV (SEQ ID NO:434)	RASQSVSSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQDDRSPYT (SEQ ID NO:547)
Ab23	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	AKLGGHSMDV (SEQ ID NO:441)	KSSQSVLYSSNN KNYLA (SEQ ID NO:501)	WASTRES (SEQ ID NO:521)	QQAYLPPIT (SEQ ID NO:548)
Ab24	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	AKPLKRGRGFY (SEQ ID NO:442)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQAFSPPPWT (SEQ ID NO:549)

Ab25	FTFSSYAMS (SEQ ID NO:377)	VISGSGGSTYYAD SVKG (SEQ ID NO:399)	AKEGRTITMD (SEQ ID NO:443)	RASQSVSSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQDDRSPT (SEQ ID NO:550)
Ab26	FTFSSYAMS (SEQ ID NO:377)	VISGSGGSTYYAD SVKG (SEQ ID NO:399)	AKDQYSVLDY (SEQ ID NO:444)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQEFDLPFT (SEQ ID NO:551)
Ab27	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	AKKYSSRGVYFDY (SEQ ID NO:445)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQYNNFPPT (SEQ ID NO:552)
Ab28	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	ARLGGAVGARHVT YFDY (SEQ ID NO:446)	RASQSVSSYLA (SEQ ID NO:498)	DASKRAT (SEQ ID NO:516)	QQRYLRPIT (SEQ ID NO:553)
Ab29	FTFSSYGMH (SEQ ID NO:390)	VISYDGSNKYYAD SVKG (SEQ ID NO:413)	ARGQYYGGSGWF DP (SEQ ID NO:447)	RASQSVSSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQPGAVPT (SEQ ID NO:554)
Ab30	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	ARLGQEYAYFQH (SEQ ID NO:448)	RASQSISSYLN (SEQ ID NO:499)	GASSLQS (SEQ ID NO:517)	QQVYITPIT (SEQ ID NO:555)
Ab31	FTFSSYGMH (SEQ ID NO:390)	LIWYDGSNKYYA DSVKG (SEQ ID NO:414)	ARRRDGYYDEVFD I (SEQ ID NO:449)	QASQDISNFLN (SEQ ID NO:502)	DASNLET (SEQ ID NO:520)	QQPVDLPFT (SEQ ID NO:556)
Ab32	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	ARVPKHYVVLDY (SEQ ID NO:450)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQYSFFPPT (SEQ ID NO:557)

Ab33	FTFSSYGMH (SEQ ID NO:390)	VISYDGSNKYYAD SVKG (SEQ ID NO:413)	ARAGGHLFDY (SEQ ID NO:451)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQDSSFPPT (SEQ ID NO:558)
Ab34	FTFSSYGMH (SEQ ID NO:390)	VISYDGSNKYYAD SVKG (SEQ ID NO:413)	ARDRGGEYVDFAF DI (SEQ ID NO:452)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQSDFPPWT (SEQ ID NO:559)
Ab35	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	ARTRSGYGASNYF DY (SEQ ID NO:453)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQGYSAPIT (SEQ ID NO:560)
Ab36	FTFSTYGMH (SEQ ID NO:391)	VIWYDGSNKYYA DS VKG (SEQ ID NO:415)	ARGTGAAAASPAF DI (SEQ ID NO:454)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQLFDWPT (SEQ ID NO:561)
Ab37	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	ARVGQYMLGMDV (SEQ ID NO:455)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRAFLFT (SEQ ID NO:562)
Ab38	FTFSTYGMH (SEQ ID NO:391)	VIWYDGSNKYYAD S VKG (SEQ ID NO:415)	ARGAPVDYGGIEP EYFQH (SEQ ID NO:456)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQIDFLPYT (SEQ ID NO:563)
Ab39	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	AKHYHVGIAFDI (SEQ ID NO:457)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQVYSPPIT (SEQ ID NO:564)
Ab40	FTFSSYAMS (SEQ ID NO:377)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	ARTRSGYGASNYF DY (SEQ ID NO:453)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQGYAAPIT (SEQ ID NO:565)

Ab41	FTFSTYAMS (SEQ ID NO:392)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	ARAMARKSVAFDI (SEQ ID NO:458)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRYALPIT (SEQ ID NO:566)
Ab42	FTFSSSAMS (SEQ ID NO:378)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	AKVPSYQRGTAFD P (SEQ ID NO:459)	RASQSVSSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQYASPPIT (SEQ ID NO:567)
Ab43	FTFSSSAMS (SEQ ID NO:378)	AISGSGGSTYYAD SVKG (SEQ ID NO:400)	AKSPAVAGIYRAD Y (SEQ ID NO:460)	RASQSISRYLN (SEQ ID NO:503)	AASSLQS (SEQ ID NO:519)	QQVYSTPIT (SEQ ID NO:568)
Ab44	FTFSTYGMH (SEQ ID NO:391)	VIWYDGSNKYYAD SVKG (SEQ ID NO:415)	ARGTGAAAASPAF DI (SEQ ID NO:454)	RASQSVSSYLA (SEQ ID NO:498)	DSSNRAT (SEQ ID NO:522)	QQLVHWPT (SEQ ID NO:569)
Ab45	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARGPGYTTALDYY YMDV (SEQ ID NO:461)	RASQSVSSNLA (SEQ ID NO:494)	GASTRAT (SEQ ID NO:512)	QQLDDWFT (SEQ ID NO:570)
Ab46	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARPAKTADY (SEQ ID NO:462)	RASQSVSSYLA (SEQ ID NO:498)	DSSNRAT (SEQ ID NO:522)	QQRSNYPIT (SEQ ID NO:571)
Ab47	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTTYAQK FQG (SEQ ID NO:405)	ARPGKSMDV (SEQ ID NO:463)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRILYPIT (SEQ ID NO:572)
Ab48	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTTYAQK FQG (SEQ ID NO:405)	ARPGKSMDV (SEQ ID NO:463)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRAAYPIT (SEQ ID NO:573)

Ab49	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARPAKTADY (SEQ ID NO:462)	RASQSVSSYLA (SEQ ID NO:498)	DASKRAT (SEQ ID NO:516)	QQRTSHPIT (SEQ ID NO:574)
Ab50	YTFTSYYIH (SEQ ID NO:380)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARAPQESPYVFDI (SEQ ID NO:428)	RASQSVSSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQYAGSPFT (SEQ ID NO:575)
Ab51	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARGVGGQDYYYM DV (SEQ ID NO:464)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQFDDVFT (SEQ ID NO:576)
Ab53	YTFTSYYIH (SEQ ID NO:380)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARAPQESPYVFDI (SEQ ID NO:428)	RASQSVSSSYLA (SEQ ID NO:497)	GASSRAT (SEQ ID NO:515)	QQYVNSPFT (SEQ ID NO:577)
Ab54	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARGPGYTTALDYY Y MDV (SEQ ID NO:461)	RASQSINSYLN (SEQ ID NO:504)	AASSLQS (SEQ ID NO:519)	QQSDDDPFT (SEQ ID NO:578)
Ab55	YTFTGSYMH (SEQ ID NO:393)	WINPNSGGTNYAQ KFQG (SEQ ID NO:416)	ARGPLYHPMIFDY (SEQ ID NO:465)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQLSTYPLT (SEQ ID NO:579)
Ab56	YTFTGYYMH (SEQ ID NO:394)	SINPNSGGTNYAQ KFQG (SEQ ID NO:417)	ARASSVDN (SEQ ID NO:466)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRSVYPIT (SEQ ID NO:580)
Ab57	YTFTNYGIS (SEQ ID NO:395)	WISAYNGNTNYA QKLQG (SEQ ID NO:409)	ARGPTKAYYGSGS YVVFDP (SEQ ID NO:467)	RASQSVSSYLA (SEQ ID NO:498)	DASKRAT (SEQ ID NO:516)	QQVSLFPLT (SEQ ID NO:581)

Ab58	YSFTSYWIG (SEQ ID NO:383)	IIYPGDSDTRYSPS FQG (SEQ ID NO:408)	ARLGIYSTGATAF DI (SEQ ID NO:468)	RASQSISSWLA (SEQ ID NO:505)	DASSLES (SEQ ID NO:523)	LDYNSYSPIT (SEQ ID NO:582)
Ab59	YTFTGSYMH (SEQ ID NO:393)	WINPNSGGTNYAQ KFQG (SEQ ID NO:416)	ARGGVWYSLFDI (SEQ ID NO:469)	QASQDISNYLN (SEQ ID NO:496)	DASNLET (SEQ ID NO:520)	QQHIALPFT (SEQ ID NO:583)
Ab60	YTFTGYYMH (SEQ ID NO:394)	WINPNSGGTSYAQ K FQG (SEQ ID NO:418)	ARASKMGDD (SEQ ID NO:470)	RASQSVSSYLA (SEQ ID NO:498)	DASKRAT (SEQ ID NO:516)	QQRASMPIT (SEQ ID NO:584)
Ab61	YTFTSYGIH (SEQ ID NO:396)	WISAYNGNTNYA QKLQG (SEQ ID NO:409)	ARGGVPRVSYFQH (SEQ ID NO:471)	RASQSVSSYLA (SEQ ID NO:498)	DSSNRAT (SEQ ID NO:522)	QQAFNRPPT (SEQ ID NO:585)
Ab62	YSFTSYWIG (SEQ ID NO:383)	IIYPGDSDTRYSPS FQG (SEQ ID NO:408)	ARAGHYDDWSGL GLDV (SEQ ID NO:472)	RASQSVSSYLA (SEQ ID NO:498)	DASKRAT (SEQ ID NO:516)	QQSSVHPYT (SEQ ID NO:586)
Ab63	YTFTSYGIS (SEQ ID NO:386)	WISTYNGNTNYAQ KLQG (SEQ ID NO:419)	ARGSGSGYDSWY D (SEQ ID NO:473)	RASQGIDSWLA (SEQ ID NO:506)	AASSLQS (SEQ ID NO:519)	QQAYSLPPT (SEQ ID NO:587)
Ab64	YSFTSYWIG (SEQ ID NO:383)	IIYPGDSDTRYSPS F QG (SEQ ID NO:408)	ARLGRWSSGSTAF DI (SEQ ID NO:474)	RASQSVSSNLA (SEQ ID NO:494)	GASTRAT (SEQ ID NO:512)	QQDDDGYT (SEQ ID NO:588)

Ab65	YSFTSYWIG (SEQ ID NO:383)	IIYPGDSDTRYSPS FQG (SEQ ID NO:408)	ARLGRKPSGSVAF DI (SEQ ID NO:475)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQDYSWPYT (SEQ ID NO:589)
Ab66	YTFTGSYMH (SEQ ID NO:393)	WINPNSGGTNYAQ K FQG (SEQ ID NO:416)	ARAGHKTHDY (SEQ ID NO:476)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRSAYPIT (SEQ ID NO:590)
Ab67	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTTYAQK FQG (SEQ ID NO:405)	ARPGKSMDV (SEQ ID NO:463)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRSHFPIT (SEQ ID NO:591)
Ab68	FTFSSYGMH (SEQ ID NO:390)	LIWYDGSNKYYA DSVKG (SEQ ID NO:414)	AKPGSMTDY (SEQ ID NO:477)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRANYPIT (SEQ ID NO:592)
Ab69	YTFTGSYMH (SEQ ID NO:393)	WINPNSGGTNYAQ KFQG (SEQ ID NO:416)	ARAKSVDHDY (SEQ ID NO:478)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRADYPIT (SEQ ID NO:593)
Ab70	YTFTGYYMH (SEQ ID NO:394)	WINPNSGGTSYAQ KFQG (SEQ ID NO:418)	ARASKMGDD (SEQ ID NO:470)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRSVYPIT (SEQ ID NO:580)
Ab71	YTFTSYYMH (SEQ ID NO:381)	IINPSGGSTSYAQK FQG (SEQ ID NO:403)	ARDISTHDYDLAF DI (SEQ ID NO:479)	RASQSVSSSYLA (SEQ ID NO:497)	GASNRAT (SEQ ID NO:524)	QQAGSHPFT (SEQ ID NO:594)
Ab72	GSISSYYWS (SEQ ID NO:389)	SIYYSGSTNYNPSL KS (SEQ ID NO:412)	ARSGTETLFDY (SEQ ID NO:480)	QASQDITNYLN (SEQ ID NO:507)	DASNLET (SEQ ID NO:520)	QQDVNYPPT (SEQ ID NO:595)

Ab73	YSFTSYWIG (SEQ ID NO:383)	IIYPGDSDTTYSPS FQG (SEQ ID NO:407)	ARAKMLDDGYAF DI (SEQ ID NO:481)	RASQSVSSNLA (SEQ ID NO:494)	GASTRAT (SEQ ID NO:512)	QQDDNYPYT (SEQ ID NO:596)
Ab74	YTFTGSYMH (SEQ ID NO:393)	WINPNSGGTNYAQ KFQG (SEQ ID NO:416)	ARAGHKTHDY (SEQ ID NO:476)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQRSTFPIT (SEQ ID NO:597)
Ab75	YTFTGYYMH (SEQ ID NO:394)	WINPNSGGTNYAQ KFQG (SEQ ID NO:416)	ARDLGYSSLLALDI (SEQ ID NO:482)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQVSNYPFT (SEQ ID NO:598)
Ab76	FTFSSYSMN (SEQ ID NO:397)	SISSSSSYIYYADS VKG (SEQ ID NO:420)	ARGGGRRGDNNW FDP (SEQ ID NO:483)	KSSQSVLYSSNN KNYLA (SEQ ID NO:501)	WASTRES (SEQ ID NO:521)	QQYHDAPIT (SEQ ID NO:599)
Ab77	FTFSSYGMH (SEQ ID NO:390)	VISYDGSNKYYAD SVKG (SEQ ID NO:413)	ARGPPHEMDY (SEQ ID NO:484)	KSSQSVLYSSNN KNYLA (SEQ ID NO:501)	WASTRES (SEQ ID NO:521)	QQAYVVPPT (SEQ ID NO:600)
Ab78	FTFSSYGMH (SEQ ID NO:390)	VIWYDGSNKYYA DS VKG (SEQ ID NO:415)	ARTPYPWIYFDL (SEQ ID NO:485)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQADNWPFT (SEQ ID NO:601)
Ab79	FTFSSYSMN (SEQ ID NO:397)	YISGSSSTIYYADS VKG (SEQ ID NO:421)	ARGGRRHYGGMD V (SEQ ID NO:486)	RSSQSLLHSNGY NYLD (SEQ ID NO:508)	LGSHRAS (SEQ ID NO:525)	MQALESPRT (SEQ ID NO:602)
Ab80	GTFSSYAIS (SEQ ID NO:379)	GIIPIFGTANYAQK FQG (SEQ ID NO:401)	ARGGGTFWSGSW ALY (SEQ ID NO:487)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQYVNWPFT (SEQ ID NO:603)

Ab81	GTFSSYAIS (SEQ ID NO:379)	GIIPIFGTANYAQK FQG (SEQ ID NO:401)	ARDSGNYDYWSG ALRY (SEQ ID NO:488)	RASQSVSSYLA (SEQ ID NO:498)	DASNRAT (SEQ ID NO:518)	QQSSNWPWT (SEQ ID NO:604)
Ab82	GSISSGGYYWS (SEQ ID NO:387)	YIYYSGSTVYNPS LKS (SEQ ID NO:422)	ARVSSSWYKA (SEQ ID NO:489)	RASQGISSWLA (SEQ ID NO:509)	AASSLQS (SEQ ID NO:519)	QQASTFPIT (SEQ ID NO:605)
Ab83	GSFSGYYWS (SEQ ID NO:398)	EIDHSGSTKYNPSL KS (SEQ ID NO:423)	ARVGVVVGRPGYS AFDI (SEQ ID NO:490)	RASQGISSWLA (SEQ ID NO:509)	AASSLQS (SEQ ID NO:519)	QQRNSLPLT (SEQ ID NO:606)
Ab84	YTFTSYGIS (SEQ ID NO:386)	WISTYNGNTNYAQ K LQG (SEQ ID NO:419)	ARGSGSGYDSWY D (SEQ ID NO:473)	RASQSISSYLN (SEQ ID NO:499)	AASSLQS (SEQ ID NO:519)	QQSYDFPIT (SEQ ID NO:607)
Ab85	FTFSSYGMH (SEQ ID NO:390)	VIWYDGSNKYYAD SVKG (SEQ ID NO:415)	AKDLGGYYGGAA YGMDV (SEQ ID NO:491)	RASQDISSWLA (SEQ ID NO:510)	AASSLQS (SEQ ID NO:519)	QQEVDYPPLT (SEQ ID NO:608)
Ab86	FTFSSYGMH (SEQ ID NO:390)	VISYDGSNKYYAD SVKG (SEQ ID NO:413)	AKDGVYYGLGNW FDP (SEQ ID NO:492)	RASQSISSWLA (SEQ ID NO:505)	KASSLES (SEQ ID NO:526)	QQLNSYSPT (SEQ ID NO:609)
Ab87	GSISSYYWS (SEQ ID NO:389)	SIYYSGSTNYNPSL KS (SEQ ID NO:412)	ARHGWDRVGWFD P (SEQ ID NO:493)	RASQSVSRYLA (SEQ ID NO:511)	DASNRAT (SEQ ID NO:518)	QQYIFWPPT (SEQ ID NO:610)

TABLE C4: Heavy chain variable regions

Ab ID	HC Variable Region Sequences
Ab 1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGTPTLLFQHWGQGTLVTVSS (SEQ ID NO:616)
Ab 2	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVPSYDYWSGYSNYYYYMDV WGKGTTVTVSS (SEQ ID NO:618)
Ab 3	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREQYHVGMDVWGKGTTVTVSS (SEQ ID NO:620)
Ab 4	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTASY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGVDSIMDYWGQGTLVTVSS (SEQ ID NO:622)
Ab 5	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARAPQESPYVFDIWGQGTMVTV SS (SEQ ID NO:624)
Ab 6	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPGGGST SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGSPTYGYLYDPWGQGTLVT VSS (SEQ ID NO:626)
Ab 7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST TYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARTSSKERDYWGQGTLVTVSS (SEQ ID NO:628)
Ab 8	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSISYSGSTYYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPYRLLLGMDVWGQGTTVTVSS (SEQ ID NO:630)
Ab 9	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTT YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLHISGEVNWFDPWGQGTLVTV SS (SEQ ID NO:632)
Ab 10	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSNWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAREAGYDYGELAFDIWGQGTMV TVSS (SEQ ID NO:634)
Ab 11	EVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAGHYDGGHLGMDVWGQGTT VTVSS (SEQ ID NO:636)
Ab 12	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGHYSGTVSSYGMDVWGQGT TVTVSS (SEQ ID NO:638)
Ab 13	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNT NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGPSHYYDLAWGQGTLVTV SS (SEQ ID NO:640)

Ab ID	HC Variable Region Sequences
Ab 14	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGNIYYSGSTVY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGLYGYGVLDVWGQGTMVTVSS (SEQ ID NO:642)
Ab 15	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGNIYYSGSTVY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGLYGYGVLDVWGQGTMVTVSS (SEQ ID NO:642)
Ab 16	QLQLQESGPGLVKPSETLSLTCTVSGGSISSNSYYWGWIRQPPGKGLEWIGSIYYSGSTYY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGVLGYGVFDYWGQGTLVTVSS (SEQ ID NO:645)
Ab 17	QLQLQESGPGLVKPSETLSLTCTVSGGSISSNSYYWGWIRQPPGKGLEWIGSIYYSGSTYY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGVLGYGVFDYWGQGTLVTVSS (SEQ ID NO:645)
Ab 18	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYNPS LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGGGEYPSGTPFDIWGQGTMVTVSS (SEQ ID NO:648)
Ab 19	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYNPS LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGGGEYPSGTPFDIWGQGTMVTVSS (SEQ ID NO:648)
Ab 20	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYNPS LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSGMASFFDYWGQGTLVTVSS (SEQ ID NO:651)
Ab 22	EVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAGHYDGGHLGMDVWGQGTT VTVSS (SEQ ID NO:636)
Ab 23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLGGHSMDVWGQGTTVTVSS (SEQ ID NO:654)
Ab 24	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPLKRGRGFYWGQGTLVTVSS (SEQ ID NO:656)
Ab 25	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEGRTITMDWGQGTLVTVSS (SEQ ID NO:658)
Ab 26	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDQYSVLDYWGQGTLVTVSS (SEQ ID NO:660)
Ab 27	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKKYSSRGVYFDYWGQGTLVT VSS (SEQ ID NO:662)
Ab 28	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLGGAVGARHVTYFDYWGQG TLVTVSS (SEQ ID NO:664)

Ab ID	HC Variable Region Sequences
Ab 29	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGQYYGGSGWFDPWGQGTL VTVSS (SEQ ID NO:666)
Ab 30	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLGQEYAYFQHWGQGTLVTV SS (SEQ ID NO:668)
Ab 31	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVALIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRRDGYYDEVFDIWGQGTM VTVSS (SEQ ID NO:670)
Ab 32	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPKHYVVLDYWGQGTLVTV SS (SEQ ID NO:672)
Ab 33	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAGGHLFDYWGQGTLVTVS S (SEQ ID NO:674)
Ab 34	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGGEYVDFAFDIWGQGT MVTVSS (SEQ ID NO:676)
Ab 35	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTRSGYGASNYFDYWGQGTL VTVSS (SEQ ID NO:678)
Ab 36	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTGAAAASPAFDIWGQGT MVTVSS (SEQ ID NO:680)
Ab 37	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVGQYMLGMDVWGQGTTVT VSS (SEQ ID NO:682)
Ab 38	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGAPVDYGGIEPEYFQHWGQ GTLVTVSS (SEQ ID NO:684)
Ab 39	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHYHVGIAFDIWGQGTMVTVS S (SEQ ID NO:686)
Ab 40	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTRSGYGASNYFDYWGQGTL VTVSS (SEQ ID NO:678)
Ab 41	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAMARKSVAFDIWGQGTMVT VSS (SEQ ID NO:689)
Ab 42	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVPSYQRGTAFDPWGQGTLVTV SS (SEQ ID NO:691)

Ab ID	HC Variable Region Sequences
Ab 43	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSPAVAGIYRADYWGQGTLVTV SS (SEQ ID NO:693)
Ab 44	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTGAAAASPAFDIWGQGT MVTVSS (SEQ ID NO:680)
Ab 45	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGPGYTTALDYYYMDVWGK GTTVTVSS (SEQ ID NO:696)
Ab 46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPAKTADYWGQGTLVTVSS (SEQ ID NO:698)
Ab 47	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST TYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPGKSMDVWGQGTTVTVSS (SEQ ID NO:700)
Ab 48	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST TYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPGKSMDVWGQGTTVTVSS (SEQ ID NO:700)
Ab 49	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPAKTADYWGQGTLVTVSS (SEQ ID NO:698)
Ab 50	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARAPQESPYVFDIWGQGTMVTV SS (SEQ ID NO:624)
Ab 51	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGVGGQDYYYMDVWGKGT TVTVSS (SEQ ID NO:705)
Ab 53	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARAPQESPYVFDIWGQGTMVTV SS (SEQ ID NO:624)
Ab 54	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGPGYTTALDYYYMDVWGK GTTVTVSS (SEQ ID NO:696)
Ab 55	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGPLYHPMIFDYWGQGTLV TVSS (SEQ ID NO:709)
Ab 56	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGSINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARASSVDNWGQGTLVTVSS (SEQ ID NO:711)
Ab 57	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGISWVRQAPGQGLEWMGWISAYNGNT NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGPTKAYYGSGSYVVFDPW GQGTLVTVSS (SEQ ID NO:713)

Ab ID	HC Variable Region Sequences
Ab 58	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGIYSTGATAFDIWGQGTMVT VSS (SEQ ID NO:715)
Ab 59	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGVWYSLFDIWGQGTMV TVSS (SEQ ID NO:717)
Ab 60	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGG TSYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARASKMGDDWGQGTLVTVS S (SEQ ID NO:719)
Ab 61	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGIHWVRQAPGQGLEWMGWISAYNGNT NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGGVPRVSYFQHWGQGTLV TVSS (SEQ ID NO:721)
Ab 62	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAGHYDDWSGLGLDVWGQGT MVTVSS (SEQ ID NO:723)
Ab 63	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISTYNGNT NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGSGSGYDSWYDWGQGTL VTVSS (SEQ ID NO:725)
Ab 64	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGRWSSGSTAFDIWGQGTMV TVSS (SEQ ID NO:727)
Ab 65	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGRKPSGSVAFDIWGQGTMVT VSS (SEQ ID NO:729)
Ab 66	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARAGHKTHDYWGQGTLVTV SS (SEQ ID NO:731)
Ab 67	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST TYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARPGKSMDVWGQGTTVTVSS (SEQ ID NO:700)
Ab 68	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVALIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPGSMTDYWGQGTLVTVSS (SEQ ID NO:734)
Ab 69	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARAKSVDHDYWGQGTLVTV SS (SEQ ID NO:736)
Ab 70	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGG TSYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARASKMGDDWGQGTLVTVS S (SEQ ID NO:719)
Ab 71	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGST SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDISTHDYDLAFDIWGQGTM VTVSS (SEQ ID NO:739)

Ab ID	HC Variable Region Sequences
Ab 72	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYNPS LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSGTETLFDYWGQGTLVTVSS (SEQ ID NO:741)
Ab 73	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTT YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARAKMLDDGYAFDIWGQGTMVT VSS (SEQ ID NO:743)
Ab 74	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARAGHKTHDYWGQGTLVTV SS (SEQ ID NO:731)
Ab 75	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDLGYSSLLALDIWGQGTM VTVSS (SEQ ID NO:746)
Ab 76	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYY ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGGRRGDNNWFDPWGQGTLV TVSS (SEQ ID NO:748)
Ab 77	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGPPHEMDYWGQGTLVTVS S (SEQ ID NO:750)
Ab 78	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTPYPWIYFDLWGRGTLVTV SS (SEQ ID NO:752)
Ab 79	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISGSSSTIYY ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGRRHYGGMDVWGQGTTVT VSS (SEQ ID NO:754)
Ab 80	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGGGTFWSGSWALYWGQGTLVT VSS (SEQ ID NO:756)
Ab 81	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDSGNYDYWSGALRYWGQGTL VTVSS (SEQ ID NO:758)
Ab 82	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTVY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVSSSWYKAWGQGTMVTVSS (SEQ ID NO:760)
Ab 83	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEIDHSGSTKY NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVGVVVGRPGYSAFDIWGQGTM VTVSS (SEQ ID NO:762)
Ab 84	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISTYNGNT NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGSGSGYDSWYDWGQGTL VTVSS (SEQ ID NO:725)
Ab 85	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGGYYGGAAYGMDVWG QGTTVTVSS (SEQ ID NO:765)

Ab ID	HC Variable Region Sequences
Ab 86	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDGVYYGLGNWFDPWGQG TLVTVSS (SEQ ID NO:767)
Ab 87	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGSIYYSGSTNYNPS LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHGWDRVGWFDPWGQGTLVTVSS (SEQ ID NO:769)

TABLE C5: Light chain variable regions

Ab ID	LC Variable Region Sequences
Ab 1	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCQQLPYWPPTFGGGTKVEIK (SEQ ID NO:617)
Ab 2	EIVLTQSPATLSVSPGERATLSCRASQSVGSNLAWYQQKPGQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCQQYFFYPPTFGGGTKVEIK (SEQ ID NO:619)
Ab 3	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLATGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQPFNFPYTFGGGTKVEIK (SEQ ID NO:621)
Ab 4	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYSASTRATGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCQQDHDYPFTFGGGTKVEIK (SEQ ID NO:623)
Ab 5	EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPD RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYFSSPFTFGGGTKVEIK (SEQ ID NO:625)
Ab 6	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRVNLPPTFGGGTKVEIK (SEQ ID NO:627)
Ab 7	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRISYPITFGGGTKVEIK (SEQ ID NO:629)
Ab 8	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQIDDTPITFGGGTKVEIK (SEQ ID NO:631)
Ab 9	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQFSYWPWTFGGGTKVEIK (SEQ ID NO:633)
Ab 10	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQHDSSPPTFGGGTKVEIK (SEQ ID NO:635)
Ab 11	EIVLTQSPGTLSLSPGERATLSCRASQSVSSDYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQDYSYPWTFGGGTKVEIK (SEQ ID NO:637)
Ab 12	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQEYAVPYTFGGGTKVEIK (SEQ ID NO:639)
Ab 13	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQVSNYPITFGGGTKVEIK (SEQ ID NO:641)
Ab 14	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQVDNIPPTFGGGTKVEIK (SEQ ID NO:643)
Ab 15	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQFDTYPTFGGGTKVEIK (SEQ ID NO:644)
Ab 16	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQFLNFPTFGGGTKVEIK (SEQ ID NO:646)

Ab ID	LC Variable Region Sequences
Ab 17	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQFFNFPTFGGGTKVEIK (SEQ ID NO:647)
Ab 18	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQFIDLPFTFGGGTKVEIK (SEQ ID NO:649)
Ab 19	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQYYDLPFTFGGGTKVEIK (SEQ ID NO:650)
Ab 20	EIVLTQSPGTLSLSPGERATLSCRASQSVSSDYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQFSSHPFTFGGGTKVEIK (SEQ ID NO:652)
Ab 22	EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPD RFSGSGSGTDFTLTISRLEPEDFAVYYCQQDDRSPYTFGGGTKVEIK (SEQ ID NO:653)
Ab 23	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLISWASTR ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQAYLPPITFGGGTKVEIK (SEQ ID NO:655)
Ab 24	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQAFSPPPWTFGGGTKVEIK (SEQ ID NO:657)
Ab 25	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQDDRSPTFGGGTKVEIK (SEQ ID NO:659)
Ab 26	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA (SEQ ID NO:661)RFSGSGSGTDFTLTISSLEPEDFAVYYCQQEFDLPFTFGGGTKVEIK
Ab 27	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQYNNFPPTFGGGTKVEIK (SEQ ID NO:663)
Ab 28	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRYLRPITFGGGTKVEIK (SEQ ID NO:665)
Ab 29	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQPGAVPTFGGGTKVEIK (SEQ ID NO:667)
Ab 30	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQVYITPITFGGGTKVEIK (SEQ ID NO:669)
Ab 31	DIQLTQSPSSLSASVGDRVTITCQASQDISNFLNWYQQKPGKAPKLLIYDASNLETGVPSRF SGSGSGTDFTFTISSLQPEDIATYYCQQPVDLPFTFGGGTKVEIK (SEQ ID NO:671)
Ab 32	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQYSFFPPTFGGGTKVEIK (SEQ ID NO:673)
Ab 33	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQDSSFPPTFGGGTKVEIK (SEQ ID NO:675)
Ab 34	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQSDFPPWTFGGGTKVEIK (SEQ ID NO:677)
Ab 35	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQGYSAPITFGGGTKVEIK (SEQ ID NO:679)
Ab 36	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQLFDWPTFGGGTKVEIK (SEQ ID NO:681)
Ab 37	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRAFLFTFGGGTKVEIK (SEQ ID NO:683)

Ab ID	LC Variable Region Sequences
Ab 38	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQIDFLPYTFGGGTKVEIK (SEQ ID NO:685)
Ab 39	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQVYSPPITFGGGTKVEIK (SEQ ID NO:687)
Ab 40	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQGYAAPITFGGGTKVEIK (SEQ ID NO:688)
Ab 41	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFTVYYCQQRYALPITFGGGTKVEIK (SEQ ID NO:690)
Ab 42	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQYASPPITFGGGTKVEIK (SEQ ID NO:692)
Ab 43	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPITFGGGTKVEIK (SEQ ID NO:694)
Ab 44	EIVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDSSNRATGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQLVHWPTFGGGTKVEIK (SEQ ID NO:695)
Ab 45	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCQQLDDWFTFGGGTKVEIK (SEQ ID NO:697)
Ab 46	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDSSNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRSNYPITFGGGTKVEIK (SEQ ID NO:699)
Ab 47	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRILYPITFGGGTKVEIK (SEQ ID NO:701)
Ab 48	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRAAYPITFGGGTKVEIK (SEQ ID NO:702)
Ab 49	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRTSHPITFGGGTKVEIK (SEQ ID NO:703)
Ab 50	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQYAGSPFTFGGGTKVEIK (SEQ ID NO:704)
Ab 51	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQFDDVFTFGGGTKVEIK (SEQ ID NO:706)
Ab 53	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR FSGSGSGTDFTLTISRLEPEDFAVYYCQQYVNSPFTFGGGTKVEIK (SEQ ID NO:707)
Ab 54	DIQMTQSPSSLSASVGDRVTITCRASQSINSYLNWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQSDDDPFTFGGGTKVEIK (SEQ ID NO:708)
Ab 55	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQLSTYPLTFGGGTKVEIK (SEQ ID NO:710)
Ab 56	EIVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQRSVYPITFGGGTKVEIK (SEQ ID NO:712)
Ab 57	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQVSLFPLTFGGGTKVEIK (SEQ ID NO:714)
Ab 58	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSR FSGSGSGTEFTLTISSLQPDDFATYYCLDYNSYSPITFGGGTKVEIK (SEQ ID NO:716)
Ab 59	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTFTISSLQPEDIATYYCQQHIALPFTFGGGTKVEIK (SEQ ID NO:718)

Ab ID	LC Variable Region Sequences
Ab 60	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRASMPITFGGGTKVEIK (SEQ ID NO:720)
Ab 61	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDSSNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQAFNRPPTFGGGTKVEIK (SEQ ID NO:722)
Ab 62	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQSSVHPYTFGGGTKVEIK (SEQ ID NO:724)
Ab 63	DIQMTQSPSSVSASVGDRVTITCRASQGIDSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQAYSLPPTFGGGTKVEIK (SEQ ID NO:726)
Ab 64	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCQQDDDGYTFGGGTKVEIK (SEQ ID NO:728)
Ab 65	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQDYSWPYTFGGGTKVEIK (SEQ ID NO:730)
Ab 66	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRSAYPITFGGGTKVEIK (SEQ ID NO:732)
Ab 67	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRSHFPITFGGGTKVEIK (SEQ ID NO:733)
Ab 68	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRANYPITFGGGTKVEIK (SEQ ID NO:735)
Ab 69	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRADYPITFGGGTKVEIK (SEQ ID NO:737)
Ab 70	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRSVYPITFGGGTKVEIK (SEQ ID NO:738)
Ab 71	EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIPD RFSGSGSGTDFTLTISRLEPEDFAVYYCQQAGSHPFTFGGGTKVEIK (SEQ ID NO:740)
Ab 72	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLETGVPSR FSGSRSGTDFTFTISSLQPEDIATYYCQQDVNYPPTFGGGTKVEIK (SEQ ID NO:742)
Ab 73	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCQQDDNYPYTFGGGTKVEIK (SEQ ID NO:744)
Ab 74	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQRSTFPITFGGGTKVEIK (SEQ ID NO:745)
Ab 75	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQVSNYPFTFGGGTKVEIK (SEQ ID NO:747)
Ab 76	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYHDAPITFGGGTKVEIK (SEQ ID NO:749)
Ab 77	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQAYVVPPTFGGGTKVEIK (SEQ ID NO:751)
Ab 78	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQADNWPFTFGGGTKVEIK (SEQ ID NO:753)

Ab ID	LC Variable Region Sequences
Ab 79	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSHRAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALESPRTFGGGTKVEIK (SEQ ID NO:755)
Ab 80	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQYVNWPFTFGGGTKVEIK (SEQ ID NO:757)
Ab 81	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSLEPEDFAVYYCQQSSNWPWTFGGGTKVEIK (SEQ ID NO:759)
Ab 82	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQASTFPITFGGGTKVEIK (SEQ ID NO:761)
Ab 83	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQRNSLPLTFGGGTKVEIK (SEQ ID NO:763)
Ab 84	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQSYDFPITFGGGTKVEIK (SEQ ID NO:764)
Ab 85	DIQLTQSPSSVSASVGDRVTITCRASQDISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQEVDYPPLTFGGGTKVEIK (SEQ ID NO:766)
Ab 86	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPSR FSGSGSGTEFTLTISSLQPDDFATYYCQQLNSYSPTFGGGTKVEIK (SEQ ID NO:768)
Ab 87	EIVLTQSPATLSLSPGERATLSCRASQSVSRYLAWYQQKPGQAPRLLIYDASNRATGIPAR FSGSGSGTDFTLTISSLEPEDFAVYYCQQYIFWPPTFGGGTKVEIK (SEQ ID NO:770)

[00193] 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 C3** 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.

[00194] 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 C3** 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.

[00195] 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.

[00196] In some embodiments, each of the light chain variable regions disclosed in **TABLE C5** and each of the heavy chain variable regions disclosed in **TABLE C4** may be attached to the light chain constant regions **(EN1)** and heavy chain constant regions **(EN2)** 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

[00197] 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.

[00198] 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.

[00199] 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.

[00200] 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.

[00201] 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 D1-D8**.

TABLE D1: EU or Kabat light chain HVR sequences

Ab ID	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)	LVSKLDS (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:833)	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)

Ab ID	HVRL1	HVRL2	HVRL3
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:836)	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)

Ab ID	HVRL1	HVRL2	HVRL3
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 D2: 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 D3: 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:910)
1H7	FSFNTYAMN (SEQ ID NO:872)	IARIRSKSNNYATYY A (SEQ ID NO:890)	VRHGDGNLWYIDV (SEQ ID NO:909)
2H8	FSFNTYAMN (SEQ ID NO:872)	IARIRSKSNNYATYY A (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:1708)	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)
7B11v2	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 D4: 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	$XX_1XIX_2X_3X_4X_5X_6X_7X_8ATXYX_9$ X_1 is A or G

	HVR H1	HVR H2
	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)	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$_1$X$_2$XWX$_3$X X_i is S or T X_2 is N, S, or T X_3 is I or M (SEQ ID NO:1654)	IGXIX$_1$PX$_2$XX$_3$X$_4$X$_5$X$_6$X$_7$N 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 D5: EU or Kabat light chain Framework sequences

Ab ID	VL FR1	VL FR2	VL FR3	VL FR4
4D11	DIZVTQSPASLSAS VGETVTITC (SEQ ID NO:923)	WYQLKQGKSPQ LLVY (SEQ ID NO:940)	GVPSRFSGSGSGTQFS LRINSLQPEDFGSYYC (SEQ ID NO:950)	FGGGTKLEIK (SEQ ID NO:968)
78C5	DIZVTQSPASLSAS VGETVTITC (SEQ ID NO:923)	WYQLKQGKSPQ LLVY (SEQ ID NO:940)	GVPSRFSGSGSGTQFS LRINSLQPEDFGSYYC (SEQ ID NO:950)	FGGGTKLEIK (SEQ ID NO:968)
6G12	TMSQSPSSLAVSV GEKVTMSC (SEQ ID NO:924)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TLTISSVKAEDLAVY YC (SEQ ID NO:951)	FGAGTKLELK (SEQ ID NO:969)
8F11	DVZMTQTPLTLSV TIGQPASISC (SEQ ID NO:925)	WLLQRPGQSPK RLIY (SEQ ID NO:942)	GVPDRFAGSGSGTDF TLKISRLEADDLGIYY C (SEQ ID NO:952)	FGAGTKLELK (SEQ ID NO:969)
8E10	DVZMTQTPLTLSV TIGQPASISC (SEQ ID NO:925)	WLLQRPGQSPK RLIY (SEQ ID NO:942)	GVPDRFTGSGSGTDF TLKISRVEAEDLGVY YC (SEQ ID NO:953)	FGGGTKLEIK (SEQ ID NO:968)
7E5	DVZMTQTPLTLSV TIGQPASISC (SEQ ID NO:925)	WLLQRPGQSPK RLIY (SEQ ID NO:942)	GVPDRFAGSGSGTDF TLKISRLEADDLGIYY C (SEQ ID NO:952)	FGAGTKLELK (SEQ ID NO:969)

Ab ID	VL FR1	VL FR2	VL FR3	VL FR4
7E5v2	DVVMTQTPLTLSV TIGQPASISC (SEQ ID NO:931)	WLLQRPGQSPK RLIY (SEQ ID NO:942)	GVPDRFAGSGSGTDF TLKISRLEADDLGIYY C (SEQ ID NO:952)	FGAGTKLELK (SEQ ID NO:969)
7F8	VLTQSPALMSASP GEKVTMTC (SEQ ID NO:926)	WYQQKPRSSPK PWIY (SEQ ID NO:943)	GVPARFSGSGSGTSY SLTINNMEAEDAATY YC (SEQ ID NO:954)	FGGGTKLVIK (SEQ ID NO:970)
8F8	DVZMTQTPLSLPV SLGDQASISC (SEQ ID NO:927)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY FC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)
1H7	VLTQSPAIMZASP GEKVTMTC (SEQ ID NO:928)	WYQQKPRSSPK PWIY (SEQ ID NO:943)	GVPARFSGSGSGTSY SLTISSMEAEDAATY YC (SEQ ID NO:956)	FGGGTKLVIK (SEQ ID NO:970)
2H8	NVLTQSPALMSAS PGEKVTMTC (SEQ ID NO:929)	WYQQKPRSSPK PWIY (SEQ ID NO:943)	GVPARFSGSGSGTSY SLTISSMEAEDAATY YC (SEQ ID NO:956)	FGGGTKLVIK (SEQ ID NO:970)
3A2	DVVMTQTPLSLPV SLGDQASISC (SEQ ID NO:930)	WYLRKPGQSPK LLIY (SEQ ID NO:945)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY YC (SEQ ID NO:957)	FGGGTELEIK (SEQ ID NO:971)
3A7	DVVMTQTPLTLSV TIGQPASISC (SEQ ID NO:931)	WLLQRPGQSPK RLIY (SEQ ID NO:942)	GVPDRFAGSGSGTDF TZKISRLEADDLGIYY C (SEQ ID NO:958)	FGGGTKLEMK (SEQ ID NO:972)
3B10	ITMSQSPSSLAVSV GEKVTMSC (SEQ ID NO:932)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TLTISSVKAEDLAVY CC (SEQ ID NO:959)	FGAGTKLELK (SEQ ID NO:969)
4F11	DVZMTQTPLSLPV SLGDQASISC (SEQ ID NO:927)	WYLRKPGQSPK LLIY (SEQ ID NO:945)	GVPDRFSGSGSGTDF TLKISRVEGEDLGVY YC (SEQ ID NO:960)	FGGGTELEIK (SEQ ID NO:971)
6H6	QTQSPSSLAVSAG EKVTLSC (SEQ ID NO:1410)	WYQQKPGQSPK LLIS (SEQ ID NO:1413)	GVPDRFTGSGFGTDF TLTISSVQGEDLAVY YC (SEQ ID NO:1414)	FGAGTKLELK (SEQ ID NO:969)
7A9	QMSQSPACLZAZV GESVTITC (SEQ ID NO:933)	WYQQKQGKSPK LVVY (SEQ ID NO:946)	GVPSRFSGRGSGTQF FLKINSZQREDFGSY YC (SEQ ID NO:961)	FGSGTKLEIK (SEQ ID NO:973)
8A1	DIQMTQSPASLSVS VGETVTITC (SEQ ID NO:934)	WYQQKQGKSPQ LLVY (SEQ ID NO:947)	GVPSRFSASGSATQFS LKINSLQSADFGSYY C (SEQ ID NO:962)	FGGGTKLEMN (SEQ ID NO:974)
9F5	DVZMTQNPLSLPV SLGDQASISC (SEQ ID NO:935)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLKISRVEADDLGVY LC (SEQ ID NO:963)	FGGGTKLEIK (SEQ ID NO:968)
9F5v2	DVVMTQTPLSLPV SLGDQASISC (SEQ ID NO:930)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLKISRVEADDLGVY FC (SEQ ID NO:1668)	FGGGTKLEIK (SEQ ID NO:968)

Ab ID	VL FR1	VL FR2	VL FR3	VL FR4
9G1	DVLMTQTPLSLPV SLGDQASISC (SEQ ID NO:936)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLRISGVEAEDLGVY FC (SEQ ID NO:964)	FGGGTKLEIK (SEQ ID NO:968)
9G3	NVLTQSPALIWAZ PGEKVTMTC (SEQ ID NO:937)	WXXXKPRSSPK PGIY (SEQ ID NO:948)	GVPGRFSGSGSGTYX SFKISSMEGKMGPLII FC (SEQ ID NO:965)	FGGGTKLEMK (SEQ ID NO:975)
10A9	DVVMTQTPLSLPV SLGDQASISC (SEQ ID NO:930)	WYLRKPGQSPK LLIY (SEQ ID NO:945)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY YC (SEQ ID NO:957)	FGGGTELEIK (SEQ ID NO:971)
11A8	DIZMTQSPSSLTVT AGEKVTMSC (SEQ ID NO:938)	WYQQKPGQPZK LLIY (SEQ ID NO:949)	GVRDRFTGSGZGTDF TLTISSVQGEDLAIYY C (SEQ ID NO:966)	FGGGTKLEMK (SEQ ID NO:972)
12D9	TQSPSSLAVSVGE KVTMTC (SEQ ID NO:939)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TLTISTVKAEDLAVY YC (SEQ ID NO:967)	FGSGTKLEIK (SEQ ID NO:973)
12F9	TMSQSPSSLAVSV GEKVTMSC (SEQ ID NO:924)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TLTISSVKAEDLAVY CC (SEQ ID NO:959)	FGAGTKLELK (SEQ ID NO:969)
10C1	QTQVFLSLLLWVS GTCGNIMLTQSPSS LAVSAGEKVTLSC (SEQ ID NO:1411)	WYQQKPGQSPK LLIS (SEQ ID NO:1413)	GVPDRFTGSGSGTDF TLTINSVQAEDLAVY YC (SEQ ID NO:1415)	FGAGTKLELK (SEQ ID NO:969)
7E9	DIVMSQSPSSLAVS VGEKVTMSC (SEQ ID NO:1412)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TLTISSVKAEDLAVY YC (SEQ ID NO:951)	FGAGTKLELK (SEQ ID NO:969)
8C3	DVVMTQTPLSLPV SLGDQASISC (SEQ ID NO:930)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY FC (SEQ ID NO:955)	FGSGTKLEIK (SEQ ID NO:973)
IB4v1	DIVMTQSHKFMST SVGDRVSITCKA (SEQ ID NO:1531)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGFGTDF TFTISSVQAEDLAVY YC (SEQ ID NO:1535)	FGGGTKLEIK (SEQ ID NO:968)
IB4v2	ZVVZTQTPLSLPVS LGDQASFSCRS (SEQ ID NO:1591)	WFLQKPGQSPK LLIF (SEQ ID NO:1597)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY FC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)
6H2	DVLMTQTPLSLPV SLGDQASISCRS (SEQ ID NO:1532)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY YC (SEQ ID NO:957)	FGSGTKLEIK (SEQ ID NO:973)
7B11	DIVMTQSHKFMST SVGDRVSITCKA (SEQ ID NO:1531)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDY TLTISSVQAEDLALY YC (SEQ ID NO:1536)	FGGGTKLEIK (SEQ ID NO:968)

Ab ID	VL FR1	VL FR2	VL FR3	VL FR4
18D8	DIVMTQSHKFMST SIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGFGTDF TFTISSVQAEDLAVY YC (SEQ ID NO:1535)	FGGGTKLEIK (SEQ ID NO:968)
18E4v1	DIVMTQSPKSMSM SVGERVTLTCKA (SEQ ID NO:1534)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSATDF TLTISSVQAEDLADY HC (SEQ ID NO:1537)	FGGGTKLEIK (SEQ ID NO:968)
18E4v2	NIVMTQSPKSMSM SVGERVTLTCKA (SEQ ID NO:1592)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSATDF TLTISSVQAEDLADY HC (SEQ ID NO:1537)	FGGGTKLEIK (SEQ ID NO:968)
18E4v3	DVVMTQTPLSLPV SLGDQASISCRS (SEQ ID NO:1593)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLRISRVEAEDLGVY FC (SEQ ID NO:1601)	FGAGTKLELK (SEQ ID NO:969)
29F6v1	DIVMTQSHKFMST SIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TFTISSVQAEDLAVY YC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
29F6v2	DVVMTQTPLSLPV SLGDQASISCRS (SEQ ID NO:1593)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY FC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)
40D5	DIVMTQSHKFMST SIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TFTISSVQAEDLAVY YC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
43B9	DIVMTQSHKFMST SIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TFTISSVQAEDLAVY YC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
44A8v1	DIVMTQSHKFMST SVGDRVSITCKA (SEQ ID NO:1531)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TFTISSVQAEDLAVY YC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
44A8v2	DIVLTQSPASLAVS LGQRATISCRA (SEQ ID NO:1594)	WYQQKPGQPPK LLIY (SEQ ID NO:1598)	GVPARFSGSGSGTDF SLNIHPVEEDDIAMY FC (SEQ ID NO:1602)	FGGGTKLEIK (SEQ ID NO:968)
44B4v1	DIVMTQSHKFMST SIGARVSITCKA (SEQ ID NO:1533)	WYQQKPGQSPK LLIY (SEQ ID NO:941)	GVPDRFTGSGSGTDF TFTISSVQAEDLAVY YC (SEQ ID NO:1538)	FGGGTKLEIK (SEQ ID NO:968)
44B4v2	DIQMTQFPASLAA XVGESVTITCRA (SEQ ID NO:1595)	WYQQKQGKSPQ LLIY (SEQ ID NO:1599)	GVPSRFSGSGSGTQY SMKINSMQPEDTAIY FC (SEQ ID NO:1603)	FGGGTKLEIK (SEQ ID NO:968)
29F7	ILLTQSPAILSVSPG ERVSFSC (SEQ ID NO:1596)	WYQQRTNGSPR LLIK (SEQ ID NO:1600)	GIPSRFSGSGSGTDFT LNINSVESEDIADYYC (SEQ ID NO:1604)	FGAGTKLELK (SEQ ID NO:969)
32G1	DVVMTQTPLSLPV SLGDQASISC (SEQ ID NO:930)	WYLQKPGQSPK LLIY (SEQ ID NO:944)	GVPDRFSGSGSGTDF TLKISRVEAEDLGVY FC (SEQ ID NO:955)	FGAGTKLELK (SEQ ID NO:969)

TABLE D6: EU or Kabat heavy chain Framework sequences

Ab ID	VH FR1	VH FR2	VH FR3	VH FR4
44D11	EVKLVESGGGLV KPGGSLKLSCAAS G (SEQ ID NO:976)	WVRQTPEKRLEW (SEQ ID NO:995)	DSVQGRFTFSRDNA RNILYLQMSSLRSED TAMYYC (SEQ ID NO:1008)	WGQGTLVTVSA (SEQ ID NO:1029)
78C5	EVKLVESGGGLV KPGGSLKLSCAAS G (SEQ ID NO:976)	WVRQTPEKRLEW (SEQ ID NO:995)	DSVQGRFTFSRDNA RNILYLQMSSLRSED TAMYYC (SEQ ID NO:1008)	WGQGTLVTVSA (SEQ ID NO:1029)
6G12	EVQLQQSGPELVK PGTSVKISCKTSG (SEQ ID NO:977)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGKASLTVDKS SSTAYMELHSLASD DSAVYYC (SEQ ID NO:1009)	WGQGTSVTVSS (SEQ ID NO:1030)
8E10	QVQLQQSGAELV RPGASVTLSCKAS G (SEQ ID NO:978)	WVKQTPVHGLEW (SEQ ID NO:997)	QKFKGKAILTADKS SSTAYMELRSLTSED SAVYYC (SEQ ID NO:1010)	WGQGTSVTVSS (SEQ ID NO:1030)
7E5	EVKLEESGGGLVQP GGSMKLSCAASG (SEQ ID NO:979)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSK STVYLQMNTLRADD TGIYYC (SEQ ID NO:1011)	WGQGTTLTVSS (SEQ ID NO:1031)
7F8	EVQLVESGGGLV QPKGSLKLSCAA SG (SEQ ID NO:980)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRITCSRDDSE NMFYLQLSSLKTED TAMYYC (SEQ ID NO:1012)	WGTGTTVTVST (SEQ ID NO:1032)
8F8	QVQLQQSGAELVK PGASVKLSCKASG (SEQ ID NO:981)	WVKQRPGRGLEW (SEQ ID NO:1000)	EKFKTKATLTVDKP SSTAYMQVSSLTSE DSAVYYC (SEQ ID NO:1013)	WGQGTTLTVSS (SEQ ID NO:1031)
IH7	ZVQLVESGGGLV QPKGSLKLSCAA SG (SEQ ID NO:982)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTCSRDDS ENMFYLQLSSLKTE DTAIYYC (SEQ ID NO:1014)	WGTGTTVTVSS (SEQ ID NO:1033)
2HS	EVQLVESGGGLVQP KGSLKLSCAASG (SEQ ID NO:980)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTCSRDDS ENMFYLQLSSLKTE DTAMYYC (SEQ ID NO:1015)	WGTGTTVTVSS (SEQ ID NO:1033)
3A2	QVQLQQSGAELVK PGASVKMSCKTSG (SEQ ID NO:983)	WVKQRPGQGLV W (SEQ ID NO:1001)	EKFKTKATLTVDTSS STAYMHLSSLTSEDS AVYFC (SEQ ID NO:1016)	WGQGTLVTVST (SEQ ID NO:1034)

3A7	EVKLEESGGGLVQP GGSMKLSCAASG (SEQ ID NO:979)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSK STVYLQMNTLRADD TGIYYC (SEQ ID NO:1011)	WGQGTTLTVSS (SEQ ID NO:1031)
3B10	EVQLVZZGRGZSQ GKGSXZZGRAZRC (SEQ ID NO:984)	GVPQGPGKGREW (SEQ ID NO:1002)	DSVKDRFTZSRDDS ESLFYZQMSZZKZE DTAMYYZ (SEQ ID NO:1017)	WGQGTIVTVS (SEQ ID NO:1035)
4F11	QVQLQQSGAELVK PGASVKMSCKTSG (SEQ ID NO:983)	WVKQRPGQGLV W (SEQ ID NO:1001)	EKFKTKATLTVDTSS STAYMHLS SLTSEDSAVYFC (SEQ ID NO:1016)	WGQGTLVTVST (SEQ ID NO:1034)
6H6	EVKLEESGGGLVQP GGSMKLSCTASG (SEQ ID NO:985)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSK STVYLQMNSLRTED TGIYYC (SEQ ID NO:1018)	WGQGTLVTVSA (SEQ ID NO:1029)
7A9	LSCAASG (SEQ ID NO:986)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTISRDDSE SMLYLQMZNLKTED TAMYYC (SEQ ID NO:1019)	WGQGTLVTVSA (SEQ ID NO:1029)
7B3	QVQLQQSGAVLVK PGASVKLSCKASG (SEQ ID NO:987)	WVKQRPGRGPEW (SEQ ID NO:1003)	EKFRNKAILTVDKPS STAYMQLNSLTSED ZAVYYC (SEQ ID NO:1020)	WGQGTTLTVSS (SEQ ID NO:1031)
8A1	EVQLQQSGAELVK PGASVKISCKASG (SEQ ID NO:988)	WVKQRPGKGLEW (SEQ ID NO:1004)	GKFEGKATLTADKS SSTAYMQLSSLTSED SAVYFC (SEQ ID NO:1021)	WGQGTLVTVSA (SEQ ID NO:1029)
9F5	QVQLQQSGPELVK PGASLKISCKASG (SEQ ID NO:989)	WVKQRPGKGLEW (SEQ ID NO:1004)	GEFRVRATLTADTSS TTAYMQLSSLTSEDS AVYFC (SEQ ID NO:1022)	WGQGASVTVSS (SEQ ID NO:1036)
9G1	QVQLQQSGAELVK PGASVKLSCKASG (SEQ ID NO:981)	WVKQRPGRGPEW (SEQ ID NO:1003)	EKFKTKATLTVDKP SSTADMQLSSLTSED SAVYYC (SEQ ID NO:1023)	WGQGTTLTVSS (SEQ ID NO:1031)
9G3	EVQLVESGGGLVQP KGSLKLSCAAFG (SEQ ID NO:990)	WVRQTPGKGLEW (SEQ ID NO:1005)	DSVKDRFTISRDDSE SIVYVQMNNLKTED TGMYSC (SEQ ID NO:1024)	WGRGTLV (SEQ ID NO:1037)
10A9	QVQLQQSGAEVVK PGASVKMSCKTSG (SEQ ID NO:991)	WVKQRPGQGLV W (SEQ ID NO:1001)	ERFKTKATLTVDTSS STAYMHLSSLTSEDS AVYFC (SEQ ID NO:1025)	WGQGTLVTVSA (SEQ ID NO:1029)

11A8	EVQLVESGGRLVQP KGSLKLSCAASG (SEQ ID NO:992)	WVRQAPGKGLEW (SEQ ID NO:999)	DSVKDRFTISRDDSE SMLYLQMNNLKTE DTAMYYC (SEQ ID NO:1026)	WGQGTLVTVSA (SEQ ID NO:1029)
12D9	QVQLQQYGPELVK PGASVKMSCKVSG (SEQ ID NO:993)	WMKQSHGKSLE W (SEQ ID NO:1006)	QEFKGKATLTVDKS SS TAYMELRSLTFEDS AV YZC (SEQ ID NO:1027)	WGQGT (SEQ ID NO:1038)
12F9	WRIGQGKGSLKLA RAARG (SEQ ID NO:994)	RVRQGPGKGREW (SEQ ID NO:1007)	DSVKDRFRASRDDS ES MLYVQMSNWKQED T AMYYG (SEQ ID NO:1028)	WGQGTLVTVSA (SEQ ID NO:1029)
iOCi	GVQSEVKFEESGG GLVQPGGSMKLSC TASG (SEQ ID NO:1416)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSK SSVSLQMNSLRTED TGIYYC (SEQ ID NO:1419)	WGQGTLVTVSA (SEQ ID NO:1029)
7E9	QVQLQQSGPELVK PGASVKISCKTSG (SEQ ID NO:1417)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGKATLTVDRS SSTAYMELRSLTSED SAVYYC (SEQ ID NO:1420)	WGQGTSVTVSS (SEQ ID NO:1030)
SC3	QVQLQQSGPDLVKP GASVKISCKASG (SEQ ID NO:1418)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGKAILTVDKS SSTAYMELRSLTSED SAVYYC (SEQ ID NO:1421)	WGQGTTLTVSS (SEQ ID NO:1031)
1B4	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
6H2	QVQLQESGPGLVQP SQSLSIICTV (SEQ ID NO:1540)	WIRQSPGKGLEW (SEQ ID NO:1541)	AAFISRLNISKDNSK SQVFFKMNSLQSDD TAIYYC (SEQ ID NO:1543)	WGQGTLVTVSA (SEQ ID NO:1029)
7B11v1	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
7B11v2	EVQZQQSGPELVKP GASVKISCKA (SEQ ID NO:1605)	WVKQSLGKSLEW (SEQ ID NO:1613)	QKFKGKATLTVDKS SSTAYMELRSLTXEE SAVYYC (SEQ ID NO:1618)	RGTGTTVTV (SEQ ID NO:1626)

18D8	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
18E4v1	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
18E4v2	QVQLQQPGAELVK PGASVKVSCKA (SEQ ID NO:1606)	WVKEKPGQGLEW (SEQ ID NO:1614)	HNFKGKATLTVDKS SSTAYMQLNSLTSE DSAVYYC (SEQ ID NO:1619)	WGQGTSVTVSS (SEQ ID NO:1030)
29F6v1	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
29F6v2	QVQLQQSVAELVRP GASVKLSCTA (SEQ ID NO:1607)	WVKQRPEQGLEW (SEQ ID NO:1615)	PKFQATATITVATSS NSAYLQLSSLASEDT AIYYC (SEQ ID NO:1620)	WGHGTSVTVSS (SEQ ID NO:1627)
40D5v1	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
40D5v2	QVQLQQSGAELVK PGASVKVSCKA (SEQ ID NO:1608)	WVKQRPGQGLEW (SEQ ID NO:1616)	QKFKGKATLTVDKS SSTAYMQILSSLTSE DSAVYYC (SEQ ID NO:1621)	WSQGTLVTVS (SEQ ID NO:1628)
43B9	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
44A8	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
44B4v1	EVQLVESGGGLVKP GGSLKLSCEA (SEQ ID NO:1539)	WVRQTPEKRLEW (SEQ ID NO:995)	DSMKGRFTISRDNA KNFLYLQMSSLRSE DTAMYYC (SEQ ID NO:1542)	WGQGTTLTVSS (SEQ ID NO:1031)
44B4v2	XXXXXQSGTELARP GASVKMPCKA (SEQ ID NO:1609)	WVKQRPGQGLEW (SEQ ID NO:1616)	QKFKDKATLTADKS SSTAYMQLSSLTSEE SAVYYC (SEQ ID NO:1622)	WGTGTTVTVSS (SEQ ID NO:1033)

45D6	QVQLQQSGRELVKPGASVKMSCMSSG (SEQ ID NO:1610)	WVIQSHGESLEW (SEQ ID NO:1617)	QKFKGKATLTVNKSSSTAYMELRSLTSEDSAVYYC (SEQ ID NO:1623)	WGQGTSVTVSS (SEQ ID NO:1030)
29F7	QVKLEESGGGLVQPGGSMKLSCVASG (SEQ ID NO:1611)	WVRQSPEKGLEW (SEQ ID NO:998)	ESVKGRFTISRDDSKSSVYLQMNNLRAVDTGIYYC (SEQ ID NO:1624)	WGQGTTLTVSS (SEQ ID NO:1031)
32G1	QVQLQQSGPELVKPGASVQMSCEASG (SEQ ID NO:1612)	WVKQSHGKSLEW (SEQ ID NO:996)	QKFKGKATLTVNKSSSTAYIELRSLTSEDSAVYHC (SEQ ID NO:1625)	WGQGTLVTVSA (SEQ ID NO:1029)

TABLE D7: Humanized light chain variable region sequences

Antibody variant	Humanized sequences
Antibody 4D11	**Antibody 4D11**
4D11V3-15	EIVMTQSPATLSVSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIY NSKTFAEGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQHHYGTPPWTF GQGTKVEIK (SEQ ID NO:1040)
4D11V1-9	DIQLTQSPSFLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1041)
4D11V3-11	EIVLTQSPATLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIY NSKTFAEGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHYGTPPW TFGQGTKVEIK (SEQ ID NO:1042)
4D11V1-5	DIQMTQSPSTLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1043)
4D11V1-39	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1044)
4D11V1-33	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1045)
4D11V3-20	EIVLTQSPGTLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIY NSKTFAEGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHHYGTPPW TFGQGTKVEIK (SEQ ID NO:1046)
4D11V2-28	DIVMTQSPLSLPVTPGEPASISCRASENIYSFLAWYLQKPGQSPQLLIY NSKTFAEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1047)
4D11V2-30	DVVMTQSPLSLPVTLGQPASISCRASENIYSFLAWFQQRPGQSPRRLI YNSKTFAEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTP PWTFGQGTKVEIK (SEQ ID NO:1048)

Antibody variant	Humanized sequences
4D11V4-1	DIVMTQSPDSLAVSLGERATINCRASENIYSFLAWYQQKPGQPPKLLI YNSKTFAEGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHHYGTP PWTFGQGTKVEIK (SEQ ID NO:1049)
Antibody 7C5	**Antibody 7C5**
7C5V3-15	EIVMTQSPATLSVSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLI YNSKTFAEGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1040)
7C5V1-9	DIQLTQSPSFLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1041)
7C5V3-11	EIVLTQSPATLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIY NSKTFAEGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHYGTPPW TFGQGTKVEIK (SEQ ID NO:1042)
7C5V1-5	DIQMTQSPSTLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1043)
7C5V1-39	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1044)
7C5V1-33	DIQMTQSPSSLSASVGDRVTITCRASENIYSFLAWYQQKPGKAPKLLI YNSKTFAEGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1045)
7C5V3-20	EIVLTQSPGTLSLSPGERATLSCRASENIYSFLAWYQQKPGQAPRLLIY NSKTFAEGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHHYGTPPW TFGQGTKVEIK (SEQ ID NO:1046)
7C5V2-28	DIVMTQSPLSLPVTPGEPASISCRASENIYSFLAWYLQKPGQSPQLLIY NSKTFAEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPP WTFGQGTKVEIK (SEQ ID NO:1047)
7C5V2-30	DVVMTQSPLSLPVTLGQPASISCRASENIYSFLAWFQQRPGQSPRRLI YNSKTFAEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTP PWTFGQGTKVEIK (SEQ ID NO:1048)
7C5V4-1	DIVMTQSPDSLAVSLGERATINCRASENIYSFLAWYQQKPGQPPKLLI YNSKTFAEGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHHYGTP PWTFGQGTKVEIK (SEQ ID NO:1049)
Antibody 6G12	**Antibody 6G12**
6G12V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNCLAWYQQKPG QPPKLLIYWAFTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQ QYYSYPLTFGQ GTKVEIK (SEQ ID NO:1051)
6G12V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSNQKNCLAWFQQRPG QSPRRLIYWAFTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1052)

Antibody variant	Humanized sequences
6G12V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSNQKNCLAWYLQKPG QSPQLLIYWAFTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1053)
6G12V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWAFTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1054)
6G12V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWAFTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1055)
6G12V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPG QAPRLLIYWAFTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1056)
6G12V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWAFTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1057)
6G12V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWAFTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1058)
6G12V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPG QAPRLLIYWAFTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1059)
6G12V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPG QAPRLLIYWAFTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1060)
Antibody 8F11	**Antibody 8F11**
8F11V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTFLSWFQQRPGQS PRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1062)
8F11V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSNGKTFLSWYLQKPGQS PQLLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1063)
8F11V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSNGKTFLSWYQQKPGQ PPKLLIYLVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1064)
8F11V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1065)
8F11V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1066)

Antibody variant	Humanized sequences
8F11V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1067)
8F11V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1068)
8F11V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQ APRLLIYLVSKLDSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1069)
8F11V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQ APRLLIYLVSKLDSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1070)
8F11V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQA PRLLIYLVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1071)
Antibody 8E10	**Antibody 8E10**
8E10V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNWFQQRPGQ SPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1073)
8E10V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLDSDGKTYLNWYLQKPGQS PQLLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1074)
8E10V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLDSDGKTYLNWYQQKPGQ PPKLLIYLVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1075)
8E10V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCWQG THFPYTFGQGTKVEIK (SEQ ID NO:1076)
8E10V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1077)
8E10V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1078)
8E10V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1079)
8E10V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLDSDGKTYLNWYQQKPGQ APRLLIYLVSKLDSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCWQG THFPYTFGQGTKVEIK (SEQ ID NO:1080)

Antibody variant	Humanized sequences
8E10V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLDSDGKTYLNWYQQKPGQ APRLLIYLVSKLDSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1081)
8E10V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLDSDGKTYLNWYQQKPGQ APRLLIYLVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCWQ GTHFPYTFGQGTKVEIK (SEQ ID NO:1082)
Antibody 7E5	**Antibody 7E5**
7E5V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTFLSWFQQRPGQS PRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1062)
7E5V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSNGKTFLSWYLQKPGQS PQLLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1063)
7E5V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSNGKTFLSWYQQKPGQ PPKLLIYLVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1064)
7E5V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1065)
7E5V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1066)
7E5V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKA PKLLIYLVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCMQGT HFPLTFGQGTKVEIK (SEQ ID NO:1067)
7E5V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGKA PKLLIYLVSKLDSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCMQGT HFPLTFGQGTKVEIK (SEQ ID NO:1068)
7E5V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQ APRLLIYLVSKLDSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1069)
7E5V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQA PRLLIYLVSKLDSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCMQGT HFPLTFGQGTKVEIK (SEQ ID NO:1070)
7E5V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQA PRLLIYLVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1071)
Antibody 7F8	**Antibody 7F8**
7F8V3-11	EIVLTQSPATLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYL TSILASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1084)

Antibody variant	Humanized sequences
7F8V1-39	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1085)
7F8V1-5	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1086)
7F8V3-15	EIVMTQSPATLSVSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLI YLTSILASGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1087)
7F8V1-9	DIQLTQSPSFLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYL TSILASGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1088)
7F8V1-33	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1089)
7F8V3-20	EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYL TSILASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1090)
7F8V2-28	DIVMTQSPLSLPVTPGEPASISCSASSSVSYMYWYLQKPGQSPQLLIY LTSILASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1091)
7F8V2-30	DVVMTQSPLSLPVTLGQPASISCSASSSVSYMYWFQQRPGQSPRRLIY LTSILASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1092)
7F8V4-1	DIVMTQSPDSLAVSLGERATINCSASSSVSYMYWYQQKPGQPPKLLI YLTSILASGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1093)
Antibody 8F8	**Antibody 8F8**
8F8V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGNTYLHWFQQRPGQS PRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQS THVPLTFGQGTKVEIK (SEQ ID NO:1095)
8F8V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQ SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQ STHVPLTFGQGTKVEIK (SEQ ID NO:1096)
8F8V4-1	DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGNTYLHWYQQKPGQ PPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQS THVPLTFGQGTKVEIK (SEQ ID NO:1097)
8F8V3-11	EIVLTQSPATLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQST HVPLTFGQGTKV EIK (SEQ ID NO:1098)

Antibody variant	Humanized sequences
8F8V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQS THVPLTFGQGTKVEIK (SEQ ID NO:1099)
8F8V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQST HVPLTFGQGTKVEIK (SEQ ID NO:1100)
8F8V3-15	EIVMTQSPATLSVSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQA PRLLIYKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQSTHVP LTFGQGTKVEIK (SEQ ID NO:1101)
8F8V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQS THVPLTFGQGTKVEIK (SEQ ID NO:1102)
8F8V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQST HVPLTFGQGTKVEIK (SEQ ID NO:1103)
8F8V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQA PRLLIYKVSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQSTH VPLTFGQGTKVEIK (SEQ ID NO:1104)
AntibodylH7	**Antibody1H7**
1H7V1-39	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1085)
1H7V3-11	EIVLTQSPATLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYL TSILASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQWSFNPYTFGQ GTKVEIK(SEQ ID NO:1084)
1H7V1-5	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILA SGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQWSFNPYTFGQGTK VEIK (SEQ ID NO:1086)
1H7V1-9	DIQLTQSPSFLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYL TSILASGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1088)
1H7V3-15	EIVMTQSPATLSVSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLI YLTSILASGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1087)
1H7V1-33	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1089)
1H7V3-20	EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYL TSILASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1090)

Antibody variant	Humanized sequences
1H7V2-28	DIVMTQSPLSLPVTPGEPASISCSASSSVSYMYWYLQKPGQSPQLLIY LTSILASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1091)
1H7V2-30	DVVMTQSPLSLPVTLGQPASISCSASSSVSYMYWFQQRPGQSPRRLIY LTSILASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1092)
1H7V4-1	DIVMTQSPDSLAVSLGERATINCSASSSVSYMYWYQQKPGQPPKLLI YLTSILASGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1093)
Antibody 2H8	**Antibody 2H8**
2H8V3-11	EIVLTQSPATLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYL TSILASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1084)
2H8V1-39	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1085)
2H8V1-5	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1086)
2H8V3-15	EIVMTQSPATLSVSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLI YLTSILASGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1087)
2H8V1-9	DIQLTQSPSFLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLIYL TSILASGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1088)
2H8V1-33	DIQMTQSPSSLSASVGDRVTITCSASSSVSYMYWYQQKPGKAPKLLI YLTSILASGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1089)
2H8V3-20	EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYL TSILASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWSFNPYTFGQ GTKVEIK (SEQ ID NO:1090)
2H8V2-28	DIVMTQSPLSLPVTPGEPASISCSASSSVSYMYWYLQKPGQSPQLLIY LTSILASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1091)
2H8V2-30	DVVMTQSPLSLPVTLGQPASISCSASSSVSYMYWFQQRPGQSPRRLIY LTSILASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQWSFNPYT FGQGTKVEIK (SEQ ID NO:1092)
2H8V4-1	DIVMTQSPDSLAVSLGERATINCSASSSVSYMYWYQQKPGQPPKLLI YLTSILASGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQWSFNPY TFGQGTKVEIK (SEQ ID NO:1093)
Antibody 3A2	**Antibody 3A2**

Antibody variant	Humanized sequences
3A2 V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQTIIHSNGNTYLEWFQQRPGQS PRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1108)
3A2 V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQTIIHSNGNTYLEWYLQKPGQSP QLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1109)
3A2 V4-1	DIVMTQSPDSLAVSLGERATINCRSSQTIIHSNGNTYLEWYQQKPGQ PPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCFQ GSHVPYTFGQGTKVEIK (SEQ ID NO:1110)
3A2 V3-11	EIVLTQSPATLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAP RLLIYKVSNRFSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCFQGSH VPYTFGQGTKVEIK (SEQ ID NO:1111)
3A2 I-9	DIQLTQSPSFLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1112)
3A2 I-33	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1113)
3A2 VI -39	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1114)
3A2 V3-15	EIVMTQSPATLSVSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1115)
3A2 VI -5	DIQMTQSPSTLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1116)
3A2 V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQA PRLLIYKVSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCFQGS HVPYTFGQGTKV EIK (SEQ ID NO:1117)
Antibody 3A7	**Antibody 3A7**
3A7 V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTFLSWFQQRPGQS PRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1062)
3A7 V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSNGKTFLSWYLQKPGQS PQLLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1063)
3A7 V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSNGKTFLSWYQQKPGQ PPKLLIYLVSKLDSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1064)

Antibody variant	Humanized sequences
3A7 VI -39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1067)
3A7 I-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1066)
3A7 I-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1065)
3A7 VI -33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSNGKTFLSWYQQKPGK APKLLIYLVSKLDSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1068)
3A7 V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQ APRLLIYLVSKLDSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCMQG THFPLTFGQGTKVEIK (SEQ ID NO:1069)
3A7 V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQ APRLLIYLVSKLDSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1070)
3A7 V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSNGKTFLSWYQQKPGQ APRLLIYLVSKLDSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCMQ GTHFPLTFGQGTKVEIK (SEQ ID NO:1071)
Antibody 3B10	**Antibody 3B10**
3B10V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSDQKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQ QYYSYPLTFGQ GTKVEIK (SEQ ID NO:1120)
3B10V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSDQKNYLAWYLQKPG QSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1121)
3B10V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSDQKNYLAWFQQRPG QSPRRLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1122)
3B10V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1123)
3B10V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1124)
3B10V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1125)

Antibody variant	Humanized sequences
3B10V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1126)
3B10V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1127)
3B10V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1128)
3B10V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPG QAPRLLIYWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1129)
Antibody 4F11	**Antibody 4F11**
4F11V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQTIIHSNGNTYLEWFQQRPGQS PRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQ GSHVPYTFGQGTKVEIK (SEQ ID NO:1108)
4F11V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQTIIHSNGNTYLEWYLQKPGQSP QLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1109)
4F11V4-1	DIVMTQSPDSLAVSLGERATINCRSSQTIIHSNGNTYLEWYQQKPGQPP KLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCFQGSHV PYTFGQGTKVEIK (SEQ ID NO:1110)
4F11V3-11	EIVLTQSPATLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAP RLLIYKVSNRFSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCFQGSHV PYTFGQGTKVEIK (SEQ ID NO:1111)
4F11V3-15	EIVMTQSPATLSVSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1115)
4F11V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1113)
4F11V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1114)
4F11V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1112)
4F11V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1116)

Antibody variant	Humanized sequences
4F11V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAP RLLIYKVSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCFQGSH VPYTFGQGTKV EIK (SEQ ID NO:1117)
Antibody 6H6	**Antibody 6H6**
6H6V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSVFYSSNQKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCH QYLSSLTFGQGTKVEIK (SEQ ID NO:1500)
6H6V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSVFYSSNQKNYLAWYLQKPGQ SPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1501)
6H6V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSVFYSSNQKNYLAWFQQRPG QSPRRLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCH QYLSSLTFGQGTKVEIK (SEQ ID NO:1502)
6H6V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCH QYLSSLTFGQGTKVEIK (SEQ ID NO:1503)
6H6V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1504)
6H6V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1505)
6H6V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1506)
6H6V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1507)
6H6V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1508)
6H6V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPG QAPRLLIYWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1509)
Antibody 7A9	**Antibody 7A9**
7A9V1-9	DIQLTQSPSFLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLI YKAKTLAEGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQHHYGTPF TFGQGTKVEIK (SEQ ID NO:1132)
7A9V3-11	EIVLTQSPATLSLSPGERATLSCRASENIYSYLAWYQQKPGQAPRLLI YKAKTLAEGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHYGTPF TFGQGTKVEIK (SEQ ID NO:1133)

Antibody variant	Humanized sequences
7A9V1-5	DIQMTQSPSTLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLL IYKAKTLAEGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHHYGTP FTFGQGTKVEIK (SEQ ID NO:1134)
7A9V3-15	EIVMTQSPATLSVSPGERATLSCRASENIYSYLAWYQQKPGQAPRLLI YKAKTLAEGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQHHYGTPF TFGQGTKVEIK (SEQ ID NO:1135)
7A9V1-39	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLI YKAKTLAEGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHHYGTPF TFGQGTKVEIK (SEQ ID NO:1136)
7A9V1-33	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLI YKAKTLAEGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQHHYGTPFT FGQGTKVEIK (SEQ ID NO:1137)
7A9V3-20	EIVLTQSPGTLSLSPGERATLSCRASENIYSYLAWYQQKPGQAPRLLI YKAKTLAEGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHHYGTPF TFGQGTKVEIK (SEQ ID NO:1138)
7A9V2-28	DIVMTQSPLSLPVTPGEPASISCRASENIYSYLAWYLQKPGQSPQLLIY KAKTLAEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGTPF TFGQGTKVEIK (SEQ ID NO:1139)
7A9V4-1	DIVMTQSPDSLAVSLGERATINCRASENIYSYLAWYQQKPGQPPKLL IYKAKTLAEGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHHYGT PFTFGQGTKVEIK (SEQ ID NO:1140)
7A9V2-30	DVVMTQSPLSLPVTLGQPASISCRASENIYSYLAWFQQRPGQSPRRLI YKAKTLAEGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHHYGT PFTFGQGTKVEIK (SEQ ID NO:1141)
Antibody 8A1	**Antibody 8A1**
8A1V3-15	EIVMTQSPATLSVSPGERATLSCRTSENVYSNLAWYQQKPGQAPRLL IYAATNLADGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCHHFWGTP YTFGQGTKVEIK (SEQ ID NO:1143)
8A1V3-11	EIVLTQSPATLSLSPGERATLSCRTSENVYSNLAWYQQKPGQAPRLLI YAATNLADGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHHFWGTPY TFGQGTKVEIK (SEQ ID NO:1144)
8A1V1-9	DIQLTQSPSFLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLLI YAATNLADGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCHHFWGTPY TFGQGTKVEIK (SEQ ID NO:1145)
8A1V1-5	DIQMTQSPSTLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLL IYAATNLADGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCHHFWGTP YTFGQGTKVEIK (SEQ ID NO:1146)
8A1V1-39	DIQMTQSPSSLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLL IYAATNLADGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHHFWGTP YTFGQGTKVEIK (SEQ ID NO:1147)

Antibody variant	Humanized sequences
8A1V1-33	DIQMTQSPSSLSASVGDRVTITCRTSENVYSNLAWYQQKPGKAPKLL IYAATNLADGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHHFWGTP YTFGQGTKVEIK (SEQ ID NO:1148)
8A1V3-20	EIVLTQSPGTLSLSPGERATLSCRTSENVYSNLAWYQQKPGQAPRLLI YAATNLADGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCHHFWGTPY TFGQGTKVEIK (SEQ ID NO:1149)
8A1V2-28	DIVMTQSPLSLPVTPGEPASISCRTSENVYSNLAWYLQKPGQSPQLLIY AATNLADGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHHFWGTP YTFGQGTKVEIK (SEQ ID NO:1150)
8A1V2-30	DVVMTQSPLSLPVTLGQPASISCRTSENVYSNLAWFQQRPGQSPRRLI YAATNLADGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCHHFWGTP YTFGQGTKVEIK (SEQ ID NO:1151)
8A1V4-1	DIVMTQSPDSLAVSLGERATINCRTSENVYSNLAWYQQKPGQPPKLL IYAATNLADGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHHFWGT PYTFGQGTKVEIK (SEQ ID NO:1152)
Antibody 9F5	**Antibody 9F5**
9F5V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGYTYLHWFQQRPGQ SPRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQ STRVPYTFGQGTKVEIK (SEQ ID NO:1154)
9F5V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGYTYLHWYLQKPGQ SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQ STRVPYTFGQGTKVEIK (SEQ ID NO:1155)
9F5V4-1	DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGYTYLHWYQQKPGQ PPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQS TRVPYTFGQGTKVEIK (SEQ ID NO:1156)
9F5V3-11	EIVLTQSPATLSLSPGERATLSCRSSQSLVHSNGYTYLHWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQST RVPYTFGQGTKVEIK (SEQ ID NO:1157)
9F5V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQST RVPYTFGQGTKVEIK (SEQ ID NO:1158)
9F5V3-15	EIVMTQSPATLSVSPGERATLSCRSSQSLVHSNGYTYLHWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQST RVPYTFGQGTKVEIK (SEQ ID NO:1159)
9F5V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPG KAPKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQ STRVPYTFGQGTKVEIK (SEQ ID NO:1160)
9F5V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQS TRVPYTFGQGTKVEIK (SEQ ID NO:1161)

Antibody variant	Humanized sequences
9F5V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQSLVHSNGYTYLHWYQQKPGKA PKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQSTR VPYTFGQGTKVEIK (SEQ ID NO:1162)
9F5V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQSLVHSNGYTYLHWYQQKPGQ APRLLIYKVSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQST RVPYTFGQGTKVEIK (SEQ ID NO:1163)
9F5-L1	DIVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYLQKPGQ SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQ STRVPYTFGQGTKLEIK (SEQ ID NO:1663)
9F5-L2	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYLQKPGQ SPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQ STRVPYTFGQG TKLEIK (SEQ ID NO:1664)
Antibody 9G1	**Antibody 9G1**
9G1V2-30	DVVMTQSPLSLPVTLGQPASISCRFSQSLVHSNGNTYLHWFQQRPGQ SPRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQ STRVPPTFGQGTKVEIK (SEQ ID NO:1165)
9G1V2-28	DIVMTQSPLSLPVTPGEPASISCRFSQSLVHSNGNTYLHWYLQKPGQSPQ LLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTRVP PTFGQGTKVEIK (SEQ ID NO:1166)
9G1V4-1	DIVMTQSPDSLAVSLGERATINCRFSQSLVHSNGNTYLHWYQQKPGQ PPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQS TRVPPTFGQGTKVEIK (SEQ ID NO:1167)
9G1V3-11	EIVLTQSPATLSLSPGERATLSCRFSQSLVHSNGNTYLHWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQST RVPPTFGQGTKV EIK (SEQ ID NO:1168)
9G1V3-15	EIVMTQSPATLSVSPGERATLSCRFSQSLVHSNGNTYLHWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQS TRVPPTFGQGTKVEIK (SEQ ID NO:1169)
9G1V1-9	DIQLTQSPSFLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQST RVPPTFGQGTKVEIK (SEQ ID NO:1170)
9G1V1-5	DIQMTQSPSTLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQST RVPPTFGQGTKVEIK (SEQ ID NO:1171)
9G1V1-39	DIQMTQSPSSLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGKAP KLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTRVPP TFGQGTKVEIK (SEQ ID NO:1172)
9G1V1-33	DIQMTQSPSSLSASVGDRVTITCRFSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQST RVPPTFGQGTKVEIK (SEQ ID NO:1173)

Antibody variant	Humanized sequences
9G1V3-20	EIVLTQSPGTLSLSPGERATLSCRFSQSLVHSNGNTYLHWYQQKPGQ APRLLIYKVSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQS TRVPPTFGQGTKV EIK (SEQ ID NO:1174)
Antibody 9G3	**Antibody 9G3**
9G3V1-33	DIQMTQSPSSLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIY FTSNLPSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSGEVTQFTFGQG TKVEIK(SEQ ID NO:1176)
9G3V1-9	DIQLTQSPSFLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIY FTSNLPSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSGEVTQFTFGQ GTKVEIK(SEQ ID NO:1177)
9G3V1-39	DIQMTQSPSSLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIY FTSNLPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSGEVTQFTFGQ GTKVEIK (SEQ ID NO:1178)
9G3V3-11	EIVLTQSPATLSLSPGERATLSCKASSNVNYMSWYQQKPGQAPRLLIYF TSNLPSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSGEVTQFTFGQG TKVEIK (SEQ ID NO:1641)
9G3V1-5	DIQMTQSPSTLSASVGDRVTITCKASSNVNYMSWYQQKPGKAPKLLIYF TSNLPSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSGEVTQFTFGQGT KVEIK (SEQ ID NO:1179)
9G3V3-15	EIVMTQSPATLSVSPGERATLSCKASSNVNYMSWYQQKPGQAPRLLIY FTSNLPSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSGEVTQFTFGQG TKVEIK (SEQ ID NO:1180)
9G3V3-20	EIVLTQSPGTLSLSPGERATLSCKASSNVNYMSWYQQKPGQAPRLLIYF TSNLPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSGEVTQFTFGQG TKVEIK (SEQ ID NO:1181)
9G3V2-28	DIVMTQSPLSLPVTPGEPASISCKASSNVNYMSWYLQKPGQSPQLLIY FTSNLPSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSGEVTQFTF GQGTKVEIK (SEQ ID NO:1182)
9G3V2-30	DVVMTQSPLSLPVTLGQPASISCKASSNVNYMSWFQQRPGQSPRRLIYF TSNLPSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSGEVTQFTFGQ GTKVEIK (SEQ ID NO:1183)
9G3V4-1	DIVMTQSPDSLAVSLGERATINCKASSNVNYMSWYQQKPGQPPKLLI YFTSNLPSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSGEVTQFTF GQGTKVEIK (SEQ ID NO:1184)
Antibody10A9	**Antibody10A9**
10A9V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQTIIHSNGNTYLEWFQQRPGQSPRR LIYKVSNRFCGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPY TFGQGTKVEIK (SEQ ID NO:1186)
10A9V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQTIIHSNGNTYLEWYLQKPGQSP QLLIYKVSNRFCGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1187)

Antibody variant	Humanized sequences
10A9V4-1	DIVMTQSPDSLAVSLGERATINCRSSQTIIHSNGNTYLEWYQQKPGQP PKLLIYKVSNRFCGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1188)
10A9V3-11	EIVLTQSPATLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAP RLLIYKVSNRFCGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCFQGSH VPYTFGQGTKV EIK (SEQ ID NO:1189)
10A9V3-15	EIVMTQSPATLSVSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQ APRLLIYKVSNRFCGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCFQG SHVPYTFGQGTKVEIK (SEQ ID NO:1190)
10A9V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPG KAPKLLIYKVSNRFCGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCF QGSHVPYTFGQGTKVEIK (SEQ ID NO:1191)
10A9V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQTIIHSNGNTYLEWYQQKPGQAP RLLIYKVSNRFCGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCFQGSH VPYTFGQGTKV EIK (SEQ ID NO:1192)
10A9V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFCGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1193)
10A9V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFCGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1194)
10A9V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQTIIHSNGNTYLEWYQQKPGKA PKLLIYKVSNRFCGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGS HVPYTFGQGTKVEIK (SEQ ID NO:1195)
Antibody11A8	**Antibody11A8**
11A8V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQKKYLTWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQ NDYGFPLTFGQ GTKVEIK (SEQ ID NO:1197)
11A8V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLNSGNQKKYLTWFQQRPG QSPRRLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQ NDYGFPLTFGQGTKVEIK (SEQ ID NO:1198)
11A8V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLNSGNQKKYLTWYLQKPG QSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QNDYGFPLTFGQ GTKVEIK (SEQ ID NO:1199)
11A8V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQN DYGFPLTFGQGTKVEIK (SEQ ID NO:1200)
11A8V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLNSGNQKKYLTWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQN DYGFPLTFGQGTKVEIK (SEQ ID NO:1201)

Antibody variant	Humanized sequences
11A8V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLNSGNQKKYLTWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQN DYGFPLTFGQGTKVEIK (SEQ ID NO:1202)
11A8V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQ NDYGFPLTFGQGTKVEIK (SEQ ID NO:1203)
11A8V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLNSGNQKKYLTWYQQKPG QAPRLLIYWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQN DYGFPLTFGQGTKVEIK (SEQ ID NO:1204)
11A8V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQ NDYGFPLTFGQGTKVEIK (SEQ ID NO:1205)
11A8V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLNSGNQKKYLTWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ NDYGFPLTFGQGTKVEIK (SEQ ID NO:1206)
Antibody12D9	**Antibody12D9**
12D9V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSGNQKNFLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQ QYYSYPFTFGQ GTKVEIK (SEQ ID NO:1208)
12D9V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSGNQKNFLAWYLQKPGQ SPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQ YYSYPFTFGQGTKVEIK (SEQ ID NO:1209)
12D9V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSGNQKNFLAWFQQRPG QSPRRLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQ QYYSYPFTFGQGTKVEIK (SEQ ID NO:1210)
12D9V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQ YYSYPFTFGQGTKVEIK (SEQ ID NO:1211)
12D9V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQ QYYSYPFTFGQGTKVEIK (SEQ ID NO:1212)
12D9V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSGNQKNFLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQ YYSYPFTFGQGTKVEIK (SEQ ID NO:1213)
12D9V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YYSYPFTFGQGTKVEIK (SEQ ID NO:1214)
12D9V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSGNQKNFLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQ YYSYPFTFGQGTKVEIK (SEQ ID NO:1215)

Antibody variant	Humanized sequences
12D9V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSGNQKNFLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ QYYSYPFTFGQGTKVEIK (SEQ ID NO:1216)
12D9V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSGNQKNFLAWYQQKPG QAPRLLIYWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YYSYPFTFGQGTKVEIK (SEQ ID NO:1217)
Antibody12F9	**Antibody12F9**
12F9V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSDQKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQ QYYSYPLTFGQ GTKVEIK (SEQ ID NO:1120)
12F9V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSDQKNYLAWYLQKPG QSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1121)
12F9V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSDQKNYLAWFQQRPG QSPRRLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1122)
12F9V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1125)
12F9V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1123)
12F9V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1124)
12F9V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1128)
12F9V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1127)
12F9V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSDQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1126)
12F9V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSDQKNYLAWYQQKPG QAPRLLIYWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1129)
Antibody10C1	**Antibody10C1**
10C1V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSVFYSSNQKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCH QYLSSLTFGQGTKVEIK (SEQ ID NO:1423)

Antibody variant	Humanized sequences
10C1V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSVFYSSNQKNYLAWFQQRPG QSPRRLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCH QYLSSLTFGQGTKVEIK (SEQ ID NO:1424)
10C1V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSVFYSSNQKNYLAWYLQKPGQ SPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCH QYLSSLTFGQGTKVEIK (SEQ ID NO:1425)
10C1V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1426)
10C1V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1427)
10C1V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCH QYLSSLTFGQGTKVEIK (SEQ ID NO:1428)
10C1V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1429)
10C1V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1430)
10C1V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSVFYSSNQKNYLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1431)
10C1V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSVFYSSNQKNYLAWYQQKPG QAPRLLIYWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCHQ YLSSLTFGQGTKVEIK (SEQ ID NO:1432)
Antibody 7E9	**Antibody 7E9**
7E9V4-1	DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNCLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQ QYYSYPLTFGQ GTKVEIK (SEQ ID NO:1434)
7E9V2-28	DIVMTQSPLSLPVTPGEPASISCKSSQSLLYSSNQKNCLAWYLQKPG QSPQLLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1435)
7E9V2-30	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSSNQKNCLAWFQQRPG QSPRRLIYWASTRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC QQYYSYPLTFGQ GTKVEIK (SEQ ID NO:1436)
7E9V1-9	DIQLTQSPSFLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1437)

Antibody variant	Humanized sequences
7E9V3-15	EIVMTQSPATLSVSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1438)
7E9V1-5	DIQMTQSPSTLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQ QYYSYPLTFGQGTKVEIK (SEQ ID NO:1439)
7E9V1-33	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1440)
7E9V1-39	DIQMTQSPSSLSASVGDRVTITCKSSQSLLYSSNQKNCLAWYQQKPG KAPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1441)
7E9V3-11	EIVLTQSPATLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPG QAPRLLIYWASTRESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1442)
7E9V3-20	EIVLTQSPGTLSLSPGERATLSCKSSQSLLYSSNQKNCLAWYQQKPG QAPRLLIYWASTRESGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YYSYPLTFGQGTKVEIK (SEQ ID NO:1443)
Antibody 8C3	**Antibody 8C3**
8C3V2-30	DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGNTYLHWFQQRPGQ SPRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQ STHVPPTFGQGTKVEIK (SEQ ID NO:1445)
8C3V2-28	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQSP QLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV PPTFGQGTKVEIK (SEQ ID NO:1446)
8C3V4-1	DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGNTYLHWYQQKPGQ PPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQS THVPPTFGQGTKVEIK (SEQ ID NO:1447)
8C3V3-11	EIVLTQSPATLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQST HVPPTFGQGTKVEIK (SEQ ID NO:1448)
8C3V1-33	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCSQS THVPPTFGQGTKVEIK (SEQ ID NO:1449)
8C3V1-5	DIQMTQSPSTLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCSQST HVPPTFGQGTKVEIK (SEQ ID NO:1450)
8C3V1-39	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQS THVPPTFGQGTKVEIK (SEQ ID NO:1451)

Antibody variant	Humanized sequences
8C3V1-9	DIQLTQSPSFLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGK APKLLIYKVSNRFSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCSQS THVPPTFGQGTKVEIK (SEQ ID NO:1452)
8C3V3-15	EIVMTQSPATLSVSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQ APRLLIYKVSNRFSGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCSQST HVPPTFGQGTKVEIK (SEQ ID NO:1453)
8C3V3-20	EIVLTQSPGTLSLSPGERATLSCRSSQSLVHSNGNTYLHWYQQKPGQ APRLLIYKVSNRFSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCSQST HVPPTFGQGTKVEIK (SEQ ID NO:1454)

TABLE D8: Humanized heavy chain variable region sequences

Antibody variant	Humanized sequences
Antibody 4D11	**Antibody 4D11**
4D11V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEW VASISRGGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC TRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1220)
4D11V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1221)
4D11V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1222)
4D11V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1222)
4D11V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1223)
4D11V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTLSSYAMSWVRQAPGQGLE WVASISRGGSTYYPQKFQGRVTITADESTSTAYMELSSLRSEDTAVYY CTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1224)
4D11V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTLSSYAMSWVRQAPGQGLE WVASISRGGSTYYPQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1225)
4D11V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTLSSYAMSWVRQMPGKGLE WVASISRGGSTYYPPSFQGQVTISADKSISTAYLQWSSLKASDTAMYY CTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1226)
4D11V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEW VASISRGGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC TRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1227)

Antibody variant	Humanized sequences
4D11V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTLSSYAMSWIRQPPGKGLEW VASISRGGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC TRGYGYYRTP FANWGQGTLVTVSS (SEQ ID NO:1228)
Antibody 7C5	**Antibody 7C5**
7C5V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEW VASISRGGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC TRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1220)
7C5V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1221)
7C5V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1222)
7C5V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1222)
7C5V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTLSSYAMSWVRQAPGKGLE WVASISRGGSTYYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1223)
7C5V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTLSSYAMSWVRQAPGQGLE WVASISRGGSTYYPQKFQGRVTITADESTSTAYMELSSLRSEDTAVY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1224)
7C5V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTLSSYAMSWVRQAPGQGL EWVASISRGGSTYYPQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAV YYCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1225)
7C5V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTLSSYAMSWVRQMPGKGLE WVASISRGGSTYYPPSFQGQVTISADKSISTAYLQWSSLKASDTAMY YCTRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1226)
7C5V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTLSSYAMSWIRQPPGKGLEW VASISRGGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC TRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1227)
7C5V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTLSSYAMSWIRQPPGKGLEW VASISRGGSTYYPPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC TRGYGYYRTPFANWGQGTLVTVSS (SEQ ID NO:1228)
Antibody 6G12	**Antibody 6G12**
6G12V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTMHWVRQAPGQGL EWIGGINPNNGGTSYSQKFQGRVTMTRDTSTSTVYMELSSLRSEDTA VYYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1230)
6G12V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTEYTMHWVRQMPGKGLE WIGGINPNNGGTSYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMY YCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1231)

Antibody variant	Humanized sequences
6G12V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTEYTMHWVRQAPGQGL EWIGGINPNNGGTSYSQKFQGRVTITADESTSTAYMELSSLRSEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1232)
6G12V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1233)
6G12V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTEYTMHWVRQAPGKGL EWIGGINPNNGGTSYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1234)
6G12V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1235)
6G12V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1235)
6G12V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEW IGGINPNNGGTSYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1236)
6G12V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLEWI GGINPNNGGTSYSAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCA RGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1237)
6G12V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEWIGG INPNNGGTSYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGG SHYYAMDYWGQGTLVTVSS (SEQ ID NO:1238)
Antibody 8E10	**Antibody 8E10**
8E10V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGLEWI GVIDPETGGTAYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCTS PDYYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1240)
8E10V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTDYEMHWVRQMPGKGLEWIG VIDPETGGTAYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTSPD YYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1241)
8E10V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIG VIDPETGGTAYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTSP DYYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1242)
8E10V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIG VIDPETGGTAYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTSP DYYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1243)
8E10V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYEMHWVRQAPGQGLEWI GVIDPETGGTAYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCTSP DYYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1244)

Antibody variant	Humanized sequences
8E10V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIG VIDPETGGTAYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTSP DYYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1245)
8E10V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIG VIDPETGGTAYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTSP DYYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1245)
8E10V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTDYEMHWIRQPPGKGLEWIGVI DPETGGTAYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1246)
8E10V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTDYEMHWVRQAPGKGLEWIG VIDPETGGTAYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSP DYYGSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1247)
8E10V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYTFTDYEMHWIRQPPGKGLEWIGVI DPETGGTAYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTSPDYY GSSYPLYYAMDYWGQGTLVTVSS (SEQ ID NO:1248)
Antibody 7E5	**Antibody 7E5**
7E5V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1250)
7E5V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1251)
7E5V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1252)
7E5V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1251)
7E5V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1253)
7E5V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMGWVRQAPGQGLEWV AEIRDKVKNHATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC RLGVFDYWGQGTLVTVSS (SEQ ID NO:1254)
7E5V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMGWVRQAPGQGLEW VAEIRDKVKNHATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCRLGVFDYWGQGTLVTVSS (SEQ ID NO:1255)
7E5V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMGWVRQMPGKGLEWV AEIRDKVKNHATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC RLGVFDYWGQGTLVTVSS (SEQ ID NO:1256)

Antibody variant	Humanized sequences
7E5V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAE IRDKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRL GVFDYWGQGTLVTVSS (SEQ ID NO:1257)
7E5V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAE IRDKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRL GVFDYWGQGTLVTVSS (SEQ ID NO:1258)
Antibody 7F8	**Antibody 7F8**
7F8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1260)
7F8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
7F8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1262)
7F8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
7F8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1263)
7F8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFSFNTYAMNWVRQAPGQGLEWI ARIRSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC VRHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1264)
7F8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYAMNWVRQMPGKGLEWIA RIRSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1265)
7F8V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFSFNTYAMNWVRQAPGQGLEWI ARIRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC VRHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1266)
7F8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARI RSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1267)
7F8V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARI RSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1268)
Antibody 8F8	**Antibody 8F8**
8F8V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTVSRYWMHWVRQAPGQGLEWI GRIDPNSGGTKYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVL TGTDFDYWGQGTLVTVSS (SEQ ID NO:1270)

Antibody variant	Humanized sequences
8F8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWI GRIDPNSGGTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVL TGTDFDYWGQGTLVTVSS (SEQ ID NO:1271)
8F8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTVSRYWMHWVRQAPGQGLEWI GRIDPNSGGTKYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVLT GTDFDYWGQGTLVTVSS (SEQ ID NO:1272)
8F8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTVSRYWMHWVRQMPGKGLEWI GRIDPNSGGTKYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVLT GTDFDYWGQGTLVTVSS (SEQ ID NO:1273)
8F8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWI GRIDPNSGGTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVL TGTDFDYWGQGTLVTVSS (SEQ ID NO:1274)
8F8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWI GRIDPNSGGTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVL TGTDFDYWGQGTLVTVSS (SEQ ID NO:1275)
8F8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWI GRIDPNSGGTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVL TGTDFDYWGQGTLVTVSS (SEQ ID NO:1274)
8F8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTVSRYWMHWIRQPPGKGLEWIGR IDPNSGGTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1276)
8F8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTVSRYWMHWVRQAPGKGLEWI GRIDPNSGGTKYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVL TGTDFDYWGQGTLVTVSS (SEQ ID NO:1277)
8F8V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYTVSRYWMHWIRQPPGKGLEWIGR IDPNSGGTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVLTGT DFDYWGQGTLVTVSS (SEQ ID NO:1278)
Antibody1H7	**Antibody1H7**
1H7V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1260)
1H7V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1262)
1H7V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
1H7V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)

Antibody variant	Humanized sequences
1H7V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1263)
1H7V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYAMNWVRQMPGKGLEWIA RIRSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1265)
1H7V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFSFNTYAMNWVRQAPGQGLEWI ARIRSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC VRHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1264)
1H7V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFSFNTYAMNWVRQAPGQGLEWI ARIRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC VRHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1266)
1H7V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARI RSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1267)
1H7V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARI RSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1268)
Antibody 2H8	**Antibody 2H8**
2H8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1260)
2H8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
2H8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1262)
2H8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1261)
2H8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFSFNTYAMNWVRQAPGKGLEWIA RIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1263)
2H8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYAMNWVRQMPGKGLEWIA RIRSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCV RHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1265)
2H8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFSFNTYAMNWVRQAPGQGLEWI ARIRSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC VRHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1264)

Antibody variant	Humanized sequences
2H8V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFSFNTYAMNWVRQAPGQGLEWI ARIRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC VRHGDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1266)
2H8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARI RSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1267)
2H8V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFSFNTYAMNWIRQPPGKGLEWIARI RSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRH GDGNLWYIDVWGQGTLVTVSS (SEQ ID NO:1268)
Antibody 3A2	**Antibody 3A2**
3A2V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYPFSNFWITWVRQMPGKGLEWIGD IYPGSDNSNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAREAY YTNPGFAYWGQGTLVTVSS (SEQ ID NO:1282)
3A2V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYPFSNFWITWVRQAPGQGLEWIG DIYPGSDNSNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1283)
3A2V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYPFSNFWITWVRQAPGQGLEWIG DIYPGSDNSNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARE AYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1284)
3A2V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1285)
3A2V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIG DIYPGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARE AYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1286)
3A2V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1285)
3A2V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1287)
3A2V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIY PGSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1288)
IGHV3-15	EVQLVESGGGLVKPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1289)
3A2V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIY PGSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1290)
Antibody 3A7	**Antibody 3A7**

Antibody variant	Humanized sequences
3A7V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1250)
3A7V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1251)
3A7V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1252)
3A7V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1251)
3A7V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMGWVRQAPGKGLEWV AEIRDKVKNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CRLGVFDYWGQGTLVTVSS (SEQ ID NO:1253)
3A7V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMGWVRQAPGQGLEWV AEIRDKVKNHATYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC RLGVFDYWGQGTLVTVSS (SEQ ID NO:1254)
3A7V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMGWVRQAPGQGLEW VAEIRDKVKNHATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCRLGVFDYWGQGTLVTVSS (SEQ ID NO:1255)
3A7V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMGWVRQMPGKGLEWV AEIRDKVKNHATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC RLGVFDYWGQGTLVTVSS (SEQ ID NO:1256)
3A7V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAE IRDKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRL GVFDYWGQGTLVTVSS (SEQ ID NO:1257)
3A7V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMGWIRQPPGKGLEWVAE IRDKVKNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCRL GVFDYWGQGTLVTVSS (SEQ ID NO:1258)
Antibody 3B10	**Antibody 3B10**
3B10V3-15	EVQLVESGGGLVKPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWES VIRSKSNNFSTLYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCV RHKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1292)
3B10V3-30	QVQLVESGGGVVQPGRSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWES VIRSKSNNFSTLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1293)
3B10V3-23	EVQLLESGGGLVQPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWES VIRSKSNNFSTLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV RHKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1294)

Antibody variant	Humanized sequences
3B10V1-46	QVQLVQSGAEVKKPGASVKVSCKASGLTSNTYTQTWVRQAPGQGLEWE SVIRSKSNNFSTLYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC VRHKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1295)
3B10V3-48	EVQLVESGGGLVQPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWES VIRSKSNNFSTLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1296)
3B10V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGLTSNTYTQTWVRQAPGQGLEWES VIRSKSNNFSTLYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVR HKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1297)
3B10V3-7	EVQLVESGGGLVQPGGSLRLSCAASGLTSNTYTQTWVRQAPGKGLEWES VIRSKSNNFSTLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV RHKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1296)
3B10V5-51	EVQLVQSGAEVKKPGESLKISCKGSGLTSNTYTQTWVRQMPGKGLEWES VIRSKSNNFSTLYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVR HKSNRYPGVYWGQGTLVTVSS (SEQ ID NO:1298)
3B10V4-59	QVQLQESGPGLVKPSETLSLTCTVSGLTSNTYTQTWIRQPPGKGLEWESVI RSKSNNFSTLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHK SNRYPGVYWGQGTLVTVSS (SEQ ID NO:1299)
3B10V4-39	QLQLQESGPGLVKPSETLSLTCTVSGLTSNTYTQTWIRQPPGKGLEWESVI RSKSNNFSTLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRHK SNRYPGVYWGQGTLVTVSS (SEQ ID NO:1300)
Antibody 4F11	**Antibody 4F11**
4F11V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYPFSNFWITWVRQMPGKGLEWIGD IYPGSDNSNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAREAY YTNPGFAYWGQGTLVTVSS (SEQ ID NO:1282)
4F11V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYPFSNFWITWVRQAPGQGLEWIG DIYPGSDNSNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1283)
4F11V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYPFSNFWITWVRQAPGQGLEWIG DIYPGSDNSNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARE AYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1284)
4F11V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1285)
4F11V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIG DIYPGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARE AYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1286)
4F11V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1285)

Antibody variant	Humanized sequences
4F11V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1287)
4F11V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIY PGSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1288)
4F11V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLEWIGD IYPGSDNSNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCAREA YYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1289)
4F11V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWIGDIY PGSDNSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREAYY TNPGFAYWGQGTLVTVSS (SEQ ID NO:1290)
Antibody 6H6	**Antibody 6H6**
6H6V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWW VAEIRNKVNNHATYYAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYY CCTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1302)
6H6V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWW VAEIRNKVNNHATYYDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY CCTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1303)
6H6V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWW VAEIRNKVNNHATYYDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CCTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1304)
6H6V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWW VAEIRNKVNNHATYYDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY CCTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1303)
6H6V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMDWVRQAPGKGLEWW VAEIRNKVNNHATYYDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CCTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1305)
6H6V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMDWVRQAPGQGLEW WVAEIRNKVNNHATYYQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCCTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1306)
6H6V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMDWVRQAPGQGLEW WVAEIRNKVNNHATYYQKFQGRVTITADESTSTAYMELSSLRSEDTAVYY CCTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1307)
6H6V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMDWVRQMPGKGLEWW VAEIRNKVNNHATYYPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC CTSLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1308)
6H6V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMDWIRQPPGKGLEWWV AEIRNKVNNHATYYPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCCT SLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1309)

Antibody variant	Humanized sequences
6H6V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMDWIRQPPGKGLEWWV AEIRNKVNNHATYYPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCCT SLYDGYYLRFAWGQGTLVTVSS (SEQ ID NO:1310)
Antibody7A9	**Antibody 7A**
7A9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVA HIKTKZNNFATFYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCV ZHZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1312)
7A9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVA HIKTKZNNFATFYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV ZHZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1313)
7A9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVA HIKTKZNNFATFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCV ZHZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1314)
7A9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWVA HIKTKZNNFATFYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCV ZHZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1313)
7A9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFNTYSMNWVRQAPGKGLEWV AHIKTKZNNFATFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC VZHZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1315)
7A9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFNTYSMNWVRQAPGQGLEWV AHIKTKZNNFATFYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC VZHZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1316)
7A9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFNTYSMNWVRQAPGQGLEWV AHIKTKZNNFATFYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCV ZHZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1317)
7A9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFNTYSMNWVRQMPGKGLEWVA HIKTKZNNFATFYAPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVZ HZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1318)
7A9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFNTYSMNWIRQPPGKGLEWVAHI KTKZNNFATFYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVZHZ SNNYPFAYWGQGTLVTVSS (SEQ ID NO:1319)
7A9V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTFNTYSMNWIRQPPGKGLEWVAH IKTKZNNFATFYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVZH ZSNNYPFAYWGQGTLVTVSS (SEQ ID NO:1320)
Antibody 7B3	**Antibody 7B3**
7B3V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYWIHWVRQAPGQGLEWIG RNDPNSGGSNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCVR TNWDGDFWGQGTLVTVSS (SEQ ID NO:1322)
7B3V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTTYWIHWVRQMPGKGLEWIG RNDPNSGGSNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCVRT NWDGDFWGQGTLVTVSS (SEQ ID NO:1323)

Antibody variant	Humanized sequences
7B3V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTTYWIHWVRQAPGQGLEWIG RNDPNSGGSNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCVRT NWDGDFWGQGTLVTVSS (SEQ ID NO:1324)
7B3V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIG RNDPNSGGSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVR TNWDGDFWGQGTLVTVSS (SEQ ID NO:1325)
7B3V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIG RNDPNSGGSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVR TNWDGDFWGQGTLVTVSS (SEQ ID NO:1326)
7B3V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIG RNDPNSGGSNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVR TNWDGDFWGQGTLVTVSS (SEQ ID NO:1327)
7B3V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLEWIG RNDPNSGGSNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVR TNWDGDFWGQGTLVTVSS (SEQ ID NO:1326)
7B3V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTTYWIHWIRQPPGKGLEWIGRN DPNSGGSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRTNW DGDFWGQGTLVTVSS (SEQ ID NO:1328)
7B3V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTTYWIHWVRQAPGKGLE WIGRNDPNSGGSNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCVRTNWDGDFWGQGTLVTVSS (SEQ ID NO:1329)
7B3V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYTFTTYWIHWIRQPPGKGLEWI GRNDPNSGGSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC VRTNWDGDFWGQGTLVTVSS (SEQ ID NO:1330)
Antibody 8A1	**Antibody 8A1**
8A1V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYAFSNYWMSWVRQMPGKGLE WIGQIYPGDGDTKYNPSFQGQVTISADKSISTAYLQWSSLKASDTAM YYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1332)
8A1V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYAFSNYWMSWVRQAPGQG LEWIGQIYPGDGDTKYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDT AVYYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1333)
8A1V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLE WIGQIYPGDGDTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1334)
8A1V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSNYWMSWVRQAPGQGL EWIGQIYPGDGDTKYNQKFQGRVTITADESTSTAYMELSSLRSEDTAV YYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1335)
8A1V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLE WIGQIYPGDGDTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1336)

Antibody variant	Humanized sequences
8A1V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLE WIGQIYPGDGDTKYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1336)
8A1V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYAFSNYWMSWVRQAPGKGL EWIGQIYPGDGDTKYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1337)
8A1V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYAFSNYWMSWIRQPPGKGLE WIGQIYPGDGDTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVY YCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1338)
8A1V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYAFSNYWMSWVRQAPGKGLE WIGQIYPGDGDTKYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1339)
8A1V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYAFSNYWMSWIRQPPGKGLE WIGQIYPGDGDTKYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVY YCSREKGADYYGSTYSAWFSYWGQGTLVTVSS (SEQ ID NO:1340)
Antibody 9F5	**Antibody 9F5**
9F5V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYAFSSSWMNWVRQMPGKGLE WIGRIYPGDGDTNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAM YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1342)
9F5V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1343)
9F5V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAV YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1344)
9F5V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLE WIGRIYPGDGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1345)
9F5V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLE WIGRIYPGDGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1346)
9F5V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLE WIGRIYPGDGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1346)
9F5V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYAFSSSWMNWVRQAPGKGLE WIGRIYPGDGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1347)
9F5V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYAFSSSWMNWIRQPPGKGLE WIGRIYPGDGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVY YCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1348)

Antibody variant	Humanized sequences
9F5V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLE WIGRIYPGDGDTNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1349)
9F5V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYAFSSSWMNWIRQPPGKGLE WIGRIYPGDGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVY YCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1350)
9F5-H1	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDT AVYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1665)
9F5-H2	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYAQKFQGRVTMTADTSTSTVYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1666)
9F5-H3	QVQLVQSGAEVKKPGASLKISCKASGYAFSSSWMNWVRQAPGQGLE WIGRIYPGDGDTNYAQKFQGRATLTADTSTSTAYMELSSLRSEDTAV YYCARLLRNQPGESYAMDYWGQGALVTVSS (SEQ ID NO:1667)
Antibody 9G1	**Antibody 9G1**
9G1V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYIFTTYWIHWVRQMPGKGLE WIGRIDPNNGDTNYNPSFQGQVTISADKSISTAYLQWSSLKASDTAM YYCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1352)
9G1V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYIFTTYWIHWVRQAPGQGLE WIGRIDPNNGDTNYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTA VYYCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1353)
9G1V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYIFTTYWIHWVRQAPGQGLE WIGRIDPNNGDTNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAV YYCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1354)
9G1V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLEW IGRIDPNNGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1355)
9G1V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYIFTTYWIHWVRQAPGKGLE WIGRIDPNNGDTNYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1356)
9G1V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLE WIGRIDPNNGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1357)
9G1V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLE WIGRIDPNNGDTNYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1357)
9G1V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYIFTTYWIHWIRQPPGKGLEWI GRIDPNNGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1358)

Antibody variant	Humanized sequences
9G1V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYIFTTYWIHWVRQAPGKGLE WIGRIDPNNGDTNYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1359)
9G1V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYIFTTYWIHWIRQPPGKGLEWI GRIDPNNGDTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CVMTGTDFDYWGQGTLVTVSS (SEQ ID NO:1360)
Antibody 9G3	**Antibody 9G3**
9G3V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLE WIARIRSNSNDYATNYSAPVKGRFTISRDDSKNTLYLQMNSLKTEDTA VYYCVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1456)
9G3V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLE WIARIRSNSNDYATNYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1457)
9G3V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFNFNTYAMKWVRQAPGKGLE WIARIRSNSNDYATNYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1458)
9G3V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLE WIARIRSNSNDYATNYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDT AVYYCVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1459)
9G3V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMKWVRQAPGKGLE WIARIRSNSNDYATNYSDSVKGRFTISRDNAKNSLYLQMNSLRAEDT AVYYCVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1460)
9G3V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFNFNTYAMKWVRQAPGQGL EWIARIRSNSNDYATNYSQKFQGRVTITADESTSTAYMELSSLRSEDT AVYYCVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1461)
9G3V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFNFNTYAMKWVRQAPGQGL EWIARIRSNSNDYATNYSQKFQGRVTMTRDTSTSTVYMELSSLRSEDT AVYYCVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1462)
9G3V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFNFNTYAMKWVRQMPGKGL EWIARIRSNSNDYATNYSPSFQGQVTISADKSISTAYLQWSSLKASDT AMYYCVGHKI NNYPFAHWGQGTLVTVSS (SEQ ID NO:1463)
9G3V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFNFNTYAMKWIRQPPGKGLEWI ARIRSNSNDYATNYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1464)
9G3V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFNFNTYAMKWIRQPPGKGLEWI ARIRSNSNDYATNYSPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CVGHKINNYPFAHWGQGTLVTVSS (SEQ ID NO:1465)
Antibody10A9	**Antibody10A9**
10A9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYPFSNFWITWVRQMPGKGLE WIGDIYPGSDNRNFNPSFQGQVTISADKSISTAYLQWSSLKASDTAMY YCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1362)

Antibody variant	Humanized sequences
10A9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYPFSNFWITWVRQAPGQGLE WIGDIYPGSDNRNFNQKFQGRVTITADESTSTAYMELSSLRSEDTAVY YCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1363)
10A9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYPFSNFWITWVRQAPGQGLE WIGDIYPGSDNRNFNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAV YYCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1364)
10A9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLE WIGDIYPGSDNRNFNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1365)
10A9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLE WIGDIYPGSDNRNFNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1365)
10A9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYPFSNFWITWVRQAPGKGLE WIGDIYPGSDNRNFNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1366)
10A9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLE WIGDIYPGSDNRNFNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1367)
10A9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWI GDIYPGSDNRNFNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC AREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1368)
10A9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYPFSNFWITWVRQAPGKGLE WIGDIYPGSDNRNFNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCAREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1369)
10A9V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYPFSNFWITWIRQPPGKGLEWI GDIYPGSDNRNFNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC AREAYYTNPGFAYWGQGTLVTVSS (SEQ ID NO:1370)
Antibody11A8	**Antibody11A8**
11A8V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLE WVARIRSKSNNYATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDT AVYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1372)
11A8V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLE WVARIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAED TAVYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1373)
11A8V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLE WVARIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1374)
11A8V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFNFNTYAMNWVRQAPGKGL EWVARIRSKSNNYATYYADSVKGRFTISRDNSKNTLYLQMNSLRAED TAVYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1375)

Antibody variant	Humanized sequences
11A8V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFNFNTYAMNWVRQAPGKGLE WVARIRSKSNNYATYYADSVKGRFTISRDNAKNSLYLQMNSLRAED TAVYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1373)
11A8V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFNFNTYAMNWVRQAPGQGL EWVARIRSKSNNYATYYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1376)
11A8V1 -46	QVQLVQSGAEVKKPGASVKVSCKASGFNFNTYAMNWVRQAPGQGL EWVARIRSKSNNYATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSE DTAVYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1377)
11A8V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFNFNTYAMNWVRQMPGKGLE WVARIRSKSNNYATYYAPSFQGQVTISADKSISTAYLQWSSLKASDT AMYYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1378)
11A8V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFNFNTYAMNWIRQPPGKGLEW VARIRSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAV YYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1379)
11A8V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFNFNTYAMNWIRQPPGKGLEW VARIRSKSNNYATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAV YYCVRHYSNYGWGFAYWGQGTLVTVSS (SEQ ID NO:1380)
Antibody12D9	**Antibody12D9**
12D9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFSDYYIHWVRQAPGQGLE WIGYIYPNNGDNGYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTA VYYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1382)
12D9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFSDYYIHWVRQMPGKGLE WIGYIYPNNGDNGYNPSFQGQVTISADKSISTAYLQWSSLKASDTAM YYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1383)
12D9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFSDYYIHWVRQAPGQGLE WIGYIYPNNGDNGYNQKFQGRVTITADESTSTAYMELSSLRSEDTAV YYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1384)
12D9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLE WIGYIYPNNGDNGYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1385)
12D9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFSDYYIHWVRQAPGKGLE WIGYIYPNNGDNGYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1386)
12D9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLE WIGYIYPNNGDNGYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1387)
12D9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLE WIGYIYPNNGDNGYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1385)

Antibody variant	Humanized sequences
12D9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFSDYYIHWIRQPPGKGLEWI GYIYPNNGDNGYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1388)
12D9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFSDYYIHWVRQAPGKGLE WIGYIYPNNGDNGYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1389)
12D9V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGYTFSDYYIHWIRQPPGKGLEWI GYIYPNNGDNGYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CARRGYYGGSYDYWGQGTLVTVSS (SEQ ID NO:1390)
Antibody12F9	Antibody12F9
12F9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLE WEGVIRRKSSNFATLYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDT AVYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1392)
12F9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLE WEGVIRRKSSNFATLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1393)
12F9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLE WEGVIRRKSSNFATLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDT AVYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1394)
12F9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFRFNTYAMTWVRQAPGKGLE WEGVIRRKSSNFATLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1395)
12F9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFRFNTYAMTWVRQAPGKGLE WEGVIRRKSSNFATLYADSVKGRFTISRDNAKNSLYLQMNSLRAEDT AVYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1394)
12F9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFRFNTYAMTWVRQAPGQGL EWEGVIRRKSSNFATLYAQKFQGRVTITADESTSTAYMELSSLRSEDT AVYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1396)
12F9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFRFNTYAMTWVRQAPGQGL EWEGVIRRKSSNFATLYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1397)
12F9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFRFNTYAMTWVRQMPGKGLE WEGVIRRKSSNFATLYAPSFQGQVTISADKSISTAYLQWSSLKASDTA MYYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1398)
12F9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFRFNTYAMTWIRQPPGKGLEW EGVIRRKSSNFATLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAV YYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1399)
12F9V4-39	QLQLQESGPGLVKPSETLSLTCTVSGFRFNTYAMTWIRQPPGKGLEW EGVIRRKSSNFATLYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAV YYCVRHKSNKYPFVYWGQGTLVTVSS (SEQ ID NO:1400)
Antibody10C1	**Antibody10C1**

Antibody variant	Humanized sequences
10C1V3-15	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLE WVAEIRNKINNHATYYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDT AVYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1467)
10C1V3-7	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLE WVAEIRNKINNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDT AVYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1468)
10C1V3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLE WVAEIRNKINNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1469)
10C1V3-30	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDAWMDWVRQAPGKGL EWVAEIRNKINNHATYYADSVKGRFTISRDNSKNTLYLQMNSLRAED TAVYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1470)
10C1V3-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDAWMDWVRQAPGKGLE WVAEIRNKINNHATYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDT AVYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1471)
1OC1V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGFTFSDAWMDWVRQAPGQGL EWVAEIRNKINNHATYYAQKFQGRVTITADESTSTAYMELSSLRSEDT AVYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1472)
1OC1V1-46	QVQLVQSGAEVKKPGASVKVSCKASGFTFSDAWMDWVRQAPGQGL EWVAEIRNKINNHATYYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1473)
10C1V5-51	EVQLVQSGAEVKKPGESLKISCKGSGFTFSDAWMDWVRQMPGKGLE WVAEIRNKINNHATYYAPSFQGQVTISADKSISTAYLQWSSLKASDTA MYYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1474)
10C1V4-59	QVQLQESGPGLVKPSETLSLTCTVSGFTFSDAWMDWIRQPPGKGLEW VAEIRNKINNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAV YYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1475)
10C1V4-30-4	QVQLQESGPGLVKPSQTLSLTCTVSGFTFSDAWMDWIRQPPGKGLEW VAEIRNKINNHATYYAPSLKSRVTISVDTSKNQFSLKLSSVTAADTAV YYCTSLYDGSYLRFAYWGQGTLVTVSS (SEQ ID NO:1476)
Antibody 7E9	**Antibody 7E9**
7E9V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYTMHWVRQAPGQGL EWIGGINPNNGGTSYKQKFQGRVTMTRDTSTSTVYMELSSLRSEDTA VYYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1478)
7E9V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTEYTMHWVRQAPGQGL EWIGGINPNNGGTSYKQKFQGRVTITADESTSTAYMELSSLRSEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1479)
7E9V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYTFTEYTMHWVRQMPGKGLE WIGGINPNNGGTSYKPSFQGQVTISADKSISTAYLQWSSLKASDTAMY YCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1480)

Antibody variant	Humanized sequences
7E9V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYKDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1481)
7E9V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYKDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1482)
7E9V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYKDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1483)
7E9V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYKDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1484)
7E9V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEWI GGINPNNGGTSYKPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC ARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1485)
7E9V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYTFTEYTMHWVRQAPGKGLE WIGGINPNNGGTSYKAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1486)
7E9V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYTFTEYTMHWIRQPPGKGLEWI GGINPNNGGTSYKPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC ARGGSHYYAMDYWGQGTLVTVSS (SEQ ID NO:1487)
Antibody 8C3	**Antibody 8C3**
8C3V1-46	QVQLVQSGAEVKKPGASVKVSCKASGYSFTGYYMHWVRQAPGQGL EWIGRVNPNNGGTSYNQKFQGRVTMTRDTSTSTVYMELSSLRSEDTA VYYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1489)
8C3V5-51	EVQLVQSGAEVKKPGESLKISCKGSGYSFTGYYMHWVRQMPGKGLE WIGRVNPNNGGTSYNPSFQGQVTISADKSISTAYLQWSSLKASDTAM YYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1490)
8C3V3-23	EVQLLESGGGLVQPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLE WIGRVNPNNGGTSYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1491)
8C3V1-69	QVQLVQSGAEVKKPGSSVKVSCKASGYSFTGYYMHWVRQAPGQGL EWIGRVNPNNGGTSYNQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1492)
8C3V3-30	QVQLVESGGGVVQPGRSLRLSCAASGYSFTGYYMHWVRQAPGKGL EWIGRVNPNNGGTSYNDSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1493)
8C3V3-48	EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLE WIGRVNPNNGGTSYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1494)

Antibody variant	Humanized sequences
8C3V3-7	EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLE WIGRVNPNNGGTSYNDSVKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1495)
8C3V4-59	QVQLQESGPGLVKPSETLSLTCTVSGYSFTGYYMHWIRQPPGKGLEW IGRVNPNNGGTSYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CVLTGGYFD YWGQGTLVTVSS (SEQ ID NO:1496)
8C3V3-15	EVQLVESGGGLVKPGGSLRLSCAASGYSFTGYYMHWVRQAPGKGLE WIGRVNPNNGGTSYNAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1497)
8C3V4-39	QLQLQESGPGLVKPSETLSLTCTVSGYSFTGYYMHWIRQPPGKGLEW IGRVNPNNGGTSYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CVLTGGYFDYWGQGTLVTVSS (SEQ ID NO:1498)

[00202] 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 D1-D6**, 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 D1-D6**, 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.

[00203] 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.

[00204] In some embodiments, each of the light chain variable regions disclosed in listed in **TABLES D1-D6**, 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 D1-D6**, 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 EN1)** and heavy chain constant regions **(TABLE EN2)** 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

[00205] 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.

[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 '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.

[00207] 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%.

[00208] 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: $RX_1SX_2SLX_3HSNX_4YTYLH$, 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).

[00209] 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.

[00210] 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 E1-E3**). 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 E4-E6**). 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 E1-E3**); 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 E4-E6**). 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 E1-E3** and **TABLES E4-E6**).

[00211] 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 E15**); 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 E17**). 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).

[00212] 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).

[00213] 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).

[00214] 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).

[00215] 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).

[00216] 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).

[00217] 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 E15**); 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 E17**). 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.

[00218] 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.

[00219] 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 E15**); 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 E17**).

[00220] 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.

[00221] 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.

[00222] 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 E1-E18**.

TABLE E1: Heavy chain HVR H1 sequences of anti-TREM2 antibodies

Ab	HVR H1
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-5, AL2p- 6, AL2p-33, AL2p-h77, and AL2p-36	YAFSSSWMN (SEQ ID NO:1831)

Ab	HVR H1
AL2p-29, AL2p-30, AL2p-31, AL2p-37, AL2p-58, AL2p-60, AL2p-61, and AL2p-62	YAFSSQWMN (SEQ ID NO:1839)
AL2p-10, AL2p-11, AL2p-45, AL2p-46, AL2p-47, AL2p-48, and AL2p-49	YAFSSDWMN (SEQ ID NO:1843)
AL2p-7 and AL2p-8	YAFSLSWMN (SEQ ID NO:1864)
AL2p-9	YAFSRSWMN (SEQ ID NO: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 (SEQ ID NO:1866)
AL2p-32	YAFSSEWMN (SEQ ID NO:1867)
AL2P-35	YAFWSSWMN (SEQ ID NO:1868)
Formula I	$YAFX_1X_2X_3WMN$ X_1 is S or W X_2 is S, L, or R X_3 is S, D, H, Q, or E (SEQ ID NO:1828)

TABLE E2: Heavy chain HVR H2 sequences of anti-TREM2 antibodies

Ab	HVR H2
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 (SEQ ID NO:1832)
AL2p-31 and AL2p-60	RIYPGGGDTNYARKFQG (SEQ ID NO:1840)
AL2p-37 and AL2p-58	RIYPGGGDTNYAGKFQG (SEQ ID NO:1842)
AL2p47, AL2p-48, AL2p-49	RIYPGEGDTNYARKFHG (SEQ ID NO:1844)
AL2p-45, AL2p46, and AL2p-61	RIYPGEGDTNYARKFQG (SEQ ID NO:1848)
AL2p-62	RIYPGEGDTNYAGKFQG (SEQ ID NO:1850)
AL2p-2 and AL2p-24	RIYPGGGDTNYAQKFQG (SEQ ID NO:1869)
AL2p-3	RIYPGEGDTNYAQKFQG (SEQ ID NO:1870)

AL2p-4 and AL2p-27	RIYPGQGDTNYAQKFQG (SEQ ID NO:1871)
AL2p-7 and AL2p-16	RIYPGDGDTNYAQKFRG (SEQ ID NO:1872)
AL2p-8, AL2p-11, AL2p-19, AL2p-20, and AL2p-36	RIYPGDGDTNYARKFQG (SEQ ID NO:1873)
AL2p-12	RIYPGDGDTNYAHKFQG (SEQ ID NO:1874)
AL2p-13	RIYPGDGDTNYAQKFKG (SEQ ID NO:1875)
AL2p-17	RIYPGDGDTNYAQKRQG (SEQ ID NO:1876)
AL2p-18	RIYPGDGDTNYAQKWQG (SEQ ID NO:1877)
AL2p-21 and AL2p-30	RIYPGDGDTNYAWKFQG (SEQ ID NO:1878)
AL2p-22	RIYPGDGDTNYAYKFQG (SEQ ID NO:1879)
AL2p-23	RIYPGDGQTNYAQKRQG (SEQ ID NO:1880)
AL2p-25, AL2p-38, AL2p-39, and AL2p-40	RIYPGGGDTNYAQKFRG (SEQ ID NO:1881)
AL2p-26	RIYPGGGDTNYAQKRQG (SEQ ID NO:1882)
AL2p-28	RIYPGVGDTNYAQKFQG (SEQ ID NO:1883)
AL2p-41 and AL2p-42	RIYPGEGDTNYAQKFRG (SEQ ID NO:1884)
AL2p-43 and AL2p44	RIYPGGGDTNYARKFRG (SEQ ID NO:1885)
AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-54, AL2p-55, AL2p-56, and AL2p-57	RIYPGEGDTNYAQKFHG (SEQ ID NO:1886)
AL2p-59	RIYPGEGQTNYAQKRQG (SEQ ID NO:1887)
Formula II	RIYPGX1GX2TNYAX_3KX_4 X_5G 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 X_5 is Q, R, K, or H (SEQ ID NO:1829)

TABLE E3: Heavy chain HVR H3 sequences of anti-TREM2 antibodies

Ab	HVR 113
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, AL2p-50, AL2p-51, AL2p-52, AL2p-53, AL2p-58, AL2p-59. AL2p-60, AL2p-61, and AL2p-62	ARLLRNQPGESYAMDY (SEQ ID NO:1833)
AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-49, AL2p-54, AL2p-55, AL2p-56, and AL2p-57	ARLLRNKPGESYAMDY (SEQ ID NO:1845)
AL2p-8 and AL2p-18	ARLLRNQPGSSYAMDY (SEQ ID NO:1888)
AL2p-9, AL2p-16, AL2p-36, AL2p-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, and AL2p-44	ARLLRNQPGASYAMDY (SEQ ID NO:1889)
AL2p-35	ARLLRNQPGESYAHDY (SEQ ID NO:1890)
Formula III	ARLLRNX_1PGX_2SYAX_3DY X_1 is Q or K X_2 is E, S, or A X_3 is M or H (SEQ ID NO:1830)

TABLE E4: Light chain HVR Ll sequences of anti-TREM2 antibodies

Ab	HVR L1
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 (SEQ ID NO:1837)
AL2p-45, AL2p-47, AL2p-50. AL2p-52, AL2p-55, and AL2p-56	RTSQSLVHSNAYTYLH (SEQ ID NO:1846)
AL2p-61 and AL2p-62	RSSQSLVHSNQYTYLH (SEQ ID NO:1849
AL2p-5, AL2p-58, and AL2p-60	RSSQSLVHSNRYTYLH (SEQ ID NO:1851)
AL2p-6	RSSQSLVHSNWYTYLH (SEQ ID NO:1891)
AL2p-7, AL2p-8, AL2p-13, and AL2p-26	RSSQSLIHSNGYTYLH (SEQ ID NO:1892)
AL2p-9, AL2p-16, AL2p-18. AL2p-20, AL2p-23, AL2p-25, AL2p-28, and AL2p-33	RTSQSLVHSNGYTYLH (SEQ ID NO:1893)
AL2p-11, AL2p-14, AL2p-17, AL2p-19, AL2p-22, AL2p-24, AL2p-27. and AL2p-29	RSSRSLVHSNGYTYLH (SEQ ID NO:1894)

AL2p-15, AL2p-21, and AL2p-30	RSSSSLVHSNGYTYLH (SEQ ID NO:1895)
AL2p-38 and AL2p-43	RSSRSLVHSNRYTYLH (SEQ ID NO:1896)
AL2p-39 and AL2p-41	RSSRSLVHSNQYTYLH (SEQ ID NO:1897)
AL2p-40, AL2p-42, and AL2p-44	RTSRSLVHSNRYTYLH (SEQ ID NO:1898)
AL2p-46, AL2p-48, AL2p-49, AL2p-51, AL2p-53, AL2p-54, AL2p-57, and AL2p-59	RTSQSLVHSNQYTYLH (SEQ ID NO:1899)
Formula IV	$RX_1SX_2SLX_3HSNX_4YTYLH$ 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 (SEQ ID NO:1834)

TABLE E5: Light chain HVR L2 sequences of anti-TREM2 antibodies

Ab	HVR L2
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 (SEQ ID NO: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 (SEQ ID NO: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 (SEQ ID NO:1847)
AL2p-15, AL2p-21, and AL2p-30	KVSNRKS (SEQ ID NO:1900)
Formula V	$KVSNRX_1S$ X_1 is F, R, V, or K (SEQ ID NO:1835)

TABLE E6: Light chain HVR L3 sequences of anti-TR FM2 antibodies

Ab	HVR L3
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,	SQSTRVPYT (SEQ ID NO:1836)

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	

TABLE E7: Heavy chain framework I sequences of anti-TREM2 antibodies

Ab	VH FR1
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-38, AL2p-39, AL2p-40, AL2p-41, AL2p-42, AL2p-43, AL2p-44, AL2p-45, AL2p-46, AL2p-47, AL2p-48, AL2p-50, AL2p-51, AL2p-54, AL2p-59, AL2p-60, and AL2p-61	QVQLVQSGAEVKKPGSSVKVSCKASG (SEQ ID NO:1716)
AL2p-33. AL2p-49, AL2p-52. AL2p-53, AL2p-55, AL2p-56, and AL2p-57	EVQLVQSGAEVKKPGSSVKVSCKASG (SEQ ID NO:1717)
AL2p-h77, AL2p-35, AL2p-36, AL2p-37. AL2p-58. and AL2p-62	QVQLVQSGAEVKKPGASVKVSCKASG (SEQ ID NO:1718)

TABLE E8: Heavy chain framework 2 sequences of anti-TREM2 antibodies

Ab	VH FR2
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 (SEQ ID NO:1719)
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-58, and AL2 -62	WVRQAPGQRLEWIG (SEQ ID NO:1720)

TABLE E9: Heavy chain framework 3 sequences of anti-TREM2 antibodies

Ab	VH FR3
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-59, AL2p-60, and AL2p-61	RVTITADESTSTAYMEL SSLRSEDTAVYYC (SEQ ID NO:1721)

Ab	VH FR3
AL2p-h77, AL2p-35, AL2p-36, AL2p-37-AL2p-58, and AL2p-62	RVTITADTSASTAYMEL SSLRSEDTAVYYC (SEQ ID NO:1722)

TABLE E10: Heavy chain framework 4 sequences of anti-TREM2 antibodies

Ab	VH FR4
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 (SEQ ID NO:1723)

TABLE E11: Light chain framework 1 sequences of anti-TREM2 antibodies

Ab	VL FR1
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	DVVMTQTPLSLSVTPGQPASI SC (SEQ ID NO: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	GVVMTQTPLSLSVTPGQPASI SC (SEQ ID NO:1725)
AL2p-33	GVVMAQTPLSLSVTPGQPASI SC (SEQ ID NO:1726
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-58, and AL2p-62	DVVMTQSPDSLAVSLGERAT INC (SEQ ID NO:1727)

TABLE E12: Light chain framework 2 sequences of anti-TREM2 antibodies

Ab	VL FR2
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,	WYLQKPGQSPQLLIY (SEQ ID NO:1728)

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-59, AL2p-60 and AL2p-61	
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, AL2p-58, and AL2p-62	WYQQKPGQSPKLLIY (SEQ ID NO:1729)

TABLE E13: Light chain framework 3 sequences of anti-TREM2 antibodies

Ab	VL FR3
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	GVPDRFSGSGSGTDFTL KISRVEAEDVGVYYC (SEQ ID NO:1730)
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, and AL2-67	GVPDRFSGSGSGTDFTL TISSLQAEDVAVYYC (SEQ ID NO:1731)

TABLE E14: Light chain framework 4 sequences of anti-TREM2 antibodies

Ab	VL FR4
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 (SEQ ID NO:1732)
AL2p-h77. AL2p-35, AL2p-36, AL2p-37, and AL2p-62	FGGGTKVEIK (SEQ ID NO:1733

TABLE E15: Heavy chain variable region sequences of anti-TREM2 antibodies

Ab	HCVR
AL2p-h50. AL2p-5, and AL2p-6	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1734)

Ab	HCVR
AL2p-2	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGLE WMGRIYPGGGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTAV YYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1735)
AL2p-3	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGEGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1736)
AL2p-4	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGQGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1737
AL2p-7	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSLSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1738)
AL2p-8	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSLSWMNWVRQAPGQGL EWMGRIYPGDGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGSSYAMDYWGQGTLVTVSS (SEQ ID NO:1739)
AL2p-9	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSRSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGASYAMDYWGQGTLVTVSS (SEQ ID NO:1740)
AL2p-10	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1741)
AL2p-11	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGL EWMGRIYPGDGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1742)
AL2p-12	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAHKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1743)
AL2p-13	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFKGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1744)
AL2p-14 and AL2p-15	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1745)
AL2p-I6	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGASYAMDYWGQGTLVTVSS (SEQ ID NO:1746)
AL2p-1 7	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKRQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1747)
AL2p-18	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKWQGRVTITADESTSTAYMELSSLRSEDT AVYYCARLLRNQPGSSYAMDYWGQGTLVTVSS (SEQ ID NO:1748)

Ab	HCVR
AL2p-19 and AL2p-20	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1749)
AL2p-21	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAWKFQGRVTITADESTSTAYMELSSLRSEDT AVYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1750)
AL2p-22	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGDTNYAYKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1751)
AL2p-23	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGDGQTNYAQKRQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1752)
AL2p-24	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGGGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1753
AL2p-25	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGGGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1754)
AL2p-26	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGGGDTNYAQKRQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1755)
AL2p-27	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGQGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1756)
AL2p-28	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGVGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1757)
AL2p-29	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1758)
AL2p-30	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWVRQAPGQGL EWMGRIYPGDGDTNYAWKFQGRVTITADESTSTAYMELSSLRSEDT AVYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1759)
AL2p-31, AL2p-60, and AL2p-h31	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWVRQAPGQGL EWMGRIYPGGGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1760)
AL2p-32	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSEWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1761)
AL2p-33	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1762)

Ab	HCVR
AL2p-h77, AL2p–h26, and AL2p-h90	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQRL EWIGRIYPGDGDTNYAQKFQGRVTITADTSASTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1763)
AL2p-35	QVQLVQSGAEVKKPGASVKVSCKASGYAFWSSWMNWVRQAPGQR LEWIGRIYPGDGDTNYAQKFQGRVTITADTSASTAYMELSSLRSEDT AVYYCARLLRNQPGESYAHDYWGQGTLVTVSS (SEQ ID NO:1764)
AL2p-36	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQRL EWIGRIYPGDGDTNYARKFQGRVTITADTSASTAYMELSSLRSEDTA VYYCARLLRNQPGASYAMDYWGQGTLVTVSS (SEQ ID NO:1765)
AL2p-37 and AL2p-58	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWVRQAPGQRL EWIGRIYPGGGDTNYAGKFQGRVTITADTSASTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1766)
AL2p-38, AL2p-39, and AL2p-40	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGGGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGASYAMDYWGQGTLVTVSS (SEQ ID NO:1767)
AL2p-41 and AL2p-42	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGEGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGASYAMDYWGQGTLVTVSS (SEQ ID NO:1768)
AL2p-43 and AL2p-44	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGGGDTNYARKFRGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGASYAMDYWGQGTLVTVSS (SEQ ID NO:1769)
AL2p-45 and AL2p-46	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGL EWMGRIYPGEGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNKPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1770)
AL2p-47 and AL2p-48	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGL EWMGRIYPGEGDTNYARKFHGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNKPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1771)
AL2p-49	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGL EWMGRIYPGEGDTNYARKFHGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNKPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1772)
AL2p-50 and AL2p-51	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGEGDTNYAQKFHGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1773)
AL2p-52 and AL2p-53	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGEGDTNYAQKFHGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1774)
AL2p-54	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGEGDTNYAQKFHGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNKPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1775)
AL2p-55, AL2p-56, and AL2p-57	EVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGEGDTNYAQKFHGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNKPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1776)

Ab	HCVR
AL2p-61	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWVRQAPGQGL EWMGRIYPGEGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1777)
AL2p-62	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWVRQAPGQRL EWIGRIYPGEGDTNYAGKFQGRVTITADTSASTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1778)
AL2p-h19 and AL2p-h35	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRATITADTSTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1779)
AL2p-h21	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDT AVYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1780)
AL2p-h22	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYAQKFQGRVTMTADTSTSTVYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1781)
AL2p-h23	QVQLVQSGAEVKKPGASLKISCKASGYAFSSSWMNWVRQAPGQGLE WIGRIYPGDGDTNYAQKFQGRATLTADTSTSTAYMELSSLRSEDTAV YYCARLLRNQPGESYAMDYWGQGALVTVSS (SEQ ID NO:1782)
AL2p-h24	QVQLVQSGAEVVKPGASLKISCKASGYAFSSSWMNWVRQAPGQGLE WIGRIYPGDGDTNYNQKFQGRATLTADTSTSTAYMELSSLRSEDTAV YFCARLLRNQPGESYAMDYWGQGALVTVSS (SEQ ID NO:1783)
AL2p-h25	QVQLVQSGAEVKKPGASLKISCKASGYAFSSSWMNWVRQAPGQGLE WIGRIYPGDGDTNYNGEFRVRATLTADTSTSTAYMELSSLRSEDTAV YYCARLLRNQPGESYAMDYWGQGALVTVSS (SEQ ID NO:1784)
AL2p-h27	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYNGEFRVRATLTADTSTSTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1785)
AL2p-h28	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYAQKFQGRATLTADTSTSTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1786)
AL2p-h29	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYAQKFQGRATMTADTSTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1787)
AL2p-h30	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGDGDTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1788)
AL2p-h32	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYNGEFRVRATLTADTSTTTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1789)
AL2p-h33	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYAQKFQGRATLTADTSTTTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1790)

Ab	HCVR
AL2p-h34	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSSWMNWVRQAPGQGL EWIGRIYPGDGDTNYAQKFQGRATITADTSTSTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1791)
AL2p-b36	EVQLLESGGGLVQPGGSLRLSCAASGYAFSSSWMNWVRQAPGKGLE WIGRIYPGDGDTNYAQKFQGRATISADTSKNTAYLQMNSLRAEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1792)
AL2p-h42 and AL2p-h59	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQRL EWMGRIYPGDGDTNYAQKFQGRVTITRDTSASTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1793)
AL2p-h43	QVQLVQSGAEVKKPGASLKVSCKASGYAFSSSWMNWVRQAPGQRL EWIGRIYPGDGDTNYNGEFRVRATLTADTSASTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1794)
AL2p-h44	QVQLVQSGAEVKKPGASLKVSCKASGYAFSSSWMNWVRQAPGQRL EWIGRIYPGDGDTNYAQKFQGRATLTADTSASTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1795)
AL2p-h47	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQGL EWMGRIYPGDGDTNYNGEFRVRVTMTRDTSTSTVYMELSSLRSEDT AVYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1796)
AL2p-h76	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQRL EWIGRIYPGDGDTNYAQKFQGRATITADTSASTAYMELSSLRSEDTA VYFCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1797)
AL2p-59	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGL EWMGRIYPGEGQTNYAQKRQGRVTITADESTSTAYMELSSLRSEDTA VYYCARLLRNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:1798)

TABLE E16: Heavy chain sequences of anti-TREM2 antibodies

Ab	HC
AL2p-58 huIgG1	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWVRQAPGQRLEWI GRIYPGGGDTNYAGKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR LLRNQPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK (SEQ ID NO:1905)
AL2p-58 huIgG1	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWVRQAPGQRLEWI GRIYPGGGDTNYAGKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR LLRNQPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE

	EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPG (SEQ ID NO:1906)
AL2p-58 huIgG1 PSEG	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWVRQAPGQRLEWI GRIYPGGGDTNYAGKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR LLRNQPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQP REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHYTQKSLSL SPGK (SEQ ID NO:1907)
AL2p-58 huIgG1 PSEG	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQWMNWVRQAPGQRLEWI GRIYPGGGDTNYAGKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR LLRNQPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQP REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHYTQKSLSL SPG (SEQ ID NO:1908)
AL2p-47 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGLEW MGRIYPGEGDTNYARKFHGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNKPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK (SEQ ID NO:1909)
AL2p-47 hulgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGLEW MGRIYPGEGDTNYARKFHGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNKPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPG (SEQ ID NO:1910)

AL2p-47 huIgG1 PSEG	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGLEW MGRIYPGEGDTNYARKFHGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNKPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHYTQKSLSL SPGK (SEQ ID NO:1911)
AL2p-47 huIgG1 PSEG	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSDWMNWVRQAPGQGLEW MGRIYPGEGDTNYARKFHGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNKPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHGALHNHYTQKSLSL SPG (SEQ ID NO:1912)
AL2p-61 hulgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWVRQAPGQGLEW MGRIYPGEGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:1913)
AL2p-61 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSQWMNWVRQAPGQGLEW MGRIYPGEGDTNYARKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGESYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPG (SEQ ID NO:1914)
AL2p-40 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGLEW MGRIYPGGGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGASYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS

	LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK (SEQ ID NO:1915)
AL2p-40 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGLEW MGRIYPGGGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGASYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPG (SEQ ID NO:1916)
AL2p-44 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGLEW MGRIYPGGGDTNYARKFRGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGASYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:1917)
AL2p-44 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGLEW MGRIYPGGGDTNYARKFRGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGASYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPG (SEQ ID NO:1918)
AL2p-41 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGLEW MGRIYPGEGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGASYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT

	TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK (SEQ ID NO:1919)
AL2p-41 huIgG1	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSSHWMNWVRQAPGQGLEW MGRIYPGEGDTNYAQKFRGRVTITADESTSTAYMELSSLRSEDTAVYYCA RLLRNQPGASYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPG (SEQ ID NO:1920)

TABLE E17: Light chain variable region sequences of anti-TREM2 antibodies

Ab	LCVR
AL2p-h50, AL2p-2, AL2p-3, AL2p-4, AL2p-h42, AL2p-h43, AL2p-h44, and AL2p-h47	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1799)
AL2p-5	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNRYTYLHWYL QKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1800)
AL2p-6	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNWYTYLHWYL QKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1801)
AL2p-7, AL2p-8, AL2p-13, and AL2p-26	GVVMTQTPLSLSVTPGQPASISCRSSQSLIHSNGYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1802)
AL2p-9, AL2p-16, AL2p-18, AL2p-20, AL2p-23, AL2p-25, and AL2p-28	GVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1803)
AL2p-10, AL2p-12, AL2p-31, and AL2p-32	GVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1804)
AL2p-11, AL2p-17, and AL2p-19	DVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1805)
AL2p-14, AL2p-24, and AL2p-29	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAE DVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1806)
AL2p-15, AL2p-21, and AL2p-30	GVVMTQTPLSLSVTPGQPASISCRSSSSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRKSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1807)

Ab	LCVR
AL2p-22	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1808)
AL2p-27	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1809)
AL2p-33	GVVMAQTPLSLSVTPGQPASISCRTSQSLVHSNGYTYLHWY LQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1810)
AL2p-h77, AL2p-35, AL2p-36, AL2p-37, and AL2p-h76	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNGYTYLHWY QQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQ AEDVAVYYCSQSTRVPYTFGGGTKVEIK (SEQ ID NO:1811)
AL2p-38 and AL2p-43	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNRYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1812)
AL2p-39 and AL2p-41	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNQYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1813)
AL2p-40, AL2p-42, and AL2p-44	GVVMTQTPLSLSVTPGQPASISCRTSRSLVHSNRYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1814)
AL2p-45, AL2p-47, AL2p-50, AL2p-52, AL2p-55, and AL2p-56	DVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNAYTYLHWY LQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1815)
AL2p-46, AL2p-48, AL2p-49, AL2p-51, AL2p-53, AL2p-54, and AL2p-57	DVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNQYTYLHWY LQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1816)
AL2p-61	GVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNQYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1817)
AL2p-62	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNQYTYLHWY QQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQ AEDVAVYYCSQSTRVPYTFGGGTKVEIK (SEQ ID NO:1818)
AL2p-58	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNRYTYLHWY QQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1819)
AL2p-60	GVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNRYTYLHWYL QKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1820)
AL2p-h19	DIVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1821)

Ab	LCVR
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	DVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDLGVYFCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1822)
AL2p-h59	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGYTYLHWYL QKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCSQSTRVPYTFGGGTKVEIK (SEQ ID NO:1823)
AL2p-h90	DVQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGYTYLHWY QQKPGKSPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCSQSTRVPYTFGGGTKVEIK (SEQ ID NO:1824)
AL2p-59	GVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNQYTYLHWY LQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCSQSTRVPYTFGQGTKLEIK (SEQ ID NO:1825)

TABLE E18: Light chain sequences of anti-TREM2 antibodies

Ab	LC
AL2p-58 huIgG1, and AL2p-58 huIgG1 PSEG	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNRYTYLH WYQQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:1921)
AL2p-47 huIgG1, and AL2p-47 huIgG1 PSEG	DVVMTQTPLSLSVTPGQPASISCRTSQSLVHSNAYTYLH WYLQKPGQSPQLLIYKVSNRVSGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:1922)
AL2p-61 huIgG1	GVVMTQTPLSLSVTPGQPASISCRSSQSLVHSNQYTYLH WYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:1923)
AL2p-41 huIgG1	GVVMTQTPLSLSVTPGQPASISCRSSRSLVHSNQYTYLH WYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:1924)

Ab	LC
AL2p-40 huIgG1, and AL2p-44 huIgG1	GVVMTQTPLSLSVTPGQPASISCRTSRSLVHSNRYTYLH WYLQKPGQSPQLLIYKVSNRRSGVPDRFSGSGSGTDFTL KISRVEAEDVGVYYCSQSTRVPYTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:1925)

[00223] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in **TABLES E1-E18** 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 EN1)** and heavy chain constant regions **(TABLE EN2)** 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

[00224] 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.

[00225] 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.

[00226] 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.

[00227] 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.

[00228] 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.

[00229] 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.

[00230] 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.

[00231] 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.

[00232] 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.

[00233] 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.

[00234] 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.

[00235] 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.

[00236] 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.

[00237] In some embodiments, the antibody is an antibody disclosed in Figure 9 of PCT Patent Application Publication No. WO2018/015573A1, reproduced below as **TABLES F1-F4**.

TABLE F1

Clone name	Variable region of the heavy chain
14D3	EVKLLEFGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGRAPEWLGLIR NKTKGYTTEYNRSVKGRFTISRDNTQNMLYLQMNSLRPEDTATYYCARIGV NNGGSLDYWGQGVMVTVSS (SEQ ID NO:1946)
14D8	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAPEWLGLIR NKANGYTTVYNPSVKGRFTISRDNTQNMLYLQMNTLRGEDTATYYCARIGI NNGGSLDYWGQGVMVTVSS (SEQ ID NO:1947)
7A12	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAPEWLGLIR NKANGYTTQYNPSVKGRFTISRDNTQNMLYLQMNTLRGEDTATYYCARIGI NNGGSLDYWGQGVMVTVSS (SEQ ID NO:1948)
8A11	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAPEWLGLIR NKTKGYTTEYNTSVKGRFTISRDNTQNMLYLQMNSLRPEDTATYYCARIGV NNGGSLDYWGQGVMVTVSS (SEQ ID NO:1949)
21A3	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAPEWLGLIR NKANGYTTQYNPSVKGRFTISRDNTQNMLYLQMNTLRGEDTATYYCARIGI NNGGSLDYWGQGVMVTVSS (SEQ ID NO:1950)

Clone name	Variable region of the heavy chain
10C3	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGETPEWLGLIR NKTKGYTTEYNPSVKGRFTISRDNTQNMLYLQMNSLRPEDTATYYCARIGTN NGGSLDYWGQGVMVTVSS (SEQ ID NO:1951)
18F9	EVKLLESGGGLVQPGGSMRLSCVVSGFTFTDFYMNWIRQAAGKAPEWLGLI RNKVNGYRTEYNPSVKGRFTISRDNIQNMLYLQMNTLRAEDTATYYCARIGI NNGGSLDYWGQGVMVTVSS (SEQ ID NO:1952)
15C5	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAPEWLGLIR NKAYGYTTEYNPSVKGRFTISRDNTQDMLYLQMNTLRAEDTATYYCARIGIN YGGSLDYWGQGVMVTVSS (SEQ ID NO:1953)
1G6	EVKLLESGGGLVQPGGSLRLSCVASGFTFTDFYMNWIRQPAGKAPEWLGLIR NKANGFTTEYNPSVKGRFTISRDNTQHMLYLQMNTLRAEDTATYYCARIGIN NGGSLDYWGQGVMVTVSS (SEQ ID NO:1954)
Consensus sequence	EVKLLESGGGLVQPGGSMRLSCAASGFTFTDFYMNWIRQPAGKAPEWLGLIR NKANGYTTEYNPSVKGRFTISRDNTQNMLYLQMNTLREDTATYYCARIGINN GGSLDYWGQGVMVTVSS (SEQ ID NO:1955)

TABLE F2

Clone name	Variable region of the light chain
14D3	DILIIQSPASLTVSAGARVTMSCKSSQSLLYSENNQDYLAWYQQKPGQFPKLL IYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTFGA GTKLELK (SEQ ID NO:1956)
14D8	DILINQSPASLTVSTGEKVTMSCRSSQSLLYSEKNQDYLAWYQQKPGQFPKLL IYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTFGA GTKLELK (SEQ ID NO:1957)
7Al2	DILINQSPASLTVSAGEKVTMSCKSSQSLLYSEKNQDYLAWYQQKPGQSPKL LMYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTF GAGTKLELK (SEQ ID NO:1958)
8A11	DILIIQSPASLTVSAGARVTMSCKSSQSLLYSENNQDYLAWYQQKPGQFPKLL IYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTFGA GTKLELK (SEQ ID NO:1959)
21A3	DILINQSPASLTVSAGEKVTMSCKSSQSLLYSEKNQDYLAWYQQKPGQSPKL LMYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTF GAGTKLELK (SEQ ID NO:1960)

Clone name	Variable region of the light chain
10C3	DILIIQSPASLTVSAGARVTMSCKSSQSLLYSENNQDYLAWYQQKPGQFPKLL IYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTFGA GTKLELK (SEQ ID NO:1961)
18F9	DILINQSPASLTVSAGEKVTMSCKSSQSLLYSENNQDYLAWYQQKPGQFPKL LIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTFG AGTKLELK (SEQ ID NO:1962)
15C5	DILINQSPASLTVSAGEKVTVSCKSSQSLLYSESNQDYLAWYQQKPGQFPKLL IYGASYRHTGVPDRFTGSGSGTDFTLTISSVQAEDLAHYYCEQTYSYPYTFGA GTKLELK (SEQ ID NO:1963)
1G6	DILINQSPASLTVSTGEKVTMSCKSSQSLLYSENKQDYLAWYQQKPGQFPKLL IYGASNRHTGVPDRFTGSGSGTDFTLTINIVQAEDLADYYCEQTYSYPYTFGA GTKLELK (SEQ ID NO:1964)
Consensus sequence	DILINQSPASLTVSAGEKVTMSCKSSQSLLYSENNQDYLAWYQQKPGQFPKL LIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYYCEQTYSYPYTFG AGTKLELK (SEQ ID NO:1965)

TABLE F3

Clone name	Complementarity determining regions in the variable region of the heavy chain		
	CDR1	**CDR2**	**CDR3**
14D3	GFTFTDFY (SEQ ID NO:1966)	IRNKTKGYTT (SEQ ID NO:1976)	ARIGVNNGGSLDYWG (SEQ ID NO:1986)
14D8	GFTFTDFY (SEQ ID NO:1967)	IRNKANGYTT (SEQ ID NO:1977)	ARIGINNGGSLDYWG (SEQ ID NO:1987)
7Al2	GFTFTDFY (SEQ ID NO:1968)	IRNKANGYTT (SEQ ID NO:1978)	ARIGINNGGSLDYWG (SEQ ID NO:1988)
8A11	GFTFTDFY (SEQ ID NO:1969)	IRNKTKGYTT (SEQ ID NO:1979)	ARIGVNNGGSLDYWG (SEQ ID NO:1989)
21A3	GFTFTDFY (SEQ ID NO:1970)	IRNKANGYTT (SEQ ID NO:1980)	ARIGINNGGSLDYWG (SEQ ID NO:1990)
10C3	GFTFTDFY (SEQ ID NO:1971)	IRNKTKGYTT (SEQ ID NO:1981)	ARIGTNNGGSLDYWG (SEQ ID NO:1991)

18F9	GFTFTDFY (SEQ ID NO:1972)	IRNKVNGYRT (SEQ ID NO:1982)	ARIGINNGGSLDYWG (SEQ ID NO:1992)
15C5	GFTFTDFY (SEQ ID NO:1973)	IRNKAYGYTT (SEQ ID NO:1983)	ARIGINYGGSLDYWG (SEQ ID NO:1993)
1G6	GFTFTDFY (SEQ ID NO:1974)	IRNKANGFTT (SEQ ID NO:1984)	ARIGINNGGSLDYWG (SEQ ID NO:1994)
Consensus	GFTFTDFY (SEQ ID NO:1975)	IRNKANGYTT (SEQ ID NO:1985)	ARIGINNGGSLDYWG (SEQ ID NO:1995)

TABLE F4

Clone name	Complementarity determining regions in the variable region of the light chain		
	CDR1	**CDR2**	**CDR3**
14D3	QSLLYSENNQDY (SEQ ID NO:1996)	GAS (SEQ ID NO:2006)	EQTYSYPYT (SEQ ID NO:2016)
14D8	QSLLYSEKNQDY (SEQ ID NO:1997)	GAS (SEQ ID NO:2007)	EQTYSYPYT (SEQ ID NO:2017)
7Al2	QSLLYSEKNQDY (SEQ ID NO:1998)	GAS (SEQ ID NO:2008)	EQTYSYPYT (SEQ ID NO:2018)
8A11	QSLLYSENNQDY (SEQ ID NO:1999)	GAS (SEQ ID NO:2009)	EQTYSYPYT (SEQ ID NO:2019)
21A3	QSLLYSEKNQDY (SEQ ID NO:2000)	GAS (SEQ ID NO:2010)	EQTYSYPYT (SEQ ID NO:2020)
10C3	QSLLYSENNQDY (SEQ ID NO:2001)	GAS (SEQ ID NO:2011)	EQTYSYPYT (SEQ ID NO:2021)
18F9	QSLLYSENNQDY (SEQ ID NO:2002)	GAS (SEQ ID NO:2012)	EQTYSYPYT (SEQ ID NO:2022)
15C5	QSLLYSESNQDY (SEQ ID NO:2003)	GAS (SEQ ID NO:2013)	EQTYSYPYT (SEQ ID NO:2023)
1G6	QSLLYSENKQDY (SEQ ID NO:2004)	GAS (SEQ ID NO:2014)	EQTYSYPYT (SEQ ID NO:2024)

Consensus	QSLLYSENNQDY (SEQ ID NO:2005)	GAS (SEQ ID NO:2015)	EQTYSYPYT (SEQ ID NO:2025)

[00238] 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 EN1)** and heavy chain constant regions **(TABLE EN2)** 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

[00239] 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.

[00240] 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.

[00241] 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.

[00242] 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

(l) 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.

[00243] 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.

[00244] In some embodiments, the antibody is an antibody disclosed in Table 15 of PCT Patent Application Publication No. WO2019/055841A1, reproduced as **TABLE G1** 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 G1**.

TABLE G1

Description	Sequence
muIgG1 3' primer	GGACAGGGATCCAGAGTTCC (SEQ ID NO:2042)
muIgG2 3' primer	AGCTGGGAAGGTGTGCACAC (SEQ ID NO:2043)
muIgG3 3' primer	CAGGGGCCAGTGGATAGAC (SEQ ID NO:2044)
muCkappa.1 3' primer	GACATTGATGTCTTTGGGGT (SEQ ID NO:2045)
muCkappa.2 3' primer	TTCACTGCCATCAATCTTCC (SEQ ID NO:2046)
RS9.F6 VH amino acid sequence	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLE WIGRSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAV YYCVRTSGTGDYWGQGTSLTVSSAKTTAPSVYPLAPVCGGTTGSSVT (SEQ ID NO:2047)
RS9.F6 VL amino acid sequence	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHNNGNTFLHWYLQKPGQ SPKLLIYkVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTT HVPPTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCF (SEQ ID NO:2048)
RS9.F6 CDR-H1 amino acid sequence	GYTFTSY (SEQ ID NO:2049)
RS9.F6 CDR-H2 amino acid sequence	IGRSDPTTGGTNYNE (SEQ ID NO:2050)
RS9.F6 and RS.F10 CDR-H3 amino acid sequence	VRTSGTGDY (SEQ ID NO:2051)
RS9.F6 and RS.F10 CDR-L1 amino acid sequence	RSSQSLVHNNGNTFLH (SEQ ID NO:2052)
RS9.F6 CDR-L2 amino acid sequence	VSNRFS (SEQ ID NO:2053)
RS9.F6 and RS.F10 CDR-L3 amino acid sequence	SQTTHVPPT (SEQ ID NO:2054)
21D11 VH amino acid sequence	QVQLQQSGAELARPGASVKLSCKASGYTFTSYWIQWVKQRPGQGLE WIGTIYPGDGDARYTQKFKGKATLTADKSSSTTYMQLNSLASEDSAV YYCARNGITTAGYYAMDYWGQGTSVTVSS (SEQ ID NO:2055)

Description	Sequence
21D4.D1 VH amino acid sequence	QVQLQQSGADLLRPGVSVKISCKGSGYTFTDHAMHWVKQSHAESLE WIGVISTYSGDTGYNQKFKGKATMTVDKSSSTAYLELARLTSEDSAIY YCAREGHYDDAMDYWGQGTSVTVSS (SEQ ID NO:2056)
26D2 VH amino acid sequence	EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLE WIGYINPYTDGTKYNEKFKGKATLTSDKSSSTAYMDLSSLTSEDSAVY YCARGEVRRYALDYWGQGTSVTVSS (SEQ ID NO:2057)
26E2.A3 VH amino acid sequence; 24B4.A1 VH amino acid sequence	QVHLQQSGSELRSPGSSVKLSCKDFDSEVFPISYMSWIRQKPGHGFEW IGDILPSIGGRIYGVKFEDRATLDADTVSNTAYLELNSLTSEDSAIYYC ARKDYGSLAYWGQGTLVTVSA (SEQ ID NO:2058)
3D3.A1 VH amino acid sequence	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWI GGVIPNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYC ARGDDSYRRGYALDYWGQGTSVTVSS (SEQ ID NO:2059)
40H3.A4 VH amino acid sequence	EVQLQQSGAEVVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLE WIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVY YCATLFAYWGQGTLVTVSA (SEQ ID NO:2060)
42E8.H1 VH amino acid sequence	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLE WMGYINYSGRTIYNPSLKSRISITRDTSKNHFFLQLISVTTEDTATYYC ARWNGNYGFAYWGQGTLVTVSA (SEQ ID NO:2061)
49H1 LB 1 VH amino acid sequence	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNRLE WMGYISFSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYC ARWNGNYGFAYWGQGTLVTVSA (SEQ ID NO:2062)
54C2.A1 VH amino acid sequence	QVHLQQSGSELRSPGSSVKLSCKDFDSEVFPIAYMSWVRQKPGHGFE WIGDILPSIGRRIYGVKFEDKATLDADTVSNTAYLELNSLTSEDSAIYY CTRKDYGSLAYWGQGTLVTVSA (SEQ ID NO:2063)
57D7.A1 VH amino acid sequence	QVQLKESGPGLVAPSQSLSITCTVSGFSLSRYSVYWVRQPPGKGLEWL GMIWGGGNTDYNSALKSRLSISKDNSKSQVFLKMNSLQTDDSAMYY CVQYGGMDYWGQGTSVTVSS (SEQ ID NO:2064)
RS9.F6 VH amino acid sequence; RS.F10 VH amino acid sequence	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLE WIGRSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAV YYCVRTSGTGDYWGQGTSLTVSS (SEQ ID NO:2065)
2 ID 11 VL amino acid sequence	DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQGRSPQLLV YAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGYYYCQHFWGTP YTFGGGTKVEIK (SEQ ID NO:2066)
2 1D4.D 1 VL amino acid sequence	DVVMTQTPLTLSVTIGQPASFSCKSSQSLLDSDGKTYLNWLLRRPGQS PKRLIYVVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQG THFPYTFGGGTKLEIK (SEQ ID NO:2067)
26D2 VL amino acid sequence	DIQMTQSSSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLIS GATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVATYYCQQYWSTPWT FGGGTKLEIK (SEQ ID NO:2068)

Description	Sequence
26E2.A3 VL amino acid sequence; 24B4.A1 VL amino acid sequence	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHINGNTYLQWFLQKPGQS PKLLIYKVSNRFSGVPDRFSGSGSGTAFTLKISRVEAEDLGVYFCSQST HVPYTFGGGTKLEIK (SEQ ID NO:2069)
3D3.A1 VL amino acid sequence	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKSYLAWYQQKPG QSPKLLIYWASTRESGVPDRFRGSGSGTDFTLTISSVKAEDLAVYYCQ QYFSYPPTFGGGTKLEIK (SEQ ID NO:2070)
40H3.A4 VL amino acid sequence	DIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSP QLLIYQMSNLASGVPDRFSSSGSGIDFTLRINRVEAEDVGVYYCAQNL ELPTFGSGTKLEIK (SEQ ID NO:2071)
42E8.H1 VL amino acid sequence	DVVMTQNPLSLPVSLGDQASISCRSSQSLVHINGNTYLHWYLQKPGQS PKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTT HALFTFGSGTKLEIK (SEQ ID NO:2072)
49H1 LB 1 VL amino acid sequence	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHINGNTYLHWYLQKPGQS PKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQST HVTFTFGSGTKLEIK (SEQ ID NO:2073)
54C2.A1 VL amino acid	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHINGNTYLQWYLQKPGQS PKLLIYKVSNRFSGVPDRFSGSGSGTDFTLRISRVEAEDLGVYFCSQST HLPYTFGGGTKLEIK (SEQ ID NO:2074)
57D7.A1 VL amino acid sequence	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQS PKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGS HVPYTFGGGTKLEIK (SEQ ID NO:2075)
RS9.F6 VL amino acid sequence; RS.F10 VL amino acid sequence	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHNNGNTFLHWYLQKPGQ SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQT THVPPTFGGGTKLEIK (SEQ ID NO:2076)
RS9.F6 and RS.F10 CDR-H1	GYTFTSYWMH (SEQ ID NO:2077)
RS9.F6 and RS.F10 CDR-H2	RSDPTTGGTNYNEKFKT (SEQ ID NO:2078)
RS9.F6, RS.F10, 26E2.A3, 24B4.A1, 42E8.H1, 49H11.B1, 54C2.Al, and 57D7.A1 CDR-L2	KVSNRFS (SEQ ID NO:2079)
2ID11 CDR-H1	GYTFTSYWIQ (SEQ ID NO:2080)
2 ID 11 CDR-H2	TIYPGDGDARYTQKFKG (SEQ ID NO:2081)
2 ID 11 CDR-H3	ARNGITTAGYYAMDY (SEQ ID NO:2082)
2ID11 CDR-L1	RASENIYSNLA (SEQ ID NO:2083)
2 ID 11 CDR-L2	AATNLAD (SEQ ID NO:2084)
2 ID 11 CDR-L3	QHFWGTPYT (SEQ ID NO:2085)
21D4.D1 CDR-H1	GYTFTDHAMH (SEQ ID NO:2086)

Description	Sequence
21D4.D1 CDR-H2	VISTYSGDTGYNQKFKG (SEQ ID NO:2087)
21D4.D1 CDR-H3	AREGHYDDAMDY (SEQ ID NO:2088)
21D4.D1 and 51D4 CDR-L1	KSSQSLLDSDGKTYLN (SEQ ID NO:2089)
21D4.D1 CDR-L2	VVSKLDS (SEQ ID NO:2090)
21D4.D1 and 51D4 CDR-L3	WQGTHFPYT (SEQ ID NO:2091)
26D2 CDR-H1	GYTFTSYVMH (SEQ ID NO:2092)
26D2 CDR-H2	YINPYTDGTKYNEKFKG (SEQ ID NO:2093)
26D2 CDR-H3	ARGEVRRYALDY (SEQ ID NO:2094)
26D2 CDR-L1	KASEDIYNRLA (SEQ ID NO:2095)
26D2 CDR-L2	GATSLET (SEQ ID NO:2096)
26D2 CDR-L3	QQYWSTPWT (SEQ ID NO:2097)
26E2.A3 and 24B4.A1 CDR-Hl	DSEVFPISYMS (SEQ ID NO:2098)
26E2.A3 and 24B4.A1 CDR-H2	DILPSIGGRIYGVKF (SEQ ID NO:2099)
26E2.A3 and 24B4.A1 CDR-H3	ARKDYGSLAY (SEQ ID NO:2100)
26E2.A3, 24B4.A1, and 54C2.A1 CDR-L1	RSSQSLVHINGNTYLQ (SEQ ID NO:2101)
26E2.A3 and 24B4.A1 CDR-L3	SQSTHVPYT (SEQ ID NO:2102)
3D3.A1 CDR-H1	GYTLSEYTMH (SEQ ID NO:2103)
3D3.A1 CDR-H2	GVIPNSGGTSYNQKFRD (SEQ ID NO:2104)
3D3.A1 CDR-H3	ARGDDSYRRGYALDY (SEQ ID NO:2105)
3D3.A1 CDR-L1	KSSQSLLYSSNQKSYLA (SEQ ID NO:2106)
3D3.A1 CDR-L2	WASTRES (SEQ ID NO:2107)
3D3.A1 CDR-L3	QQYFSYPPT (SEQ ID NO:2108)
40H3.A4 CDR-H1	GFNIKDTYMH (SEQ ID NO:2109)
40H3.A4 CDR-H2	RIDPANGNTKYDPKFQG (SEQ ID NO:2110)
40H3.A4 CDR-H3	ATLFAY (SEQ ID NO:2111)
40H3.A4 CDR-L1	RSSKSLLHSNGITYLY (SEQ ID NO:2112)
40H3.A4 CDR-L2	QMSNLAS (SEQ ID NO:2113)
40H3.A4 CDR-L3	AQNLELPT (SEQ ID NO:2114)
42E8.H1 and 49Hll.Bl CDR-H1	GYSITSDYAWN (SEQ ID NO:2115)
42E8.H1 CDR-H2	YINYSGRTIYNPSLKS (SEQ ID NO:2116)

Description	Sequence
42E8.H1 and 49Hll.Bl CDR-H3	ARWNGNYGFAY (SEQ ID NO:2117)
42E8.H1 and 49Hll.Bl CDR-L1	RSSQSLVHINGNTYLH (SEQ ID NO:2118)
42E8.H1 CDR-L3	SQTTHALFT (SEQ ID NO:2119)
49H11.B1 CDR-H2	YISFSGSTSYNPSLKS (SEQ ID NO:2120)
49H11.B1 CDR-L3	SQSTHVTFT (SEQ ID NO:2121)
54C2.A1 CDR-H1	DSEVFPIAYMS (SEQ ID NO:2122)
54C2.A1 CDR-H2	DILPSIGRRIYGVKFED (SEQ ID NO:2123)
54C2.A1 CDR-H3	KDYGSLAY (SEQ ID NO:2124)
54C2.A1 CDR-L3	SQSTHLPYT (SEQ ID NO:2125)
57D7.A1 CDR-H1	GFSLSRYSVY (SEQ ID NO:2126)
57D7.A1 CDR-H2	MIWGGGNTDYNSALKS (SEQ ID NO:2127)
57D7.A1 CDR-H3	YGGMDY (SEQ ID NO:2128)
57D7.A1 CDR-L1	RSSQSIVHSNGNTYLE (SEQ ID NO:2129)
57D7.A1 CDR-L3	FQGSHVPYT (SEQ ID NO:2130)
RS9.F6-Fd	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLE WIGRSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAV YYCVRTSGTGDYWGQGTSLTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH (SEQ ID NO:2131)
RS9.F6-Fd fused to Fc with LALAPG, TfR binding, and knob mutations	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLE WIGRSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAV YYCVRTSGTGDYWGQGTSLTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAP IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVL WESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGFVFSCSV MHEALHNHYTQKSLSLSPGK (SEQ ID NO:2132)
RS9.F6-Fd fused to Fc with LALAPG and hole mutations	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQSPGRGLE WIGRSDPTTGGTNYNEKFKTKATLTVDKPSSTAYMQLSSLTSDDSAV YYCVRTSGTGDYWGQGTSLTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAP IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK (SEQ ID NO:2133)

Description	Sequence
3D3.A1-Fd	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWI GGVIPNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYC ARGDDSYRRGYALDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH (SEQ ID NO:2134)
3D3.A1-Fd fused to Fc with LALAPG, TfR binding, and knob mutations	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWI GGVIPNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYC ARGDDSYRRGYALDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYP SDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQGF VFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2135)
3D3.A1-Fd fused to Fc with LALAPG and hole mutations	EVQLQQSGPELVKPGASVKISCKTSGYTLSEYTMHWVIQSHGKSLEWI GGVIPNSGGTSYNQKFRDKASLTVDKSSSTAYLELRSLTSEDSAVYYC ARGDDSYRRGYALDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2136)
Human TREM2 protein	MEPLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKH WGRRKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAIT DDTLGGTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVL ADPLDHRDAGDLWFPGESESFEDAHVEHSISRSLLEGEIPFPPTSI LLLLACIFLIKILAASALWAAAWHGQKPGTHPPSELDCGHDPGY QLQTLPGLRDT (SEQ ID NO:1)
Human transferrin receptor protein 1 (TFR1)	MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEE NADNNTKANVTKPKRCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEP KTECERLAGTESPVREEPGEDFPAARRLYWDDLKRKLSEKLDSTDFTG TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKVWRDQHFVK IQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHAN FGTKKDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMD QTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPV QTISRAAAEKLFGNMEGDCPSDWKTDSTCRMVTSESKNVKLTVSNVL KEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLK LAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHL KAFTYINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQ

Description	Sequence
	DSNWASKVEKLTLDNAAFPFLAYSGIPAVSFCFCEDTDYPYLGTTMD TYKELIERIPELNKVARAAAEVAGQFVIKLTHDVELNLDYERYNSQLL SFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFGNAEKT DRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALL ENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNE F (SEQ ID NO:2137)
Wild-type human Fc sequence positions 231-447 EU index numbering	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2138)
Human IgG1 hinge sequence	EPKSCDKTHTCPPCP (SEQ ID NO:2139)
Clone CH3C.35.20	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2140)
Clone CH3C.35.21	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2141)
Clone CH3C.35.22	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2142)
Clone CH3C.35.23	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2143)
Clone CH3C.35.24	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2144)
Clone CH3C.35.21. 17	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2145)

Description	Sequence
Clone CH3C.35.20.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2146)
Clone CH3C.35.20.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2147)
Clone CH3C.35.20.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2148)
Clone CH3C.35.20.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2149)
Clone CH3C.35.20.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2150)
Clone CH3C.35.20.6	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2151)
Clone CH3C.35.21.a.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2152)
Clone CH3C.35.21.a.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2153)
Clone CH3C.35.21.a.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF

Description	Sequence
	YPSDIAVWWESYGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2154)
Clone CH3C.35.21.a.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2155)
Clone CH3C.35.21.a.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESFGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2156)
Clone CH3C.35.21.a.6	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESFGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2157)
Clone CH3C.35.23.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2158)
Clone CH3C.35.23.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2159)
Clone CH3C.35.23.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2160)
Clone CH3C.35.23.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2161)
Clone CH3C.35.23.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2162)

Description	Sequence
Clone CH3C.35.23.6	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2163)
Clone CH3C.35.24.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2164)
Clone CH3C.35.24.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2165)
Clone CH3C.35.24.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2166)
Clone CH3C.35.24.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2167)
Clone CH3C.35.24.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESFGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2168)
Clone CH3C.35.24.6	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESFGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2169)
Clone CH3C.35.21. 17.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2170)
Clone CH3C.35.21. 17.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF

Description	Sequence
	YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2171)
Clone CH3C.35.21. 17.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2172)
Clone CH3C.35.21. 17.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2173)
Clone CH3C.35.21. 17.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESFGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2174)
Clone CH3C.35.21. 17.6	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESFGTEWVSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2175)
Clones CH3C.35.N390 and CH3C.35.N163	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2176)
Clone CH3C.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGLVWVGYKTTPPVLDSDGSFFLYSKLTVAKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2177)
Clone CH3C.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTVWSHYKTTPPVLDSDGSFFLYSKLTVSKSEWQQ GYVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2178)
Clone CH3C.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSQYKTTPPVLDSDGSFFLYSKLTVEKSDWQQ GHVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2179)

Description	Sequence
Clone CH3C.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESVGTPWALYKTTPPVLDSDGSFFLYSKLTVLKSEWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2180)
Clone CH3C. 17	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTVWSKYKTTPPVLDSDGSFFLYSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2181)
Clone CH3C. 18	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2182)
Clone CH3C.21	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGLVWVGYKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2183)
Clone CH3C.25	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESMGHVWVGYKTTPPVLDSDGSFFLYSKLTVDKSTWQ QGWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2184)
Clone CH3C.34	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGLVWVFSKTTPPVLDSDGSFFLYSKLTVPKSTWQQG WVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2185)
Clone CH3C.35	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKSEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2186)
Clone CH3C.44	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2187)
Clone CH3C.51	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF

Description	Sequence
	YPSDIAVEWESLGHVWVGYKTTPPVLDSDGSFFLYSKLTVSKSEWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2188)
Clone CH3C.3. 1-3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVATKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2189)
Clone CH3C.3. 1-9	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGPVWVHTKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2190)
Clone CH3C.3.2-5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVDQKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2191)
Clone CH3C.3.2-19	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVNQKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2192)
Clone CH3C.3.2-1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVNFKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2193)
Clone CH3C. 18 variant	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2194)
Clone CH3C. 18 variant	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2195)
Clone CH3C. 18 variant	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVYWESLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2196)

Description	Sequence
Clone CH3C. 18 variant	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWAVYQTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2197)
Clone CH3C. 18 variant	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWAVYFTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2198)
Clone CH3C. 18 variant	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWAVYHTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2199)
Clone CH3C.35. 13	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESLGHVWAVYKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2200)
Clone CH3C.35. 14	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWAVYQTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2201)
Clone CH3C.35. 15	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESLGHVWAVYQTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2202)
Clone CH3C.35. 16	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESLGHVWVNQKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2203)
Clone CH3C.35. 17	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVNQQTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2204)
Clone CH3C.35. 18	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF

Description	Sequence
	YPSDIAVWWESLGHVWVNQQTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2205)
Clone CH3C.35. 19	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2206)
Clone CH3C.35.K165Q	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSSYQTTPPVLDSDGSFFLYSKLTVTKSEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2207)
Clone CH3C.35.N163. K165Q	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYQTTPPVLDSDGSFFLYSKLTVTKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2208)
Clone CH3C.35.21.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKSEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2209)
Clone CH3C.35.21.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTKSEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2210)
Clone CH3C.35.21.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2211)
Clone CH3C.35.21.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTGEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2212)
Clone CH3C.35.21.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQG FVFSCWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2213)

Description	Sequence
Clone CH3C.35.21.6	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTKEEWQQG FVFSCWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2214)
Clone CH3C.35.21.7	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQG FVFTCWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2215)
Clone CH3C.35.21.8	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQG FVFTCGVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2216)
Clone CH3C.35.21.9	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQG FVFECWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2217)
Clone CH3C.35.21. 10	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQG FVFKCWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2218)
Clone CH3C.35.21.il	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTPEEWQQG FVFKCWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2219)
Clone CH3C.35.21. 12	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2220)
Clone CH3C.35.21. 13	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTGEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2221)
Clone CH3C.35.21. 14	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF

Description	Sequence
	YPSDIAVWWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQ GFVFTCWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2222)
Clone CH3C.35.21. 15	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTGEEWQQ GFVFTCWVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2223)
Clone CH3C.35.21. 16	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTREEWQQ GFVFTCGVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2224)
Clone CH3C.35.21. 18	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWSSYRTTPPVLDSDGSFFLYSKLTVTKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2225)
Clone CH3B.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRFDYVTTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYGFHDLSLSPGK (SEQ ID NO:2226)
Clone CH3B.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRFDMVTTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYGFHDLSLSPGK (SEQ ID NO:2227)
Clone CH3B.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRFEYVTTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYGFHDLSLSPGK (SEQ ID NO:2228)
Clone CH3B.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRFEMVTTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYGFHDLSLSPGK (SEQ ID NO:2229)
Clone CH3B.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRFELVTTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYGFHDLSLSPGK (SEQ ID NO:2230)

Description	Sequence
Clone CH2A2.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVEFIWYV DGVDVRYEWQLPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2231)
Clone CH2A2.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVGFVWY VDGVPVSWEWYWPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2232)
Clone CH2A2.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFDWY VDGVMVRREWHRPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2233)
Clone CH2A2.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVSFEWY VDGVPVRWEWQWPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2234)
Clone CH2A2.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVAFTWY VDGVPVRWEWQNPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2235)
Clone CH2C.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDPQTPPWEVKFNWY VDGVEVHNAKTKPREEEYYTYYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2236)
Clone CH2C.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDPPSPPWEVKFNWY VDGVEVHNAKTKPREEEYYSNYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2237)
Clone CH2C.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDPQTPPWEVKFNWY VDGVEVHNAKTKPREEEYYSNYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2238)
Clone CH2C.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDFRGPPWEVKFNWY VDGVEVHNAKTKPREEEYYHDYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF

Description	Sequence
	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2239)
Clone CH2C.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDPQTVPWEVKFNWY VDGVEVHNAKTKPREEEYYSNYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2240)
Clone CH2D.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSVPPRMVKFNWY VDGVEVHNAKTKSLTSQHNSTVRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2241)
Clone CH2D.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSVPPWMVKFNW YVDGVEVHNAKTKSLTSQHNSTVRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2242)
Clone CH2D.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDMWEYVKFNW YVDGVEVHNAKTKPWVKQLNSTWRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2243)
Clone CH2D.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDDWTWVKFNW YVDGVEVHNAKTKPWIAQPNSTWRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2244)
Clone CH2D.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDDWEWVKFNW YVDGVEVHNAKTKPWKLQLNSTWRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2245)
Clone CH2E3.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPWVWFYW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCS VVNIALWWSIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2246)
Clone CH2E3.2	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPVVGFRWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCRVS NSALTWKIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2247)

Description	Sequence
Clone CH2E3.3	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPVVGFRWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCRVS NSALSWRIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2248)
Clone CH2E3.4	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPIVGFRWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCRVS NSALRWRIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2249)
Clone CH2E3.5	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPAVGFEWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCQV FNWALDWVIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2250)
Fc sequence with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2251)
Fc sequence with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2252)
Fc sequence with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2253)
Fc sequence with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2254)
Fc sequence with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2255)
Fc sequence with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG

Description	Sequence
	FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2256)
Fc sequence with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2257)
Fc sequence with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2258)
Clone CH3C.35.21 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2259)
Clone CH3C.35.21 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2260)
Clone CH3C.35.21 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2261)
Clone CH3C.35.21 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2262)
Clone CH3C.35.21 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2263)
Clone CH3C.35.21 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2264)

Description	Sequence
Clone CH3C.35.21 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2265)
Clone CH3C.35.21 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2266)
Clone CH3C.35.20.1 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2267)
Clone CH3C.35.20.1 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2268)
Clone CH3C.35.20.1 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2269)
Clone CH3C.35.20.1 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2270)
Clone CH3C.35.20.1 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2271)
Clone CH3C.35.20.1 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2272)
Clone CH3C.35.20.1 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF

Description	Sequence
	YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2273)
Clone CH3C.35.20.1 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2274)
Clone CH3C.35.20.1 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2275)
Clone CH3C.35.20.1 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2276)
Clone CH3C.35.20.1 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2277)
Clone CH3C.35.20.1 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2278)
Clone CH3C.35.23.2 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2279)
Clone CH3C.35.23.2 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2280)
Clone CH3C.35.23.2 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2281)

Description	Sequence
Clone CH3C.35.23.2 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2282)
Clone CH3C.35.23.2 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2283)
Clone CH3C.35.23.2 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2284)
Clone CH3C.35.23.2 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2285)
Clone CH3C.35.23.2 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2286)
Clone CH3C.35.23.2 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2287)
Clone CH3C.35.23.2 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2288)
Clone CH3C.35.23.2 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2289)
Clone CH3C.35.23.2 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG

Description	Sequence
	FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2290)
Clone CH3C.35.23.3 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2291)
Clone CH3C.35.23.3 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2292)
Clone CH3C.35.23.3 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2293)
Clone CH3C.35.23.3 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2294)
Clone CH3C.35.23.3 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2295)
Clone CH3C.35.23.3 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2296)
Clone CH3C.35.23.3 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2297)
Clone CH3C.35.23.3 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2298)

Description	Sequence
Clone CH3C.35.23.3 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2299)
Clone CH3C.35.23.3 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2300)
Clone CH3C.35.23.3 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2301)
Clone CH3C.35.23.3 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2302)
Clone CH3C.35.23.4 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2303)
Clone CH3C.35.23.4 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2304)
Clone CH3C.35.23.4 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2305)
Clone CH3C.35.23.4 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2306)
Clone CH3C.35.23.4 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG

Description	Sequence
	FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2307)
Clone CH3C.35.23.4 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2308)
Clone CH3C.35.23.4 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2309)
Clone CH3C.35.23.4 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2310)
Clone CH3C.35.23.4 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2311)
Clone CH3C.35.23.4 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2312)
Clone CH3C.35.23.4 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2313)
Clone CH3C.35.23.4 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2314)
Clone CH3C.35.21. 17.2 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2315)

Description	Sequence
Clone CH3C.35.21.17.2 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2316)
Clone CH3C.35.21.17.2 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2317)
Clone CH3C.35.21.17.2 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2318)
Clone CH3C.35.21.17.2 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2319)
Clone CH3C.35.21.17.2 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2320)
Clone CH3C.35.21.17.2 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2321)
Clone CH3C.35.21.17.2 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2322)
Clone CH3C.35.21.17.2 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2323)
Clone CH3C.35.21.17.2 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF

Description	Sequence
	YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2324)
Clone CH3C.35.21. 17.2 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2325)
Clone CH3C.35.21. 17.2 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2326)
Clone CH3C.35.23 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2327)
Clone CH3C.35.23 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2328)
Clone CH3C.35.23 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2329)
Clone CH3C.35.23 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2330)
Clone CH3C.35.23 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2331)
Clone CH3C.35.23 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2332)

Description	Sequence
Clone CH3C.35.23 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2333)
Clone CH3C.35.23 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2334)
Clone CH3C.35.23 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2335)
Clone CH3C.35.23 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2336)
Clone CH3C.35.23 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2337)
Clone CH3C.35.23 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2338)
CH3C motif	YxTEWSS (SEQ ID NO:2339)
CH3C motif	TxxExxxxF (SEQ ID NO:2340)
mulgGI 3' VH PCR primer	GGACAGGGATCCAGAGTTCC (SEQ ID NO:2341)
mu3/4G2 3' VH PCR primer	AGCTGGGAAGGTGTGCACAC (SEQ ID NO:2342)
mu3/4G3 3' VH PCR primer	CAGGGGCCAGTGGATAGAC (SEQ ID NO:2343)
muCkappa.1 3' VL PCR primer	GACATTGATGTCTTTGGGGT (SEQ ID NO:2344)
muCkappa.2 3' VL PCR primer	TTCACTGCCATCAATCTTCC (SEQ ID NO:2345)

Description	Sequence
7B10.A2 VH amino acid sequence	EVQLQQSGPELVKPGASVKMSCKASGYTFTDYNMHWVKQSHGKSLE WIGYINPNNGGTTYNQKFKGKATLTVNKSSSTAYMELRSLTSEDSAV YYCATYNNHYFDSWGQGTTLTVSS (SEQ ID NO:2346)
7B10.A2 CDR-H1	GYTFTDYNMH (SEQ ID NO:2347)
7B10.A2 CDR-H2	YINPNNGGTTYNQKFKG (SEQ ID NO:2348)
7B10.A2 CDR-H3	ATYNNHYFDS (SEQ ID NO:2349)
7B10.A2 VL amino acid sequence	DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLI YYTSNLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYSNLPYT FGGGTKLEIK (SEQ ID NO:2350)
7B10.A2 CDR-L1	SASQGISNYLN (SEQ ID NO:2351)
7B10.A2 CDR-L2	YTSNLHS (SEQ ID NO:2352)
7B10.A2 CDR-L3	QQYSNLPYT (SEQ ID NO:2353)
51D4 VH amino acid sequence	QVHLQQSGPEVVRPGVSVKISCKGSGYTFTDYGMHWVKQSHAKSLE WIGVISTYNGNTSYNQKYKGKATVTVDKPSSTAYMELVRLTSEDSAI YYCARDFGYVPFDYWGQGTTLTVSS (SEQ ID NO:2354)
51D4 CDR-H1	GYTFTDYGMH (SEQ ID NO:2355)
51D4 CDR-H2	VISTYNGNTSYNQKYKG (SEQ ID NO:2356)
51D4 CDR-H3	ARDFGYVPFDY (SEQ ID NO:2357)
51D4 VL amino acid sequence	DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRP GQSPKRLIYLVSYLDSGVPDRFTGSGSGTDFTLKISRVEADDLGV YYCWQGTHFPYTFGGGTKLEIK (SEQ ID NO:2358)
51D4 CDR-L2	LVSYLDS (SEQ ID NO:2359)
CDR-H1 consensus sequence	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 (SEQ ID NO:2360)
CDR-H1 consensus sequence	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 (SEQ ID NO:2361)
CDR-H1 consensus sequence	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 (SEQ ID NO:2362)
CDR-H1 consensus sequence	GYTX4X5X6X8X9X10X11, wherein X4 is F or L; X is T or S; X6 is D, S, or E; X8 is H, Y; X9 is A, N, G, V, W, T; X10 is M or I; and X11 is H or Q (SEQ ID NO:2363)
CDR-H2 consensus sequence	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 (SEQ ID NO:2364)

Description	Sequence
CDR-H2 consensus sequence	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 (SEQ ID NO:2365)
CDR-H2 consensus sequence	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 (SEQ ID NO:2366)
CDR-H3 consensus sequence	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 (SEQ ID NO:2367)
CDR-L1 consensus sequence	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 (SEQ ID NO:2368)
CDR-L1 consensus sequence	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 (SEQ ID NO:2369)
CDR-L2 consensus sequence	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 (SEQ ID NO:2370)
CDR-L3 consensus sequence	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 (SEQ ID NO:2371)
CDR-L3 consensus sequence	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 (SEQ ID NO:2372)
Human TREM2 extracellular domain (ECD) amino acid sequence (without signal peptide and His tag)	SGAHNTTVFQGVAGQSLQVSCPYDSMKHWGRRKAWCRQLGEK GPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLGGTLTITLRNLQP HDAGLYQCQSLHGSEADTLRKVLVEVLADPLDHRDAGDLWFPG ESESFEDAHVEHSISRSLLEGEIPFPPTS (SEQ ID NO:2373)
Human TREM2 peptide	DLWFPGESES (SEQ ID NO:2374)
Human TREM2 peptide 9-mer amino acid sequence	DLWFPGESE (SEQ ID NO:2375)
Human TREM2 peptide sequence	DLWFP (SEQ ID NO:2376)

Description	Sequence
(residues 140-144 of full-length TREM2)	
Clone CH3C.18.3.4-1 (CH3C.3.4-1)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESWGFVWSTYKTTPPVLDSDGSFFLYSKLTVPKSNWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2377)
Clone CH3C.18.3.4-19 (CH3C.3.4-19)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESWGHVWSTYKTTPPVLDSDGSFFLYSKLTVPKSNWQQ GYVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2378)
Clone CH3C.18.3.2-3 (CH3C.3.2-3)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVEQKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2379)
Clone CH3C.18.3.2-14 (CH3C.3.2-14)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVGVKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2380)
Clone CH3C.18.3.2-24 (CH3C.3.2-24)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVHTKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2381)
Clone CH3C.18.3.4-26 (CH3C.3.4-26)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESWGTVWGTYKTTPPVLDSDGSFFLYSKLTVPKSNWQQ GYVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2382)
Clone CH3C.18.3.2-17 (CH3C.3.2-17)	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESLGHVWVGTKTTPPVLDSDGSFFLYSKLTVPKSTWQQ GWVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2383)
Clone CH3C.35.20.1.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2384)

Description	Sequence
Clone CH3C.35.23.2.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2385)
Clone CH3C.35.23. 1.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2386)
Clone CH3C.35.S413	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKSEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2387)
Clone CH3C.35.23.3.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2388)
Clone CH3C.35.N390.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2389)
Clone CH3C.35.23.6.1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWVNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2390)
Clone CH3C.35.21 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2391)
Clone CH3C.35.21 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2392)
Clone CH3C.35.21 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG

Description	Sequence
	FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2393)
Clone CH3C.35.21 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2394)
Clone CH3C.35.20.1.1 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2395)
Clone CH3C.35.20.1.1 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2396)
Clone CH3C.35.20.1.1 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2397)
Clone CH3C.35.20.1.1 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2398)
Clone CH3C.35.20.1.1 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2399)
Clone CH3C.35.20.1.1 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2400)
Clone CH3C.35.20.1.1 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2401)

Description	Sequence
Clone CH3C.35.20.1.1 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2402)
Clone CH3C.35.20.1.1 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2403)
Clone CH3C.35.20.1.1 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2404)
Clone CH3C.35.20.1.1 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2405)
Clone CH3C.35.20.1.1 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2406)
Clone CH3C.35.23.2.1 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2407)
Clone CH3C.35.23.2.1 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2408)
Clone CH3C.35.23.2.1 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2409)
Clone CH3C.35.23.2.1 with	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG

Description	Sequence
knob and YTE mutations	FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2410)
Clone CH3C.35.23.2.1 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2411)
Clone CH3C.35.23.2.1 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2412)
Clone CH3C.35.23.2.1 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2413)
Clone CH3C.35.23.2.1 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2414)
Clone CH3C.35.23.2.1 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2415)
Clone CH3C.35.23.2.1 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2416)
Clone CH3C.35.23.2.1 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2417)
Clone CH3C.35.23.2.1 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQ QGFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2418)

Description	Sequence
Clone CH3C.35.23.1.1 with knob mutation	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2419)
Clone CH3C.35.23.1.1 with knob and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2420)
Clone CH3C.35.23.1.1 with knob and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2421)
Clone CH3C.35.23.1.1 with knob and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2422)
Clone CH3C.35.23.1.1 with knob, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2423)
Clone CH3C.35.23.1.1 with knob, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2424)
Clone CH3C.35.23.1.1 with hole mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2425)
Clone CH3C.35.23.1.1 with hole and LALA mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2426)
Clone CH3C.35.23.1.1 with hole and LALAPG mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG

Description	Sequence
	FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2427)
Clone CH3C.35.23. 1.1 with hole and YTE mutations	APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2428)
Clone CH3C.35.23. 1.1 with hole, LALA, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2429)
Clone CH3C.35.23. 1.1 with hole, LALAPG, and YTE mutations	APEAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2430)
Clone CH3C.35.20.1 M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2431)
Clone CH3C.35.20.1 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2432)
Clone CH3C.35.20.1 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2433)
Clone CH3C.35.20.1 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2434)
Clone CH3C.35.20.1 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2435)

Description	Sequence
Clone CH3C.35.20.1 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2436)
Clone CH3C.35.20.1 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2437)
Clone CH3C.35.20.1.1 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2438)
Clone CH3C.35.20.1.1 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2439)
Clone CH3C.35.20.1.1 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2440)
Clone CH3C.35.20.1.1 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2441)
Clone CH3C.35.20.1.1 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2442)
Clone CH3C.35.20.1.1 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2443)
Clone CH3C.35.20.1.1 with hole, LALAPG, and	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG

Description	Sequence
M428L and N434S mutations	FYPSDIAVEWESFGTEWSSYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2444)
Clone CH3C.35.21 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2445)
Clone CH3C.35.21 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2446)
Clone CH3C.35.21 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2447)
Clone CH3C.35.21 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2448)
Clone CH3C.35.21 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2449)
Clone CH3C.35.21 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2450)
Clone CH3C.35.21 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVWWESYGTEWSSYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2451)
Clone CH3C.35.21. 17.2 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2452)

Description	Sequence
Clone CH3C.35.21.17.2 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2453)
Clone CH3C.35.21.17.2 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2454)
Clone CH3C.35.21.17.2 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2455)
Clone CH3C.35.21.17.2 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2456)
Clone CH3C.35.21.17.2 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2457)
Clone CH3C.35.21.17.2 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVLWESYGTEWASYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2458)
Clone CH3C.35.23 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2459)
Clone CH3C.35.23 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2460)
Clone CH3C.35.23 with knob, LALA,	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG

Description	Sequence
and M428L and N434S mutations	FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2461)
Clone CH3C.35.23 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2462)
Clone CH3C.35.23 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2463)
Clone CH3C.35.23 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2464)
Clone CH3C.35.23 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2465)
Clone CH3C.35.23. 1.1 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2466)
Clone CH3C.35.23. 1.1 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2467)
Clone CH3C.35.23. 1.1 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2468)
Clone CH3C.35.23. 1.1 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2469)

Description	Sequence
Clone CH3C.35.23.1.1 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2470)
Clone CH3C.35.23.1.1 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQG FVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2471)
Clone CH3C.35.23.1.1 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESFGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2472)
Clone CH3C.35.23.2 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2473)
Clone CH3C.35.23.2 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2474)
Clone CH3C.35.23.2 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2475)
Clone CH3C.35.23.2 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2476)
Clone CH3C.35.23.2 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2477)
Clone CH3C.35.23.2 with hole, LALA, and	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF

Description	Sequence
M428L and N434S mutations	YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2478)
Clone CH3C.35.23.2 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2479)
Clone CH3C.35.23.2.1 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2480)
Clone CH3C.35.23.2.1 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2481)
Clone CH3C.35.23.2.1 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2482)
Clone CH3C.35.23.2.1 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLYSKLTVSKSEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2483)
Clone CH3C.35.23.2.1 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2484)
Clone CH3C.35.23.2.1 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2485)
Clone CH3C.35.23.2.1 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWANYKTTPPVLDSDGSFFLVSKLTVSKSEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2486)

Description	Sequence
Clone CH3C.35.23.3 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2487)
Clone CH3C.35.23.3 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2488)
Clone CH3C.35.23.3 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2489)
Clone CH3C.35.23.3 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLYSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2490)
Clone CH3C.35.23.3 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2491)
Clone CH3C.35.23.3 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2492)
Clone CH3C.35.23.3 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWVNYKTTPPVLDSDGSFFLVSKLTVTKEEWQ QGFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2493)
Clone CH3C.35.23.4 with M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2494)
Clone CH3C.35.23.4 with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG

Description	Sequence
	FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2495)
Clone CH3C.35.23.4 with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2496)
Clone CH3C.35.23.4 with knob, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLYSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2497)
Clone CH3C.35.23.4 with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2498)
Clone CH3C.35.23.4 with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2499)
Clone CH3C.35.23.4 with hole, LALAPG, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKG FYPSDIAVEWESYGTEWSNYKTTPPVLDSDGSFFLVSKLTVSKEEWQQ GFVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2500)
Fc sequence with hole and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2501)
Fc sequence with hole, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2502)
Fc sequence with knob and M428L and N434S mutations	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2503)

Description	Sequence
Fc sequence with knob, LALA, and M428L and N434S mutations	APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:2504)
SS2_NHis_TREM2	MPALLSLVSLLSVLLMGCVAETGGSGHHHHHHSGTHNTTVFQGVAG QSLQVSCPYDSMKHWGRRKAWCRQLGEKGPCQRVVSTHNLWLLSFL RRWNGSTAITDDTLGGTLTITLRNLQPHDAGLYQCQSLHGSEADTLR KVLVEVLADPLDHRDAGDLWFPGESESFEDAHVEHSISRSLLEGEIPFP PTSAS (SEQ ID NO:2505)

[00245] 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 EN1)** and heavy chain constant regions **(TABLE EN2)** 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

[00246] 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.

[00247] 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.

[00248] 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.

[00249] 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.

[00250] 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.

[00251] 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.

[00252] In some embodiments, the antibody comprises the VH sequence shown in SEQ ID NO:2506, 2508, or 2510.

[00253] 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.

[00254] 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.

[00255] In some embodiments, the antibody is the 37012 antibody (see **TABLE H1**)

[00256] 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 H1** and **H2** respectively.

TABLE H1

Name	Sequence
37012 VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSLTNSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CTREWAGSGYFDYWGQGTLVTVSS (SEQ ID NO:2506)
37012 VL	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIY YTSNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFG QGTKLEIK (SEQ ID NO:2507)
37013VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSLTNSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CTREWAGSGYFDYWGQGTLVTVSS (SEQ ID NO:2508)

Name	Sequence
37013VL	DIQMTQSPSSLSASVGDRVTMTCKASQNVGNNLAWYQQKPGKAPKLL LYYTSNRFTGVPSRFSGSGSGTDFTLTISSVQPEDFATYYCQRIYNSPWT FGQGTKLELK (SEQ ID NO:2509)
37014VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VASLTNSGGSTYYADSVKGRFTLSRDNSKNTLYLQMNSLRAEDTAVYY CTREWAGSGYFDYWGQGTLVTVSS (SEQ ID NO:2510)
37014VL	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIY YTSNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFG QGTKLEIK (SEQ ID NO:2511)
37017VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSLTNSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKEWAGSGYFDYWGQGTLVTVSS (SEQ ID NO:2512)
37017VL	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIY YTSNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFG QGTKLEIK (SEQ ID NO:2513)
Full 37012_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSLTNSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CTREWAGSGYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (SEQ ID NO:2529)
Full 37012 L	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIY YTSNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFG QGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC (SEQ ID NO:2530)
Full 37013_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSLTNSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CTREWAGSGYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (SEQ ID NO:2531)
Full 37013 L	DIQMTQSPSSLSASVGDRVTMTCKASQNVGNNLAWYQQKPGKAPKLL LYYTSNRFTGVPSRFSGSGSGTDFTLTISSVQPEDFATYYCQRIYNSPWT FGQGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV

Name	Sequence
	QWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2532)
Full 37014_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VASLTNSGGSTYYADSVKGRFTLSRDNSKNTLYLQMNSLRAEDTAVYY CTREWAGSGYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (SEQ ID NO:2533)
Full 37014 L	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIY YTSNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFG QGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC (SEQ ID NO:2534)
Full 37017_H	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSLTNSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKEWAGSGYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (SEQ ID NO:2535)
Full 37017_L	DIQMTQSPSSLSASVGDRVTITCKASQNVGNNLAWYQQKPGKAPKLLIY YTSNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRIYNSPWTFG QGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC (SEQ ID NO:2536)

TABLE H2: CDR's of humanized antibodies

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

[00257] 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 EN1)** and heavy chain constant regions **(TABLE EN2)** 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

[00258] 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.

[00259] 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.

[00260] 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.

[00261] 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.

[00262] 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.

[00263] 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.

[00264] 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.

[00265] 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.

[00266] 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.

[00267] 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.

[00268] 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.

[00269] 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.

[00270] 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.

[00271] 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.

[00272] 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 in **TABLE I1**:

TABLE I1

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

Antibody (ATCC # of the hybridoma)	Light chain variable region	Heavy chain variable region
HJ23.13 (PTA-125173)	SEQ ID NO:2574	SEQ ID NO:2575

[00273] 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 I2-4**.

TABLE I2

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		

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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	

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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	

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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					

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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				

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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 I3

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	

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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		

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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	

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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	

Antibody	Light Chain HVR			Heavy Chain HVR		
	L1	L2	L3	H1	H2	H3
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 I4

Comments	Sequence
HJ23.4 light chain variable region	DVVMTQTPLSLPVSLGDQAFISCRSSQNLVHSNGNTYLHWYLQK PGQSPKLLIYIVSNRFSGVPDRFSGSGSGTDFTLEISRVEAEDLGV YFCSQSTHVPLTFGAGTKLELK (SEQ ID NO:2539)
HJ23.4 heavy chain variable region	EVQLQQSGPDLVKPGASVKMSCKASGYTFTDYNIHWVKQSHGK TLEWIGYINPNTGGTYYNQKFKGKATMTVNKSSSTAYMELRSLT SEDSAVYYCVATRWDGVNWAQGTLVTVSA (SEQ ID NO:2540)
HJ23.4 L1	QNLVHSNGNTY (SEQ ID NO:2541)
HJ23.4 L2	IVS
HJ23.4 L3	SQSTHVPLT (SEQ ID NO:2542)
HJ23.4 H1	GYTFTDYN (SEQ ID NO:2543)
HJ23.4 H2	INPNTGGT (SEQ ID NO:2544)
HJ23.4 H3	VATRWDGVN (SEQ ID NO:2545)
HJ23.7 light chain variable region	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQK PGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGV YFCSQSTHVPLTFGAGTKLELK (SEQ ID NO:2546)
HJ23.7 heavy chain variable region	EVQLQQSGAELVKPGASVKLSCTSSGFNIKGYYIHWVKQRTEQG LEWIGRIDPEDGETKNAPKFQGKATFGTDTFSNTAYLRLSSLTSE DTGVYYCVRTETRGAYWGPGTLVTVSA (SEQ ID NO:2547)
HJ23.7 L1	QSLVHSNGNTY (SEQ ID NO:2548)
HJ23.7 L2	KVS
HJ23.7 L 3	SQSTHVPLT (SEQ ID NO:2549)
HJ23.7 H1	GFNIKGYY (SEQ ID NO:2550)
HJ23.7 H2	IDPEDGET (SEQ ID NO:2551)
HJ23.7 H3	VRTETRGAY (SEQ ID NO:2552)
HJ23.8 light chain variable region	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGDTYLHWYLQK RGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGV YFCSQTTHVPLTFGAGTKLELK (SEQ ID NO:2553)
HJ23.8 heavy chain variable region	QVPLQQPGAEFVKPGASVKLSCKASAYTFTRYWMHWVKQRPGR GLEWIGRIDPNSGGTNYNEKFKSKATFTVDKPSSTSYMQLSSLTS EDSAVYFCVFTGTLFDYWGQGTTLTVSS (SEQ ID NO:2554)
HJ23.8 L1	QSLVHSNGDTY (SEQ ID NO:2555)
HJ23.8 L2	KVS
HJ23.8 L3	SQTTHVPLT (SEQ ID NO:2556)
HJ23.8 H1	AYTFTRYW (SEQ ID NO:2557)
HJ23.8 H2	IDPNSGGT (SEQ ID NO:2558)
HJ23.8 H3	VFTGTLFDY (SEQ ID NO:2559)
HJ23.9 light chain variable region	DVVMTQTPLSLPVSLGDQASISCKSSQSLVHSNGNTYLHWYLQK PGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGV YFCSQSTHVPPTFGGGTKLEIK (SEQ ID NO:2560)

Comments	Sequence
HJ23.9 heavy chain variable region	EVQLQHSGPVLVKPGASVKMSCKSSGYTFTDYYLNWVKQSHGK SPEWIGVINPNTGSTSYNQKFKGKATLTVDKSSSTAYMDLNSLTS EDSAVYYCATHYYGSIYKQAWFAYWGQGTLVT (SEQ ID NO:2561)
HJ23.9 L1	QSLVHSNGNTY (SEQ ID NO:2562)
HJ23.9 L2	KVS
HJ23.9 L3	SQSTHVPPT (SEQ ID NO:2563)
HJ23.9 H1	GYTFTDYY (SEQ ID NO:2564)
HJ23.9 H2	INPNTGST (SEQ ID NO:2565)
HJ23.9 H3	ATHYYGSIYKQAWFAY (SEQ ID NO:2566)
HJ23.10 light chain variable region	DVVMTQTPLSLPVSLGDQASISCKSSQSLVHSNGNTYLHWYLQK PGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGI YFCSQSTHVPPTFGGGTKLEIK (SEQ ID NO:2567)
HJ23.10 heavy chain variable region	EVQLQHSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHG KSPEWIGVINPNTGSTSYNQKFKGKATLTVDKSSSTAYMDLNSLT SEDSAVYYCATHYYGSIYKQAWFAYWGQGTLVTV (SEQ ID NO:2568)
HJ23.10 L1	QSLVHSNGNTY (SEQ ID NO:2569)
HJ23.10 L2	KVS
HJ23.10 L3	SQSTHVPPT (SEQ ID NO:2570)
HJ23.10 H1	GYTFTDYY (SEQ ID NO:2571)
HJ23.10 H2	INPNTGST (SEQ ID NO:2572)
HJ23.10 H3	ATHYYGSIYKQAWFAY (SEQ ID NO:2573)
HJ23.13 light chain variable region	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNLKNYLAWFQQ KPGQSPKLLIYWASIRESGVPDRFTGSGSGTDFTLTINSVKAEDLA VYYCQQYYTFPLTFGAGTKLELK (SEQ ID NO:2574)
HJ23.13 heavy chain variable region	EVQLVETGGGLVQPKGSLKLSCAASGFSFNINAMHWVRQAPGT GLKWVARIRSGSNDFATYYADSVKDRFTISRDDSHSMLYLQMN NLKTEDTAIYFCVREYVNYFVHWGQGTLVTVSA (SEQ ID NO:2575)
HJ23.13 L1	QSLLYSSNLKNY (SEQ ID NO:2576)
HJ23.13 L2	WAS
HJ23.13 L3	QQYYTFPLT (SEQ ID NO:2577)
HJ23.13 H1	GFSFNINA (SEQ ID NO:2578)
HJ23.13 H2	IRSGSNDFAT (SEQ ID NO:2579)
HJ23.13 H3	VREYVNYFVH (SEQ ID NO:2580)
	DHRDAGDLWFPGES (SEQ ID NO:2581)
Consensus L1	QX1LVHSNGX2TY, where X1 is S, T, N, or Q and X2 is D or N (SEQ ID NO:2582)
Consensus L2	X1VS, where X1 is I or K

Comments	Sequence
Consensus L3	SQX1THVPX2T, where X1 is S, T, N, or Q and X2 is P or L (SEQ ID NO:2583)

[00274] 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 EN1**) and heavy chain constant regions (**TABLE EN2**) 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

[00275] 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.

[00276] 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.

[00277] 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.

[00278] 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.

[00279] In some embodiments, the antibody or antigen-binding fragment thereof comprises:

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.

[00280] 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.

[00281] 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.

[00282] 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.

[00283] 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.

[00284] 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.

[00285] 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.

[00286] In some embodiments, the antibody is an antibody disclosed in Table 1 of PCT Patent Application Publication No. WO2020/079580A1, reproduced below as **TABLE J1**.

TABLE J1: Sequences of Exemplary Monoclonal Antibodies That Bind Human TREM2

Description	**Sequence**
MOR44698A	
HCDR1 (Combined)	GYTFTGYHMS (SEQ ID NO: 2586)
HCDR2 (Combined)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Combined)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Kabat)	GYHMS (SEQ ID NO: 2589)
HCDR2 (Kabat)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Kabat)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Chothia)	GYTFTGY (SEQ ID NO: 2590)
HCDR2 (Chothia)	NPVSGN (SEQ ID NO: 2591)

HCDR3 (Chothia)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (IMGT)	GYTFTGYH (SEQ ID NO: 2592)
HCDR2 (IMGT)	INPVSGNT (SEQ ID NO: 2593)
HCDR3 (IMGT)	ARIPSYTYAFDY (SEQ ID NO: 2594)
VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSS (SEQ ID NO: 2595)
DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAG CGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTACCATAT GTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATGGGCGTTAT CAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTTCAGGGCCGGGT GACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTATCCCGTCTT ACACTTACGCTTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGTTAGCT CA (SEQ ID NO: 2596)
Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2597)
DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAG CGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTACCATAT GTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATGGGCGTTAT CAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTTCAGGGCCGGGT GACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTATCCCGTCTT ACACTTACGCTTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGTTAGCT CAGCCTCCACCAAGGGTCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGA GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC GTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCAGC GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACG AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGT GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGT ACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC

	CCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGG TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG CTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 2598)
LCDR1 (Combined)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Combined)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Combined)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Kabat)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Kabat)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Kabat)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Chothia)	SQDISNY (SEQ ID NO: 2602)
LCDR2 (Chothia)	RAS (SEQ ID NO: 2603)
LCDR3 (Chothia)	YRHMPSQ (SEQ ID NO: 2604)
LCDR1 (IMGT)	QDISNY (SEQ ID NO: 2605)
LCDR2 (IMGT)	RAS (SEQ ID NO: 2603)
LCDR3 (IMGT)	FQYRHMPSQT (SEQ ID NO: 2601)
VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK (SEQ ID NO: 2606)
DNA VL	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCTGGC TTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACCGTG CTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATCCG GCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGA CCTATTATTGCTTCCAGTACCGTCATATGCCGTCTCAGACCTTTGGCCAGGG CACGAAAGTTGAAATTAAA (SEQ ID NO: 2607)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 2608)
DNA Light Chain	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCTGGC TTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACCGTG CTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATCCG

	GCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGA CCTATTATTGCTTCCAGTACCGTCATATGCCGTCTCAGACCTTTGGCCAGGG CACGAAAGTTGAAATTAAACGTACGGTGGCCGCTCCCAGCGTGTTCATCTT CCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCC TGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGAC AACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACA GCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCT GTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGT (SEQ ID NO: 2609)
MOR44698B	
HCDR1 (Combined)	GYTFTGYHMS (SEQ ID NO: 2586)
HCDR2 (Combined)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Combined)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Kabat)	GYHMS (SEQ ID NO: 2589)
HCDR2 (Kabat)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Kabat)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Chothia)	GYTFTGY (SEQ ID NO: 2590)
HCDR2 (Chothia)	NPVSGN (SEQ ID NO: 2591)
HCDR3 (Chothia)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (IMGT)	GYTFTGYH (SEQ ID NO: 2592)
HCDR2 (IMGT)	INPVSGNT (SEQ ID NO: 2593)
HCDR3 (IMGT)	ARIPSYTYAFDY (SEQ ID NO: 2594)
VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSS (SEQ ID NO: 2595)
DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CG (SEQ ID NO: 2610)
Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV

	TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2611)
DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CGGCCTCCACTAAGGGCCCAAGTGTGTTTCCCCTGGCCCCCAGCAGCAAGT CTACTTCCGGCGGAACTGCTGCCCTGGGTTGCCTGGTGAAGGACTACTTCC CCGAGCCCGTGACAGTGTCCTGGAACTCTGGGGCTCTGACTTCCGGCGTGC ACACCTTCCCCGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGCG TGGTGACAGTGCCCTCCAGCTCTCTGGGAACCCAGACCTATATCTGCAACG TGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTGGAGCCCAA GAGCTGCGACAAGACCCACACCTGCCCCCCCTGCCCAGCTCCAGAACTGCT GGGAGGGCCTTCCGTGTTCCTGTTCCCCCCCAAGCCCAAGGACACCCTGAT GATCAGCAGGACCCCCGAGGTGACCTGCGTGGTGGTGGACGTGTCCCACG AGGACCCAGAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAC AACGCCAAGACCAAGCCCAGAGAGGAGCAGTACAACAGCACCTACAGGGT GGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAAT ACAAGTGCAAAGTCTCCAACAAGGCCCTGCCAGCCCCAATCGAAAAGACA ATCAGCAAGGCCAAGGGCCAGCCACGGGAGCCCCAGGTGTACACCCTGCC CCCCAGCCGGGAGGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGG TGAAGGGCTTCTACCCCAGCGATATCGCCGTGGAGTGGGAGAGCAACGGC CAGCCCGAGAACAACTACAAGACCACCCCCCCAGTGCTGGACAGCGACGG CAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGTCCAGGTGGCAGCA GGGCAACGTGTTCAGCTGCAGCGTGATGCACGAGGCCCTGCACAACCACT ACACCCAGAAGTCCCTGAGCCTGAGCCCCGGCAAG (SEQ ID NO: 2612)
LCDR1 (Combined)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Combined)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Combined)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Kabat)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Kabat)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Kabat)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Chothia)	SQDISNY (SEQ ID NO: 2602)
LCDR2 (Chothia)	RAS (SEQ ID NO: 2603)

LCDR3 (Chothia)	YRHMPSQ (SEQ ID NO: 2604)
LCDR1 (IMGT)	QDISNY (SEQ ID NO: 2605)
LCDR2 (IMGT)	RAS (SEQ ID NO: 2603)
LCDR3 (IMGT)	FQYRHMPSQT (SEQ ID NO: 2601)
VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK (SEQ ID NO: 2606)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAG (SEQ ID NO: 2613)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 2608)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTT CCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCC TGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGAC AACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACA GCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCC GACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCT GTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2614)
MOR44698C	
HCDR1 (Combined)	GYTFTGYHMS (SEQ ID NO: 2586)
HCDR2 (Combined)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Combined)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Kabat)	GYHMS (SEQ ID NO: 2589)
HCDR2 (Kabat)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)

HCDR3 (Kabat)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Chothia)	GYTFTGY (SEQ ID NO: 2590)
HCDR2 (Chothia)	NPVSGN (SEQ ID NO: 2591)
HCDR3 (Chothia)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (IMGT)	GYTFTGYH (SEQ ID NO: 2592)
HCDR2 (IMGT)	INPVSGNT (SEQ ID NO: 2593)
HCDR3 (IMGT)	ARIPSYTYAFDY (SEQ ID NO: 2594)
VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSS (SEQ ID NO: 2595)
DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CG (SEQ ID NO: 2610)
Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2615)
DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGT CAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGACTATTTCC CGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGC ATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGT CGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGT CAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGT CCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTG GTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGATGA

	TCTCCCGCACTCCGGAAGTCACTTGCGTGGTCGTGGCCGTGTCCCACGAGG ACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAAC GCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGT GTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACA AGTGCAAAGTGTCCAACAAGGCACTGGCTGCCCCTATCGAAAAGACTATCT CCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCTT CCCGCGAAGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAA GGGTTCTACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCT GAGAACAACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTC TTCCTGTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAAC GTGTTCTCTTGCTCCGTGATGCACGAAGCCCTGCACAACCACTACACCCAA AAGTCGCTCAGCCTCTCCCCCGGAAAG (SEQ ID NO: 2616)
LCDR1 (Combined)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Combined)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Combined)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Kabat)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Kabat)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Kabat)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Chothia)	SQDISNY (SEQ ID NO: 2602)
LCDR2 (Chothia)	RAS (SEQ ID NO: 2603)
LCDR3 (Chothia)	YRHMPSQ (SEQ ID NO: 2604)
LCDR1 (IMGT)	QDISNY (SEQ ID NO: 2605)
LCDR2 (IMGT)	RAS (SEQ ID NO: 2603)
LCDR3 (IMGT)	FQYRHMPSQT (SEQ ID NO: 2601)
VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK (SEQ ID NO: 2606)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAG (SEQ ID NO: 2613)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ

	ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 2608)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTT CCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCC TGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGAC AACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACA GCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCC GACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCT GTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2614)
MOR44698D	
HCDR1 (Combined)	GYTFTGYHMS (SEQ ID NO: 2586)
HCDR2 (Combined)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Combined)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Kabat)	GYHMS (SEQ ID NO: 2589)
HCDR2 (Kabat)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Kabat)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Chothia)	GYTFTGY (SEQ ID NO: 2590)
HCDR2 (Chothia)	NPVSGN (SEQ ID NO: 2591)
HCDR3 (Chothia)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (IMGT)	GYTFTGYH (SEQ ID NO: 2592)
HCDR2 (IMGT)	INPVSGNT (SEQ ID NO: 2593)
HCDR3 (IMGT)	ARIPSYTYAFDY (SEQ ID NO: 2594)
VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSS (SEQ ID NO: 2595)
DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC

	GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CG (SEQ ID NO: 2610)
Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 2617)
DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGT CAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGACTATTTCC CGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGC ATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGT CGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGT CAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGT CCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTG GTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGATGA TCTCCCGCACTCCGGAAGTCACTTGCGTGGTCGTGGACGTGTCCCACGAGG ACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAAC GCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGT GTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACA AGTGCAAAGTGTCCAACAAGGCACTGCCAGCCCCTATCGAAAAGACTATC TCCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCT TCCCGCGAAGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAA GGGTTCTACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCT GAGAACAACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTC TTCCTGTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAAC GTGTTCTCTTGCTCCGTGCTGCACGAAGCCCTGCACAGCCACTACACCCAA AAGTCGCTCAGCCTCTCCCCCGGAAAG (SEQ ID NO: 2618)
LCDR1 (Combined)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Combined)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Combined)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Kabat)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Kabat)	RASSLQS (SEQ ID NO: 2600)

LCDR3 (Kabat)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Chothia)	SQDISNY (SEQ ID NO: 2602)
LCDR2 (Chothia)	RAS (SEQ ID NO: 2603)
LCDR3 (Chothia)	YRHMPSQ (SEQ ID NO: 2604)
LCDR1 (IMGT)	QDISNY (SEQ ID NO: 2605)
LCDR2 (IMGT)	RAS (SEQ ID NO: 2603)
LCDR3 (IMGT)	FQYRHMPSQT (SEQ ID NO: 2601)
VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK (SEQ ID NO: 2606)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAG (SEQ ID NO: 2613)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 2608)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTT CCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCC TGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGAC AACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACA GCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCC GACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCT GTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2614)
MOR44698E	
HCDR1 (Combined)	GYTFTGYHMS (SEQ ID NO: 2586)
HCDR2 (Combined)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)

HCDR3 (Combined)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Kabat)	GYHMS (SEQ ID NO: 2589)
HCDR2 (Kabat)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Kabat)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Chothia)	GYTFTGY (SEQ ID NO: 2590)
HCDR2 (Chothia)	NPVSGN (SEQ ID NO: 2591)
HCDR3 (Chothia)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (IMGT)	GYTFTGYH (SEQ ID NO: 2592)
HCDR2 (IMGT)	INPVSGNT (SEQ ID NO: 2593)
HCDR3 (IMGT)	ARIPSYTYAFDY (SEQ ID NO: 2594)
VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSS (SEQ ID NO: 2595)
DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CG (SEQ ID NO: 2610)
Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 2619)
DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGT CAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGACTATTTCC

	CGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGC ATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGT CGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGT CAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGT CCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTG GTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGATGA TCTCCCGCACTCCGGAAGTCACTTGCGTGGTCGTGGCCGTGTCCCACGAGG ACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAAC GCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGT GTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACA AGTGCAAAGTGTCCAACAAGGCACTGGCTGCCCCTATCGAAAAGACTATCT CCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCTT CCCGCGAAGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAA GGGTTCTACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCT GAGAACAACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTC TTCCTGTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAAC GTGTTCTCTTGCTCCGTGCTGCACGAAGCCCTGCACAGCCACTACACCCAA AAGTCGCTCAGCCTCTCCCCCGGAAAG (SEQ ID NO: 2620)
LCDR1 (Combined)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Combined)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Combined)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Kabat)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Kabat)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Kabat)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Chothia)	SQDISNY (SEQ ID NO: 2602)
LCDR2 (Chothia)	RAS (SEQ ID NO: 2603)
LCDR3 (Chothia)	YRHMPSQ (SEQ ID NO: 2604)
LCDR1 (IMGT)	QDISNY (SEQ ID NO: 2605)
LCDR2 (IMGT)	RAS (SEQ ID NO: 2603)
LCDR3 (IMGT)	FQYRHMPSQT (SEQ ID NO: 2601)
VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK (SEQ ID NO: 2606)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG

	GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAG (SEQ ID NO: 2613)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 2608)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTT CCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCC TGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGAC AACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACA GCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCC GACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCT GTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2614)
MOR44698F	
HCDR1 (Combined)	GYTFTGYHMS (SEQ ID NO: 2586)
HCDR2 (Combined)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Combined)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Kabat)	GYHMS (SEQ ID NO: 2589)
HCDR2 (Kabat)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Kabat)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Chothia)	GYTFTGY (SEQ ID NO: 2590)
HCDR2 (Chothia)	NPVSGN (SEQ ID NO: 2591)
HCDR3 (Chothia)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (IMGT)	GYTFTGYH (SEQ ID NO: 2592)
HCDR2 (IMGT)	INPVSGNT (SEQ ID NO: 2593)
HCDR3 (IMGT)	ARIPSYTYAFDY (SEQ ID NO: 2594)

VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSS (SEQ ID NO: 2595)
DNA VH	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CG (SEQ ID NO: 2610)
Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLYITREPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2621)
DNA Heavy Chain	CAAGTGCAACTCGTGCAGTCAGGAGCCGAAGTCAAGAAGCCTGGAGCCTC GGTCAAGGTGTCCTGCAAGGCCAGCGGATACACTTTCACTGGATACCACAT GTCGTGGGTCAGACAGGCTCCTGGCCAAGGGCTGGAGTGGATGGGCGTCA TCAACCCGGTGTCGGGTAATACCGTGTACGCCCAGAAGTTCCAGGGTCGCG TGACCATGACCCGGGATACCTCCATTAGCACCGCGTACATGGAGCTCAGCC GGTTGAGATCCGAGGATACCGCCGTGTACTACTGTGCGCGGATCCCGTCCT ACACTTACGCCTTCGACTATTGGGGCCAGGGGACTCTTGTCACCGTGTCCT CGGCCTCCACTAAGGGCCCGTCAGTGTTCCCCCTTGCGCCATCCTCGAAGT CAACCTCCGGAGGAACTGCCGCACTGGGTTGCCTCGTGAAAGACTATTTCC CGGAACCCGTCACTGTCTCCTGGAACTCAGGAGCGCTCACCAGCGGAGTGC ATACCTTTCCTGCGGTGCTGCAGTCCAGCGGCCTGTACTCCCTGAGCTCCGT CGTGACCGTCCCCTCGTCGTCCCTGGGAACCCAAACCTACATTTGCAACGT CAATCACAAGCCAAGCAACACTAAGGTGGACAAGAGAGTGGAGCCCAAGT CCTGCGATAAGACCCACACCTGTCCTCCCTGTCCGGCACCTGAACTGCTTG GTGGACCTTCCGTGTTCCTGTTCCCGCCCAAGCCAAAAGACACCCTGTATA TCACTCGCGAACCGGAAGTCACTTGCGTGGTCGTGGACGTGTCCCACGAGG ACCCCGAGGTCAAGTTTAATTGGTACGTGGACGGAGTGGAAGTGCACAAC GCCAAGACCAAGCCGCGGGAAGAACAGTACAACTCCACCTACCGCGTGGT GTCCGTCCTGACTGTGCTCCACCAGGACTGGCTGAACGGAAAGGAGTACA AGTGCAAAGTGTCCAACAAGGCACTGCCAGCCCCTATCGAAAAGACTATC TCCAAGGCCAAGGGCCAACCTAGGGAGCCCCAGGTGTACACGTTGCCTCCT TCCCGCGAAGAAATGACTAAGAACCAGGTGTCGCTGACCTGTCTCGTGAAA GGGTTCTACCCCTCTGACATCGCCGTGGAATGGGAGTCAAACGGACAGCCT GAGAACAACTATAAGACCACACCACCTGTCCTGGACTCCGACGGCTCCTTC TTCCTGTACTCAAAGTTGACCGTGGACAAGTCGCGGTGGCAACAGGGCAAC GTGTTCTCTTGCTCCGTGATGCACGAAGCCCTGCACAACCACTACACCCAA AAGTCGCTCAGCCTCTCCCCCGGAAAG (SEQ ID NO: 2622)
LCDR1 (Combined)	RASQDISNYLA (SEQ ID NO: 2599)

LCDR2 (Combined)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Combined)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Kabat)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Kabat)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Kabat)	FQYRHMPSQT (SEQ ID NO: 2601)
LCDR1 (Chothia)	SQDISNY (SEQ ID NO: 2602)
LCDR2 (Chothia)	RAS (SEQ ID NO: 2603)
LCDR3 (Chothia)	YRHMPSQ (SEQ ID NO: 2604)
LCDR1 (IMGT)	QDISNY (SEQ ID NO: 2605)
LCDR2 (IMGT)	RAS (SEQ ID NO: 2603)
LCDR3 (IMGT)	FQYRHMPSQT (SEQ ID NO: 2601)
VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK (SEQ ID NO: 2606)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAG (SEQ ID NO: 2613)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQYRHMPSQTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 2608)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGATATTTCCAACTACCTGGCC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACCGGGC GTCCTCCTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCTTCCAGTACCGGCACATGCCCTCACAAACCTTCGGACAGGG CACCAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTT CCCCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCC TGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGAC AACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACA GCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCC GACTACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCT

	GTCCAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2614)
MOR44746A	
HCDR1 (Combined)	GDSVSSSSAAWN (SEQ ID NO: 2623)
HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Combined)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Kabat)	SSSAAWN (SEQ ID NO: 2626)
HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Kabat)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Chothia)	GDSVSSSSA (SEQ ID NO: 2627)
HCDR2 (Chothia)	GYRSKWY (SEQ ID NO: 2628)
HCDR3 (Chothia)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (IMGT)	GDSVSSSSAA (SEQ ID NO: 2629)
HCDR2 (IMGT)	IGYRSKWYN (SEQ ID NO: 2630)
HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI (SEQ ID NO: 2631)
VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSS (SEQ ID NO: 2632)
DNA VH	CAGGTGCAATTGCAGCAGAGCGGTCCGGGCCTGGTGAAACCGAGCCAGAC CCTGAGCCTGACCTGCGCGATTTCCGGAGATAGCGTGAGCTCTTCTTCTGCT GCTTGGAACTGGATTCGTCAGAGCCCGAGCCGTGGCCTCGAGTGGCTGGGC CATATCGGTTACCGTAGCAAATGGTACAACGAATATGCCGTGAGCGTGAA AAGCCGCATTACCATTAACCCGGATACTTCGAAAAACCAGTTTAGCCTGCA ACTGAACAGCGTGACCCCGGAAGATACGGCCGTGTATTATTGCGCGCGTGG TATGTACGGTTCTGTTCCCTACAAAGAAGGTTACTACTTCGATATTTGGGGC CAAGGCACCCTGGTGACTGTTAGCTCA (SEQ ID NO: 2633)
Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2634)
DNA Heavy Chain	CAGGTGCAATTGCAGCAGAGCGGTCCGGGCCTGGTGAAACCGAGCCAGAC CCTGAGCCTGACCTGCGCGATTTCCGGAGATAGCGTGAGCTCTTCTTCTGCT

	GCTTGGAACTGGATTCGTCAGAGCCCGAGCCGTGGCCTCGAGTGGCTGGGC CATATCGGTTACCGTAGCAAATGGTACAACGAATATGCCGTGAGCGTGAA AAGCCGCATTACCATTAACCCGGATACTTCGAAAAACCAGTTTAGCCTGCA ACTGAACAGCGTGACCCCGGAAGATACGGCCGTGTATTATTGCGCGCGTGG TATGTACGGTTCTGTTCCCTACAAAGAAGGTTACTACTTCGATATTTGGGGC CAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTC TTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAAC TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCC CACCGTGCCCAGCACCTGAAGCAGCGGGGGGACCGTCAGTCTTCCTCTTCC CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCA GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAA CCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGC CGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCG TGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA (SEQ ID NO: 2635)
LCDR1 (Combined)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Combined)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Combined)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Kabat)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Kabat)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Kabat)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Chothia)	SQGISSD (SEQ ID NO: 2639)
LCDR2 (Chothia)	AAS (SEQ ID NO: 2640)
LCDR3 (Chothia)	YTDESM (SEQ ID NO: 2641)
LCDR1 (IMGT)	QGISSD (SEQ ID NO: 2642)
LCDR2 (IMGT)	AAS (SEQ ID NO: 2640)

LCDR3 (IMGT)	QQYTDESMT (SEQ ID NO: 2638)
VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIK (SEQ ID NO: 2643)
DNA VL	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGGTATTTCTTCTGACCTGAA CTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACGCTG CTTCTAACCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATCCG GCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGA CCTATTATTGCCAGCAGTACACTGACGAATCTATGACCTTTGGCCAGGGCA CGAAAGTTGAAATTAAA (SEQ ID NO: 2644)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2645)
DNA Light Chain	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGGTATTTCTTCTGACCTGAA CTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACGCTG CTTCTAACCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATCCG GCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGA CCTATTATTGCCAGCAGTACACTGACGAATCTATGACCTTTGGCCAGGGCA CGAAAGTTGAAATTAAACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCC CCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTG CTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAA CGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCA AGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGAC TACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTC CAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGT (SEQ ID NO: 2646)
MOR44746B	
HCDR1 (Combined)	GDSVSSSSAAWN (SEQ ID NO: 2623)
HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Combined)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Kabat)	SSSAAWN (SEQ ID NO: 2626)
HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Kabat)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Chothia)	GDSVSSSSA (SEQ ID NO: 2627)
HCDR2 (Chothia)	GYRSKWY (SEQ ID NO: 2628)
HCDR3 (Chothia)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)

HCDR1 (IMGT)	GDSVSSSSAA (SEQ ID NO: 2629)
HCDR2 (IMGT)	IGYRSKWYN (SEQ ID NO: 2630)
HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI (SEQ ID NO: 2631)
VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSS (SEQ ID NO: 2632)
DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCG (SEQ ID NO: 2647)
Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2648)
DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCCCAAGTG TGTTTCCCCTGGCCCCCAGCAGCAAGTCTACTTCCGGCGGAACTGCTGCCC TGGGTTGCCTGGTGAAGGACTACTTCCCCGAGCCCGTGACAGTGTCCTGGA ACTCTGGGGCTCTGACTTCCGGCGTGCACACCTTCCCCGCCGTGCTGCAGA GCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACAGTGCCCTCCAGCTCTC TGGGAACCCAGACCTATATCTGCAACGTGAACCACAAGCCCAGCAACACC AAGGTGGACAAGAGAGTGGAGCCCAAGAGCTGCGACAAGACCCACACCTG CCCCCCCTGCCCAGCTCCAGAACTGCTGGGAGGGCCTTCCGTGTTCCTGTT CCCCCCCAAGCCCAAGGACACCCTGATGATCAGCAGGACCCCCGAGGTGA CCTGCGTGGTGGTGGACGTGTCCCACGAGGACCCAGAGGTGAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCCAGAGAG GAGCAGTACAACAGCACCTACAGGGTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGCAAAGAATACAAGTGCAAAGTCTCCAACAAGG CCCTGCCAGCCCCAATCGAAAAGACAATCAGCAAGGCCAAGGGCCAGCCA CGGGAGCCCCAGGTGTACACCCTGCCCCCCAGCCGGGAGGAGATGACCAA GAACCAGGTGTCCCTGACCTGTCTGGTGAAGGGCTTCTACCCCAGCGATAT

	CGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCA CCCCCCCAGTGCTGGACAGCGACGGCAGCTTCTTCCTGTACAGCAAGCTGA CCGTGGACAAGTCCAGGTGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTG ATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAG CCCCGGCAAG (SEQ ID NO: 2649)
LCDR1 (Combined)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Combined)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Combined)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Kabat)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Kabat)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Kabat)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Chothia)	SQGISSD (SEQ ID NO: 2639)
LCDR2 (Chothia)	AAS (SEQ ID NO: 2640)
LCDR3 (Chothia)	YTDESM (SEQ ID NO: 2641)
LCDR1 (IMGT)	QGISSD (SEQ ID NO: 2642)
LCDR2 (IMGT)	AAS (SEQ ID NO: 2640)
LCDR3 (IMGT)	QQYTDESMT (SEQ ID NO: 2638)
VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIK (SEQ ID NO: 2643)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAG (SEQ ID NO: 2650)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2645)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC

	CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCC CCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGC TGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAAC GCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACAGCA AGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGAC TACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTC CAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2651)
MOR44746C	
HCDR1 (Combined)	GDSVSSSSAAWN (SEQ ID NO: 2623)
HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Combined)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Kabat)	SSSAAWN (SEQ ID NO: 2626)
HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Kabat)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Chothia)	GDSVSSSSA (SEQ ID NO: 2627)
HCDR2 (Chothia)	GYRSKWY (SEQ ID NO: 2628)
HCDR3 (Chothia)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (IMGT)	GDSVSSSSAA (SEQ ID NO: 2629)
HCDR2 (IMGT)	IGYRSKWYN (SEQ ID NO: 2630)
HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI (SEQ ID NO: 2631)
VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSS (SEQ ID NO: 2632)
DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCG (SEQ ID NO: 2647)
Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR

	TPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2652)
DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCCCGTCAG TGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACTGCCGCAC TGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGTCTCCTGGA ACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGGTGCTGCAGT CCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCT GGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCCAAGCAACACTA AGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGACCCACACCTGT CCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCC CGCCCAAGCCAAAAGACACCCTGATGATCTCCCGCACTCCGGAAGTCACTT GCGTGGTCGTGGCCGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGT ACGTGGACGGAGTGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGA ACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCA GGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCAC TGGCTGCCCCTATCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGG GAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAAC CAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCC GTGGAATGGGAGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACC ACCTGTCCTGGACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTG GACAAGTCGCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGATGCAC GAAGCCCTGCACAACCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGA AAG (SEQ ID NO: 2653)
LCDR1 (Combined)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Combined)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Combined)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Kabat)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Kabat)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Kabat)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Chothia)	SQGISSD (SEQ ID NO: 2639)
LCDR2 (Chothia)	AAS (SEQ ID NO: 2640)

LCDR3 (Chothia)	YTDESM (SEQ ID NO: 2641)
LCDR1 (IMGT)	QGISSD (SEQ ID NO: 2642)
LCDR2 (IMGT)	AAS (SEQ ID NO: 2640)
LCDR3 (IMGT)	QQYTDESMT (SEQ ID NO: 2638)
VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIK (SEQ ID NO: 2643)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAG (SEQ ID NO: 2650)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2645)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCC CCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGC TGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAAC GCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACAGCA AGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGAC TACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTC CAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2651)
MOR44746D	
HCDR1 (Combined)	GDSVSSSSAAWN (SEQ ID NO: 2623)
HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Combined)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Kabat)	SSSAAWN (SEQ ID NO: 2626)
HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Kabat)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)

HCDR1 (Chothia)	GDSVSSSSA (SEQ ID NO: 2627)
HCDR2 (Chothia)	GYRSKWY (SEQ ID NO: 2628)
HCDR3 (Chothia)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (IMGT)	GDSVSSSSAA (SEQ ID NO: 2629)
HCDR2 (IMGT)	IGYRSKWYN (SEQ ID NO: 2630)
HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI (SEQ ID NO: 2631)
VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSS (SEQ ID NO: 2632)
DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCG (SEQ ID NO: 2647)
Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 2654)
DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCCCGTCAG TGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACTGCCGCAC TGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGTCTCCTGGA ACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGGTGCTGCAGT CCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCT GGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCCAAGCAACACTA AGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGACCCACACCTGT CCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCC CGCCCAAGCCAAAAGACACCCTGATGATCTCCCGCACTCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGT

	ACGTGGACGGAGTGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGA ACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCA GGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCAC TGCCAGCCCCTATCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGG GAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAAC CAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCC GTGGAATGGGAGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACC ACCTGTCCTGGACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTG GACAAGTCGCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGCTGCAC GAAGCCCTGCACAGCCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGA AAG (SEQ ID NO: 2655)
LCDR1 (Combined)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Combined)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Combined)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Kabat)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Kabat)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Kabat)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Chothia)	SQGISSD (SEQ ID NO: 2639)
LCDR2 (Chothia)	AAS (SEQ ID NO: 2640)
LCDR3 (Chothia)	YTDESM (SEQ ID NO: 2641)
LCDR1 (IMGT)	QGISSD (SEQ ID NO: 2642)
LCDR2 (IMGT)	AAS (SEQ ID NO: 2640)
LCDR3 (IMGT)	QQYTDESMT (SEQ ID NO: 2638)
VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIK (SEQ ID NO: 2643)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAG (SEQ ID NO: 2650)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE

	SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2645)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCC CCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGC TGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAAC GCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACAGCA AGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGAC TACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTC CAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2651)
MOR44746E	
HCDR1 (Combined)	GDSVSSSSAAWN (SEQ ID NO: 2623)
HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Combined)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Kabat)	SSSAAWN (SEQ ID NO: 2626)
HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Kabat)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Chothia)	GDSVSSSSA (SEQ ID NO: 2627)
HCDR2 (Chothia)	GYRSKWY (SEQ ID NO: 2628)
HCDR3 (Chothia)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (IMGT)	GDSVSSSSAA (SEQ ID NO: 2629)
HCDR2 (IMGT)	IGYRSKWYN (SEQ ID NO: 2630)
HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI (SEQ ID NO: 2631)
VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSS (SEQ ID NO: 2632)
DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG

	GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCG (SEQ ID NO: 2647)
Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 2656)
DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCCCGTCAG TGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACTGCCGCAC TGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGTCTCCTGGA ACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGGTGCTGCAGT CCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCT GGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCCAAGCAACACTA AGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGACCCACACCTGT CCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCC CGCCCAAGCCAAAAGACACCCTGATGATCTCCCGCACTCCGGAAGTCACTT GCGTGGTCGTGGCCGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGT ACGTGGACGGAGTGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGA ACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCA GGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCAC TGGCTGCCCCTATCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGG GAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAAC CAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCC GTGGAATGGGAGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACC ACCTGTCCTGGACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTG GACAAGTCGCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGCTGCAC GAAGCCCTGCACAGCCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGA AAG (SEQ ID NO: 2657)
LCDR1 (Combined)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Combined)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Combined)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Kabat)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Kabat)	AASNLQS (SEQ ID NO: 2637)

LCDR3 (Kabat)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Chothia)	SQGISSD (SEQ ID NO: 2639)
LCDR2 (Chothia)	AAS (SEQ ID NO: 2640)
LCDR3 (Chothia)	YTDESM (SEQ ID NO: 2641)
LCDR1 (IMGT)	QGISSD (SEQ ID NO: 2642)
LCDR2 (IMGT)	AAS (SEQ ID NO: 2640)
LCDR3 (IMGT)	QQYTDESMT (SEQ ID NO: 2638)
VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIK (SEQ ID NO: 2643)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAG (SEQ ID NO: 2650)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2645)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCC CCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGC TGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAAC GCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACAGCA AGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGAC TACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTC CAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2651)
MOR44746F	
HCDR1 (Combined)	GDSVSSSSAAWN (SEQ ID NO: 2623)
HCDR2 (Combined)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Combined)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)

HCDR1 (Kabat)	SSSAAWN (SEQ ID NO: 2626)
HCDR2 (Kabat)	HIGYRSKWYNEYAVSVKS (SEQ ID NO: 2624)
HCDR3 (Kabat)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (Chothia)	GDSVSSSSA (SEQ ID NO: 2627)
HCDR2 (Chothia)	GYRSKWY (SEQ ID NO: 2628)
HCDR3 (Chothia)	GMYGSVPYKEGYYFDI (SEQ ID NO: 2625)
HCDR1 (IMGT)	GDSVSSSSAA (SEQ ID NO: 2629)
HCDR2 (IMGT)	IGYRSKWYN (SEQ ID NO: 2630)
HCDR3 (IMGT)	ARGMYGSVPYKEGYYFDI (SEQ ID NO: 2631)
VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSS (SEQ ID NO: 2632)
DNA VH	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCG (SEQ ID NO: 2647)
Heavy Chain	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSSSAAWNWIRQSPSRGLEWLGHI GYRSKWYNEYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGMYG SVPYKEGYYFDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLYITR EPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2658)
DNA Heavy Chain	CAAGTGCAACTCCAGCAGTCAGGACCGGGGTTGGTCAAGCCTTCGCAGAC CCTGTCCCTCACTTGCGCCATTAGCGGAGATTCGGTGTCGTCGTCGTCAGC CGCCTGGAACTGGATTAGACAGTCCCCTTCCCGAGGGCTGGAGTGGCTGGG CCACATCGGATACCGCAGCAAGTGGTACAACGAATACGCCGTCAGCGTGA AGTCACGCATCACCATCAACCCGGATACTAGCAAGAACCAGTTCAGCCTCC AGTTGAACTCCGTGACCCCGGAGGATACCGCCGTGTACTACTGTGCGCGGG GCATGTACGGATCCGTGCCGTACAAGGAGGGATACTACTTCGACATTTGGG GCCAGGGGACTCTTGTCACCGTGTCCTCGGCCTCCACTAAGGGCCCGTCAG TGTTCCCCCTTGCGCCATCCTCGAAGTCAACCTCCGGAGGAACTGCCGCAC TGGGTTGCCTCGTGAAAGACTATTTCCCGGAACCCGTCACTGTCTCCTGGA ACTCAGGAGCGCTCACCAGCGGAGTGCATACCTTTCCTGCGGTGCTGCAGT

	CCAGCGGCCTGTACTCCCTGAGCTCCGTCGTGACCGTCCCCTCGTCGTCCCT GGGAACCCAAACCTACATTTGCAACGTCAATCACAAGCCAAGCAACACTA AGGTGGACAAGAGAGTGGAGCCCAAGTCCTGCGATAAGACCCACACCTGT CCTCCCTGTCCGGCACCTGAACTGCTTGGTGGACCTTCCGTGTTCCTGTTCC CGCCCAAGCCAAAAGACACCCTGTATATCACTCGCGAACCGGAAGTCACTT GCGTGGTCGTGGACGTGTCCCACGAGGACCCCGAGGTCAAGTTTAATTGGT ACGTGGACGGAGTGGAAGTGCACAACGCCAAGACCAAGCCGCGGGAAGA ACAGTACAACTCCACCTACCGCGTGGTGTCCGTCCTGACTGTGCTCCACCA GGACTGGCTGAACGGAAAGGAGTACAAGTGCAAAGTGTCCAACAAGGCAC TGCCAGCCCCTATCGAAAAGACTATCTCCAAGGCCAAGGGCCAACCTAGG GAGCCCCAGGTGTACACGTTGCCTCCTTCCCGCGAAGAAATGACTAAGAAC CAGGTGTCGCTGACCTGTCTCGTGAAAGGGTTCTACCCCTCTGACATCGCC GTGGAATGGGAGTCAAACGGACAGCCTGAGAACAACTATAAGACCACACC ACCTGTCCTGGACTCCGACGGCTCCTTCTTCCTGTACTCAAAGTTGACCGTG GACAAGTCGCGGTGGCAACAGGGCAACGTGTTCTCTTGCTCCGTGATGCAC GAAGCCCTGCACAACCACTACACCCAAAAGTCGCTCAGCCTCTCCCCCGGA AAG (SEQ ID NO: 2659)
LCDR1 (Combined)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Combined)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Combined)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Kabat)	RASQGISSDLN (SEQ ID NO: 2636)
LCDR2 (Kabat)	AASNLQS (SEQ ID NO: 2637)
LCDR3 (Kabat)	QQYTDESMT (SEQ ID NO: 2638)
LCDR1 (Chothia)	SQGISSD (SEQ ID NO: 2639)
LCDR2 (Chothia)	AAS (SEQ ID NO: 2640)
LCDR3 (Chothia)	YTDESM (SEQ ID NO: 2641)
LCDR1 (IMGT)	QGISSD (SEQ ID NO: 2642)
LCDR2 (IMGT)	AAS (SEQ ID NO: 2640)
LCDR3 (IMGT)	QQYTDESMT (SEQ ID NO: 2638)
VL	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIK (SEQ ID NO: 2643)
DNA VL	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC

	CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAG (SEQ ID NO: 2650)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSDLNWYQQKPGKAPKLLIYAASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYTDESMTFGQGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2645)
DNA Light Chain	GACATTCAGATGACCCAGTCCCCGTCGTCCCTGTCCGCATCCGTGGGCGAC AGAGTCACCATCACTTGCCGGGCCTCACAGGGAATTTCCTCCGACCTGAAC TGGTATCAGCAGAAGCCTGGAAAGGCCCCGAAGCTGCTGATCTACGCCGC GTCCAACTTGCAATCGGGAGTGCCAAGCCGCTTTTCTGGTTCCGGGAGCGG GACTGACTTCACCCTGACTATTAGCAGCCTGCAGCCCGAAGATTTCGCTAC CTACTACTGCCAACAGTACACAGATGAATCCATGACCTTCGGACAGGGCAC CAAAGTCGAGATCAAGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCC CCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGC TGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAAC GCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTCACCGAGCAGGACAGCA AGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGAC TACGAGAAGCATAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTC CAGCCCCGTGACCAAGAGCTTCAACAGGGGCGAGTGC (SEQ ID NO: 2651)
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HCDR1 (Combined)	GYTFTGYHMS (SEQ ID NO: 2586)
HCDR2 (Combined)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Combined)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Kabat)	GYHMS (SEQ ID NO: 2589)
HCDR2 (Kabat)	VINPVSGNTVYAQKFQG (SEQ ID NO: 2587)
HCDR3 (Kabat)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (Chothia)	GYTFTGY (SEQ ID NO: 2590)
HCDR2 (Chothia)	NPVSGN (SEQ ID NO: 2591)
HCDR3 (Chothia)	IPSYTYAFDY (SEQ ID NO: 2588)
HCDR1 (IMGT)	GYTFTGYH (SEQ ID NO: 2592)
HCDR2 (IMGT)	INPVSGNT (SEQ ID NO: 2593)
HCDR3 (IMGT)	ARIPSYTYAFDY (SEQ ID NO: 2594)
VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSS (SEQ ID NO: 2595)

DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAG CGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTACCATAT GTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATGGGCGTTAT CAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTTCAGGGCCGGGT GACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTATCCCGTCTT ACACTTACGCTTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGTTAGCT CA (SEQ ID NO: 2596)
Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHMSWVRQAPGQGLEWMGV INPVSGNTVYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARIPSYT YAFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2597)
DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAG CGTGAAAGTTAGCTGCAAAGCGTCCGGATATACCTTCACTGGTTACCATAT GTCTTGGGTGCGCCAGGCCCCGGGCCAGGGCCTCGAGTGGATGGGCGTTAT CAACCCGGTTTCTGGCAACACGGTTTACGCGCAGAAATTTCAGGGCCGGGT GACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTATCCCGTCTT ACACTTACGCTTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGTTAGCT CAGCCTCCACCAAGGGTCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGA GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC GTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCAGC GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACG AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGT GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGT ACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGG TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG CTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 2598)
LCDR1 (Combined)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Combined)	RASSLQS (SEQ ID NO: 2600)

LCDR3 (Combined)	QQHGHSPTT (SEQ ID NO: 2660)
LCDR1 (Kabat)	RASQDISNYLA (SEQ ID NO: 2599)
LCDR2 (Kabat)	RASSLQS (SEQ ID NO: 2600)
LCDR3 (Kabat)	QQHGHSPTT (SEQ ID NO: 2660)
LCDR1 (Chothia)	SQDISNY (SEQ ID NO: 2602)
LCDR2 (Chothia)	RAS (SEQ ID NO: 2603)
LCDR3 (Chothia)	HGHSPT (SEQ ID NO: 2661)
LCDR1 (IMGT)	QDISNY (SEQ ID NO: 2605)
LCDR2 (IMGT)	RAS (SEQ ID NO: 2603)
LCDR3 (IMGT)	QQHGHSPTT (SEQ ID NO: 2660)
VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHGHSPTTFGQGTKVEIK (SEQ ID NO: 2662)
DNA VL	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCTGGC TTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACCGTG CTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATCCG GCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGA CCTATTATTGCCAGCAGCATGGTCATTCTCCGACTACCTTTGGCCAGGGCA CGAAAGTTGAAATTAAA (SEQ ID NO: 2663)
Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKLLIYRASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHGHSPTTFGQGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 2664)
DNA Light Chain	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGA TCGCGTGACCATTACCTGCAGAGCCAGCCAGGACATTTCTAACTACCTGGC TTGGTACCAGCAGAAACCGGGCAAAGCGCCGAAACTATTAATCTACCGTG CTTCTTCTCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGGCAGCGGATCCG GCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGA CCTATTATTGCCAGCAGCATGGTCATTCTCCGACTACCTTTGGCCAGGGCA CGAAAGTTGAAATTAAACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCC CCCCCAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTG CTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAA CGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCA AGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGAC TACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTC CAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGTGT (SEQ ID NO: 2665)
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HCDR1 (Combined)	GFSLSTSGVGVS (SEQ ID NO: 2666)
HCDR2 (Combined)	LIFSDHDKIYSTSLKT (SEQ ID NO: 2667)
HCDR3 (Combined)	TLIDRSVYFDY (SEQ ID NO: 2668)
HCDR1 (Kabat)	TSGVGVS (SEQ ID NO: 2669)
HCDR2 (Kabat)	LIFSDHDKIYSTSLKT (SEQ ID NO: 2667)
HCDR3 (Kabat)	TLIDRSVYFDY (SEQ ID NO: 2668)
HCDR1 (Chothia)	GFSLSTSGV (SEQ ID NO: 2670)
HCDR2 (Chothia)	FSDHD (SEQ ID NO: 2671)
HCDR3 (Chothia)	TLIDRSVYFDY (SEQ ID NO: 2668)
HCDR1 (IMGT)	GFSLSTSGVG (SEQ ID NO: 2672)
HCDR2 (IMGT)	IFSDHDK (SEQ ID NO: 2673)
HCDR3 (IMGT)	ARTLIDRSVYFDY (SEQ ID NO: 2674)
VH	QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVSWIRQPPGKALEWLALIF SDHDKIYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARTLIDRSVY FDYWGQGTLVTVSS (SEQ ID NO: 2675)
DNA VH	CAGGTGCAATTGAAAGAAAGCGGTCCGGCGCTGGTGAAACCGACCCAGAC CCTGACCCTGACGTGCACCTTTTCCGGATTCAGCCTGTCTACTTCCGGTGTT GGTGTGAGCTGGATTCGCCAGCCGCCGGGCAAAGCGCTCGAGTGGCTGGC GCTGATCTTCTCTGACCATGACAAGATCTATAGCACCAGCCTGAAAACCCG TCTGACCATTAGCAAAGATACTTCGAAAAACCAGGTGGTGCTGACCATGAC CAACATGGACCCGGTGGATACCGCGACCTATTATTGCGCGCGTACTCTGAT CGACCGTTCTGTTTACTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGTT AGCTCA (SEQ ID NO: 2676)
Heavy Chain	QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVSWIRQPPGKALEWLALIF SDHDKIYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARTLIDRSVY FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK VDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 2677)
DNA Heavy Chain	CAGGTGCAATTGAAAGAAAGCGGTCCGGCGCTGGTGAAACCGACCCAGAC CCTGACCCTGACGTGCACCTTTTCCGGATTCAGCCTGTCTACTTCCGGTGTT GGTGTGAGCTGGATTCGCCAGCCGCCGGGCAAAGCGCTCGAGTGGCTGGC GCTGATCTTCTCTGACCATGACAAGATCTATAGCACCAGCCTGAAAACCCG TCTGACCATTAGCAAAGATACTTCGAAAAACCAGGTGGTGCTGACCATGAC

	CAACATGGACCCGGTGGATACCGCGACCTATTATTGCGCGCGTACTCTGAT CGACCGTTCTGTTTACTTCGATTACTGGGGCCAAGGCACCCTGGTGACTGTT AGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCCCCTGGCACCCTCCTCC AAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC AACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGC AGCGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGG GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCT GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 2678)
LCDR1 (Combined)	SGSSSNIGHHYVS (SEQ ID NO: 2679)
LCDR2 (Combined)	DNTNRPS (SEQ ID NO: 2680)
LCDR3 (Combined)	ATWDGLMNSIV (SEQ ID NO: 2681)
LCDR1 (Kabat)	SGSSSNIGHHYVS (SEQ ID NO: 2679)
LCDR2 (Kabat)	DNTNRPS (SEQ ID NO: 2680)
LCDR3 (Kabat)	ATWDGLMNSIV (SEQ ID NO: 2681)
LCDR1 (Chothia)	SSSNIGHHY (SEQ ID NO:2682)
LCDR2 (Chothia)	DNT (SEQ ID NO:2683)
LCDR3 (Chothia)	WDGLMNSI (SEQ ID NO:2684)
LCDR1 (IMGT)	SSNIGHHY (SEQ ID NO:2685)
LCDR2 (IMGT)	DNT (SEQ ID NO:2683)
LCDR3 (IMGT)	ATWDGLMNSIV (SEQ ID NO: 2681)
VL	DIVLTQPPSVSGAPGQRVTISCSGSSSNIGHHYVSWYQQLPGTAPKLLIYDNTN RPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCATWDGLMNSIVFGGGTKL TVL (SEQ ID NO:2686)

DNA VL	GATATCGTGCTGACCCAGCCGCCGAGCGTGAGCGGTGCACCGGGCCAGCG CGTGACCATTAGCTGTAGCGGCAGCAGCAGCAACATTGGTCATCATTACGT GTCTTGGTACCAGCAGCTGCCGGGCACGGCGCCGAAACTGCTGATCTACGA CAACACTAACCGCCCGAGCGGCGTGCCGGATCGCTTTAGCGGATCCAAAA GCGGCACCAGCGCCAGCCTGGCGATTACCGGCCTGCAAGCAGAAGACGAA GCGGATTATTACTGCGCTACTTGGGACGGTCTGATGAACTCTATCGTGTTTG GCGGCGGCACGAAGTTAACCGTCCTA (SEQ ID NO:2687)
Light Chain	DIVLTQPPSVSGAPGQRVTISCSGSSSNIGHHYVSWYQQLPGTAPKLLIYDNTN RPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCATWDGLMNSIVFGGGTKL TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO:2688)
DNA Light Chain	GATATCGTGCTGACCCAGCCGCCGAGCGTGAGCGGTGCACCGGGCCAGCG CGTGACCATTAGCTGTAGCGGCAGCAGCAGCAACATTGGTCATCATTACGT GTCTTGGTACCAGCAGCTGCCGGGCACGGCGCCGAAACTGCTGATCTACGA CAACACTAACCGCCCGAGCGGCGTGCCGGATCGCTTTAGCGGATCCAAAA GCGGCACCAGCGCCAGCCTGGCGATTACCGGCCTGCAAGCAGAAGACGAA GCGGATTATTACTGCGCTACTTGGGACGGTCTGATGAACTCTATCGTGTTTG GCGGCGGCACGAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCG GTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACA CTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGG AAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTC CAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGC CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO:2689)

[00287] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed above, including those in **TABLE J1** above, may be attached to the light chain constant regions **(TABLE EN1)** and heavy chain constant regions **(TABLE EN2)** 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

[00288] 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.

[00289] 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.

[00290] 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.

[00291] 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.

[00292] 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.

[00293] 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.

[00294] 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 EN1**) and heavy chain constant regions (**TABLE EN2**) 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

[00295] 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.

[00296] 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 W-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).

[00297] In some embodiments, the CDR-H2 sequence is selected from SEQ ID NOS:2718, 2727, 2729, and 2731.

[00298] 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.

[00299] 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.

[00300] 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.

[00301] 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.

[00302] 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;

a CDR-L2 sequence comprising the sequence of WMSTRAS (SEQ ID NO: 2696); and

(e) a CDR-L3 sequence comprising the sequence of Q-Q-F-L-E-ϕ_6-P-F-T (SEQ ID NO:2740), wherein ϕ_6 is Y or F.

[00303] 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.

[00304] 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.

[00305] 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.

[00306] 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.

[00307] 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.

[00308] 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.

[00309] 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.

[00310] 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.

[00311] 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.

[00312] 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.

[00313] 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.

[00314] 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 L1**.

TABLE L1

Description	Sequence
Human TREM2 Protein	MEPLRLLILLFVTELSGAHNTTVFQGVAGQSLQVS CPYDSMKHWGRRKAWCRQLGEKGPCQRVVSTH NLWLLSFLRRWNGSTAITDDTLGGTLTITLRNLQP HDAGLYQCQSLHGSEADTLRKVLVEVLADPLDH RDAGDLWFPGESESFEDAHVEHSISRSLLEGEIPFP PTSILLLLACIFLIKILAASALWAAAWHGQKPGTH PPSELDCGHDPGY QLQTLPGLRDT (SEQ ID NO:1)
CL0020306 VH	EVKLLDSGGGLVQAGGSLRLSCAGSGFTFTDFYM SWIRQPPGKAPEWLGVIRNKANGYTAGYNPSVK GRFTISRDNTQNILYLQMNTL RAEDTAIYYCARLSYGFDYWGQGVMVTVSS (SEQ ID NO:2690)
CL0020306 VL	DIVMTQGALPNPVPSGESASITCQSSKSLLHSNGK TYLNWYLQRPGQSPQLLIYWMSTRASGVSDRFSG SGSGTDFTLKIS SVEAEDVG VYYCQQFLEFPFTFGSGTKLEIK (SEQ ID NO:2691)
CL0020306 CDR-H1; CDR-H1 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3, CL0020188-	GFTFTDFYMS (SEQ ID NO:2692)

Description	Sequence
4, CL0020188-5, CL0020188-6, CL0020188-7, and CL0020188-8	
CL0020306 CDR-H2; CDR-H2 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3, and CL0020188-4	VIRNKANGYTAGYNPSVKG (SEQ ID NO:2693)
CL0020306 CDR-H3	ARLSYGFDY (SEQ ID NO:2694)
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	QSSKSLLHSNGKTYLN (SEQ ID NO:2695)
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	WMSTRAS (SEQ ID NO:2696)
CL0020306 CDR-L3; CL0020307 CDR-L3; CL0020307-1 CDR-L3	QQFLEFPFT (SEQ ID NO:2697)
CL0020307 V_H	EVKLLESGGGLVQPGGSLRLSCAASGFTFTNFYM SWIRQPPGRAPEWLGVIRNRPNGYTTDYNPSVKG RFTISRDNTQNILYLQMSTLRADDTAFYYCTRLTY GFDYWGQGVMVTVSS (SEQ ID NO:2698)
CL0020307 VL	DIVMTQGALPNPVPSGESASITCQSSKSLLHSNGK TYLNWYLQRPGQSPQLLIYWMSTRASGVSDRFSG SGSGTDFTLKIS SVEAEVVGVYYCQQFLEFPFTFGSGTKLEIK (SEQ ID NO:2699)
CL0020307 CDR-H1	GFTFTNFYMS (SEQ ID NO:2700)
CL0020307 CDR-H2	VIRNRPNGYTTDYNPSVKG (SEQ ID NO:2701)
CL0020307 CDR-H3	TRLTYGFDY (SEQ ID NO:2702)
CL0020188 VH	EVKLLDSGGGLVQAGGSLRLSCAGSGFTFTDFYM SWIRQPPGKAPEWLGVIRNKANGYTAGYNPSVK GRFTISRDNTQNILYLQMNTLRAEDTAIYYCARLT YGFDYWGQGVMVTVSS (SEQ ID NO:2703)
CL0020188 VL	DIVMTQGALPNPVPSGESASITCQSSKSLLHSNGK TYLNWYLQR PGQSPQLLIYWMSTRASGVSDRFSGSGSGTDFTLK IS SVEAEDVG VYYCQQFLEYPFTFGSGTKLEIK (SEQ ID NO:2704)

Description	Sequence
CDR-H3 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3, CL0020188-4, CL0020188-5, CL0020188-6, CL0020188-7, and CL0020188-8	ARLTYGFDY (SEQ ID NO:2705)
CDR-L3 for CL0020188 and variants CL0020188-1, CL0020188-2, CL0020188-3, CL0020188-4, CL0020188-5, CL0020188-6, CL0020188-7, and CL0020188-8	QQFLEYPFT (SEQ ID NO:2706)
CL0020188-1 VH; CL0020188-3 VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDFYM SWVRQAPGKGLEWVSVIRNKANGYTAGYNPSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARL TYGFDYWGQGTLVTVSS (SEQ ID NO:2707)
CL0020188-1 VL; CL0020188-2 VL; CL0020188-5 VL; CL0020188-6 VL	DIVMTQTPLSLPVTPGEPASISCQSSKSLLHSNGKT YLNWYLQKPGQSPQLLIYWMSTRASGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYCQQFLEYPFTFG QGTKVEIK (SEQ ID NO:2708)
CL0020188-2 VH	EVQLVESGGGLVQPGGSLRLSCAGSGFTFTDFYM SWVRQAPGKGLEWVSVIRNKANGYTAGYNPSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARL TYGFDYWGQGTLVTVSS (SEQ ID NO:2709)
CL0020188-3 VL; CL0020188-4 VL; CL0020188-7 VL; CL0020188-8 VL	DIVMTQTPLSLPVTPGEPASISCQSSKSLLHSTGKT YLNWYLQKPGQSPQLLIYWMSTRASGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYCQQFLEYPFTFG QGTKVEIK (SEQ ID NO:2710)
CDR-L1 for variants CL0020188-3, CL0020188-4, CL0020188-7, and CL0020188-8	QSSKSLLHSTGKTYLN (SEQ ID NO:2711)
CL0020188-5 VH; CL0020188-7 VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFTDFYM SWVRQAPGKGLEWVSVIRNKANAYTAGYNPSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARL TYGFDYWGQGTLVTVSS (SEQ ID NO:2712)
CDR-H2 for variants CL0020188-5, CL0020188-6, CL0020188-7, and CL0020188-8	VIRNKANAYTAGYNPSVKG (SEQ ID NO:2713)
CL0020188-6 VH; CL0020188-8 VH	EVQLVESGGGLVQPGGSLRLSCAGSGFTFTDFYM SWVRQAPGKGPEWLSVIRNKANAYTAGYNPSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARL TYGFDYWGQGTLVTVSS (SEQ ID NO:2714)
CL0020123 VH	EVQLQQSGAELVRSGASVKLSCTASGFSIEDFYIH WVKQRPEQGLEWIGWIDPENGDSKYAPKFQGKA

Description	Sequence
	TMTADTSSNTAYLHLSSLTSEDTAVYYCHADHGN YGSTMDYWGQGTSVTVSS (SEQ ID NO:2715)
CL0020123 VL	DIQMNQSPSSLSASLGDTVTITCHASQHINVWLSW YQQKPGDHPKLLIYKASNLHTGVPSRFSGSGSGT GFTLTISSLQPEDIATYYCQQGQTYPRTFGGGTKL EIK (SEQ ID NO:2716)
CDR-H1 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3, CL0020123-4, CL0020123-5, CL0020123-6, CL0020123-7, and CL0020123-8	GFSIEDFYIH (SEQ ID NO:2717)
CDR-H2 for CL0020123 and variants CL0020123-1 and CL0020123-2	WIDPENGDSKYAPKFQG (SEQ ID NO:2718)
CDR-H3 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3, CL0020123-4, CL0020123-5, CL0020123-6, CL0020123-7, and CL0020123-8	HADHGNYGSTMDY (SEQ ID NO:2719)
CDR-L1 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3, CL0020123-4, CL0020123-5, CL0020123-6, CL0020123-7, and CL0020123-8	HASQHINVWLS (SEQ ID NO:2720)
CDR-L2 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3, CL0020123-4, CL0020123-5, CL0020123-6, CL0020123-7, and CL0020123-8	KASNLHT (SEQ ID NO:2721)
CDR-L3 for CL0020123 and variants CL0020123-1, CL0020123-2, CL0020123-3, CL0020123-4, CL0020123-5, CL0020123-6, CL0020123-7, and CL0020123-8	QQGQTYPRT (SEQ ID NO:2722)
CL0020123-1 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPENGDSKYAPKFQG RATITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2723)
CL0020123-1 VL; CL0020123-2 VL; CL0020123-3 VL; CL0020123-4 VL CL0020123-5 VL; CL0020123-6 VL; CL0020123-7 VL; CL0020123-8 VL	DIQMTQSPSSLSASVGDRVTITCHASQHINVWLS WYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQGQTYPRTFGQGTK VEIK (SEQ ID NO:2724)

Description	Sequence
CL0020123-2 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPENGDSKYAPKFQG RVTITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2725)
CL0020123-3 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPEQGDSKYAPKFQG RATITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2726)
CDR-H2 for variants CL0020123-3 and CL0020123-6	WIDPEQGDSKYAPKFQG (SEQ ID NO:2727)
CL0020123-4 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPENGESKYAPKFQG RATITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2728)
CDR-H2 for variants CL0020123-4 and CL0020123-7	WIDPENGESKYAPKFQG (SEQ ID NO:2729)
CL0020123-5 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPEQGESKYAPKFQG RATITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2730)
CDR-H2 for variants CL0020123-5 and CL0020123-8	WIDPEQGESKYAPKFQG (SEQ ID NO:2731)
CL0020123-6 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPEQGDSKYAPKFQG RVTITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2732)
CL0020123-7 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPENGESKYAPKFQG RVTITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2733)
CL0020123-8 VH	QVQLVQSGAEVKKPGASVKVSCKASGFSIEDFYI HWVRQAPGQGLEWMGWIDPEQGESKYAPKFQG RVTITADTSTSTAYMELSSLRSEDTAVYYCHADH GNYGSTMDYWGQGTLVTVSS (SEQ ID NO:2734)
CDR-H2 consensus sequence	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 (SEQ ID NO:2735)
CDR-H1 consensus sequence	G-F-T-F-T-α6-F-Y-M-S, wherein α6 is D or N (SEQ ID NO:2736)
CDR-H2 consensus sequence	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; β8 is G or A; β11 is A or T; and β12 is G or D (SEQ ID NO:2737)

Description	Sequence
CDR-H3 consensus sequence	γ1-R-L-γ4-Y-G-F-D-Y, wherein γ1 is A or T; and γ4 is T or S (SEQ ID NO:2738)
CDR-L1 consensus sequence	Q-S-S-K-S-L-L-H-S-δ10-G-K-T-Y-L-N, wherein δ10 is N or T (SEQ ID NO:2739)
CDR-L3 consensus sequence	Q-Q-F-L-E-f6-P-F-T, wherein f6 is Y or F (SEQ ID NO:2740)
CL0020307-1 VL	DIVMTQSPDSLAVSLGERATINCQSSKSLLHSNGK TYLNWYQQKPGQPPKLLIYWMSTRASGVPDRFS GSGSGTDFTLTISSLQAEDVAVYYCQQFLEFPFTF GQGTKVEIK (SEQ ID NO:2741)
TREM2 epitope	FPGESES (SEQ ID NO:2742)
TREM2 epitope	GEKGPCQRV (SEQ ID NO:2743)
TREM2 epitope	TLRNLQPHDAGL (SEQ ID NO:2744)
TREM2 epitope	VEVL (SEQ ID NO:2745)
Reference antibody #1 VL	DIQMTQSPSSVSASVGDRVTITCRASQGISNWLA WYQQKPGKAPKLLIYAASSLQVGVPLRFSGSGSG TDFTLTISSLQPEDFATYYCQQADSFPRNFGQGTK LEIK (SEQ ID NO:2746)
Reference antibody #1 VH	EVQLVQSGAEVKKPGESLKISCKGSGHSFTNYWI AWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQ VTISADKSISTAYLQWSSLKASDTAVYFCARQRTF YYDSSGYFDYWGQGTLVTVSS (SEQ ID NO:2747)
Reference antibody #2 VL	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAW YQQKPGKAPKLLIYAASSLQNGVPSRFSGSGSGT DFTLTISSLQPEDFATYFCQQADSFPRTFGQGTKL EIK (SEQ ID NO:2748)
Reference antibody #2 VH	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIA WVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQV TISADKSISTAYLQWSSLKASDTAMYFCARQRTF YYDSSDYFDYWGQGTLVTVSS (SEQ ID NO:2749)
Reference antibody #3 VL	DVVMTQSPDSLAVSLGERATINCRSSQSLVHSNR YTYLHWYQQKPGQSPKLLIYKVSNRFSGVPDRFS GSGSGTDFTLKISRVEAEDVGVYYCSQSTRVPYTF GQGTKLEIK (SEQ ID NO:2750)
Reference antibody #3 VH	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSQW MNWVRQAPGQRLEWIGRIYPGGGDTNYAGKFQG RVTITADTSASTAYMELSSLRSEDTAVYYCARLL RNQPGESYAMDYWGQGTLVTVSS (SEQ ID NO:2751)
CL0020188-4 VH	EVQLVESGGGLVQPGGSLRLSCAGSGFTFTDFYM SWVRQAPGKGPEWLSVIRNKANGYTAGYNPSVK

Description	Sequence
	GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARL TYGFDYWGQGTLVTVSS (SEQ ID NO:2752)

[00315] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in **TABLE L1** 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 EN1**) and heavy chain constant regions (**TABLE EN2**) 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

[00316] 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.

[00317] 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).

[00318] 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.

[00319] 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.

[00320] 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.

[00321] 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.

[00322] 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.

[00323] 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.

[00324] 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 M1**.

TABLE M1

Description	Sequence
'823 Antibody 1 CDR-H1	GFSFNTYWIG (SEQ ID NO:2753)
'823 Antibody 1 CDR-H2	IIYPGDQDIRYSPSFQG (SEQ ID NO:2754)
'823 Antibody 1 CDR-H3	ARYGRYIYGYGGYHGMDV (SEQ ID NO:2755)
'823 Antibody 1 CDR-L1	RASQAIRDDLG (SEQ ID NO:2756)
'823 Antibody 1 CDR-L2	YAASSLQS (SEQ ID NO:2757
'823 Antibody 1 CDR-L3	LQNYNYPHT (SEQ ID NO:2758)
'823 Antibody 1 VH	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYWIGWVRQMPG KGLEWMGIIYPGDQDIRYSPSFQGQVTISADKSISTAYLQWSSL KASDTAMYYCARYGRYIYGYGGYHGMDVWGQGTTVTVSS (SEQ ID NO:2759)
'823 Antibody 1 VL	DIQMTQSPSSLSASVGDRVTITCRASQAIRDDLGWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC LQNYNYPHTFGQGTKLEIK (SEQ ID NO:2760)
'823 Antibody 1 Heavy Chain	EVQLVQSGAEVKKPGESLKISCKGSGFSFNTYWIGWVRQMPG KGLEWMGIIYPGDQDIRYSPSFQGQVTISADKSISTAYLQWSSL KASDTAMYYCARYGRYIYGYGGYHGMDVWGQGTTVTVSSA STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH KPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG (SEQ ID NO:2761)
'823 Antibody 1 Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQAIRDDLGWYQQKPGKA PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC LQNYNYPHTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2762)
Human TREM2 ECD-His	HNTTVFQGVAGQSLQVSCPYDSMKHWGRRKAWCRQLGEKG PCQRVVSTHNLWLLSFLRRWNGSTAITDDTLGGTLTITLRNLQ PHDAGLYQCQSLHGSEADTLRKVLVEVLADPLDHRDAGDLW FPGESESFEDAHVEHSISRSLLEGEIPFPPTSHHHHHH (SEQ ID NO:2763)

Mouse TREM2 ECD-His	LNTTVLQGMAGQSLRVSCTYDALKHWGRRKAWCRQLGEEG PCQRVVSTHGVWLLAFLKKRNGSTVIADDTLAGTVTITLKNL QAGDAGLYQCQSLRGREAEVLQKVLVEVLEDPLDDQDAGDL WVPEESSSFEGAQVEHSTSRNQETSFPPTSHHHHHH (SEQ ID NO:2764)
Rat TREM2 ECD-His	NTTVFQGVAGQSLRVSCPYDSATHWGRRKAWCRQLGEEGPC ERVVSTHSWWLLSFLKRRNGSTAITDDALGGTLTVTLRDLQA QDAGVYQCQSLQGREASTLQKILVEVLTEPLEHEHAGDFWVP EESGSFEDPPVERSSSRSPSEGEPSFPPASGGGGQHHHHHH (SEQ ID NO:2765)
Rabbit TREM2 ECD-His	NTTVLQGVAGQSLRVSCTYDALRHWGRRKAWCRQLAEEGPC QRVVSTHGVWLLAFLRKQNGSTVITDDTLAGTVTITLRNLQA GDAGLYQCQSLRGREAEVLQKVVVEVLEDPLDDQDAGDLWV PEESESFEGAQVEHSTSRSQSGGGGQHHHHHH (SEQ ID NO:2766)
Cynomolgus monkey TREM2 ECD-His	HNTTVFQGVEGQSLQVSCPYDSMKHWGRRKAWCRQLGEKGP CQRVVSTHNLWLLSFLRRRNGSTAITDDTLGGTLTITLRNLQPH DAGFYQCQSLHGSEADTLRKVLVEVLADPLDHRDAGDLWVP GESESFEDAHVEHSISRPSQGSHLPSCLSKEGGGGQHHHHHH (SEQ ID NO:2767)

[00325] In some embodiments, each of the light chain variable regions and each of the heavy chain variable regions disclosed in **TABLE M1** 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 EN1)** and heavy chain constant regions **(TABLE EN2)** 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.

Exemplary Anti-TREM2 Antibodies

[00326] 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 EX1** and **EX2** below, along with exemplary light chain and variable regions.

TABLE EX1: Exemplary Anti-TREM2 Antibody Light Chain Variable Regions

VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
EIVMTQSPATLSVSPGERATLSCR ASQSVSSNLAWFQQKPGQAPRLL IYGASTRATGIPARFSGSGSGTEF TLTISSLQPEDFAVYYCLQDNNFP PTFGQGTKVDIK (SEQ ID NO:330)	RASQSVSSNLA (SEQ ID NO:10)	GASTRAT (SEQ ID NO:23)	LQDNNFPPT (SEQ ID NO:372)

TABLE EX2: Exemplary Anti-TREM2 Antibody Heavy Chain Variable Regions

VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
EVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIGWVRQMP GKGLEWMGIIYPGDADARYS PSFQGQVTISADKSISTAYLQ WSSLKASDTAMYFCARRRQ GIFGDALDFWGQGTLVTVSS (SEQ ID NO:331)	SYWIG (SEQ ID NO:81)	IIYPGDADARYSPSF QG (SEQ ID NO:373)	RRQGIFGDALDF (SEQ ID NO:374)

[00327] As noted above, anti-TREM2 antibodies may comprise one or more of the CDRs presented in **TABLE EX1** (light chain CDRs; i.e. CDRLs) and **TABLE EX2** (heavy chain CDRs, i.e. CDRHs).

[00328] In some embodiments, an anti-TREM2 antibody comprises a light chain comprising a CDRL1 having an amino acid sequence according to SEQ ID NO:10, a CDRL2 having an amino acid sequence according to SEQ ID NO:23, a CDRL3 having an amino acid sequence according to SEQ ID NO:372, or any CDRL1, CDRL2, or CDRL3 amino acid sequence 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 to any of SEQ ID NOS:10, 23, and 372. Such substitutions, deletions, and insertions would retain significant anti-TREM2 binding activity In these and other embodiments, an anti-TREM2 antibody comprises a CDRH1 having an amino acid sequence according to SEQ ID NO:81, a CDRH2 having an amino acid sequence according to SEQ ID NO:373, a CDRH3 having an amino acid sequence according to SEQ ID NO:374, or any CDRH1, CDRH2, or CDRH3 having an amino acid sequence 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 to any of SEQ ID NOS:81, 373, and 374. Such substitutions, deletions, and insertions would retain significant anti-TREM2 binding activity

[00329] In some embodiments, an anti-TREM2 antibody comprises a light chain variable region comprising a CDRL1 having an amino acid sequence according to SEQ ID NO:10; a CDRL2 having an

amino acid sequence according to SEQ ID NO:23; and a CDRL3 having an amino acid sequence according to SEQ ID NO:372, and a heavy chain variable region comprising a CDRH1 having an amino acid sequence according to SEQ ID NO:81; a CDRH2 having an amino acid sequence according to SEQ ID NO:373; and a CDRH3 having an amino acid sequence according to SEQ ID NO:374.

[00330] In some embodiments, an anti-TREM2 antibody comprises a light chain variable region having an amino acid sequence according to SEQ ID NO:330, or any amino acid sequence 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 to SEQ ID NO:330. Such substitutions, deletions, and insertions would retain significant anti-TREM2 binding activity. In some embodiments, an anti-TREM2 antibody comprises a heavy chain variable region having an amino acid sequence according to SEQ ID NO:331, or any amino acid sequence 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 to SEQ ID NO:331. Such substitutions, deletions, and insertions would retain significant anti-TREM2 binding activity.

[00331] In specific embodiments, an anti-TREM2 antibody comprises a light chain variable region having an amino acid sequence according to SEQ ID NO:330, and a heavy chain variable region having an amino acid sequence according to SEQ ID NO:331.

[00332] In some embodiments, an anti-TREM2 antibody comprises a heavy chain amino acid sequence, and/or a light chain amino acid sequence selected from **TABLE EX3**. TABLE EX3 shows exemplary anti-TREM2 antibody heavy and light chains for exemplary antibodies "Ab-1", "Ab-2", and "Ab-3".

TABLE EX3: Exemplary Anti-TREM2 Antibody Heavy and Light Chains

Chain	Description	Amino Acid Sequence
Light Chain	Ab-1	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLI YGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQDNNFPPT FGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:2777)

Chain	Description	Amino Acid Sequence
	Ab-1 w/ leader sequence	MDMRVPAQLLGLLLLWLRGARCEIVMTQSPATLSVSPGERATLSCR ASQSVSSNLAWFQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFT LTISSLQPEDFAVYYCLQDNNFPPTFGQGTKVDIKRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO:339)
	Ab-2	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLI YGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQDNNFPPT FGQGTKVDIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDIN VKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNS YTCEATHKTSTSPIVKSFNRNEC (SEQ ID NO:2780)
	Ab-3	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWFQQKPGQAPRLLI YGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFAVYYCLQDNNFPPT FGQGTKVDIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDIN VKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNS YTCEATHKTSTSPIVKSFNRNEC (SEQ ID NO:2780)
Heavy Chain	Ab-1	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLE WMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAM YFCARRRQGIFGDALDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:2774)
	Ab-1 w/ leader sequence	MDMRVPAQLLGLLLLWLRGARCEVQLVQSGAEVKKPGESLKISCK GSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDADARYSPSFQGQVT ISADKSISTAYLQWSSLKASDTAMYFCARRRQGIFGDALDFWGQGTL VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK (SEQ ID NO:340)

Chain	Description	Amino Acid Sequence
	Ab-2	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLE WMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAM YFCARRRQGIFGDALDFWGQGTLVTVSSAKTTPPSVYPLAPGSAAQT NSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSS SVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVH TAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPI EKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFT CSVLHEGLHNHHTEKSLSHSPGK (SEQ ID NO:2781)
	Ab-3	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLE WMGIIYPGDADARYSPSFQGQVTISADKSISTAYLQWSSLKASDTAM YFCARRRQGIFGDALDFWGQGTLVTVSSAKTTPPSVYPLAPGSAAQT NSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSS SVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVH TAQTQPREEQFGSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPI EKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFT CSVLHEGLHNHHTEKSLSHSPGK (SEQ ID NO:2779)

[00333] In some embodiments, an anti-TREM2 antibody comprises a light chain having an amino acid sequence according to any one of SEQ ID NOS:2777, 339, and 2780, or any amino acid sequence 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 to any one of SEQ ID NOS:2777, 339, and 2780. Such substitutions, deletions, and insertions would retain significant anti-TREM2 binding activity. In these and other embodiments, an anti-TREM2 antibody comprises a heavy chain having an amino acid sequence according to any one of SEQ ID NOS:2774, 340, 2779, and 2781, or any amino acid sequence 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 to any one of SEQ ID NOS:2774, 340, 2779, and 2781. Such substitutions, deletions, and insertions would retain significant anti-TREM2 binding activity.

[00334] In some embodiments, an anti-TREM2 antibody comprises a light chain having an amino acid sequence according to SEQ ID NO:2777, and a heavy chain variable region having an amino acid sequence according to SEQ ID NO:2774. In some embodiments, an anti-TREM2 antibody comprises a light chain having an amino acid sequence according to SEQ ID NO:339, and a heavy chain variable

region having an amino acid sequence according to SEQ ID NO:340. In some embodiments, an anti-TREM2 antibody comprises a light chain having an amino acid sequence according to SEQ ID NO:2780, and a heavy chain variable region having an amino acid sequence according to SEQ ID NO:2781. In some embodiments, an anti-TREM2 antibody comprises a light chain having an amino acid sequence according to SEQ ID NO:2780, and a heavy chain variable region having an amino acid sequence according to SEQ ID NO:2779.

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 EN1**.

TABLE EN1: Exemplary Human Immunoglobulin Light Chain Constant Regions

Designation	CL Domain Amino Acid Sequence
Human lambda v1	GQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD GSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS (SEQ ID NO:191)
Human lambda v2	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS SPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS (SEQ ID NO:192)
Human lambda v3	QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:193)
Human lambda v4	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS SPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTH EGSTVEKTVAPTECS (SEQ ID NO:194)
Human lambda v5	GQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKAD GSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVT HEGSTVEKTVAPAECS (SEQ ID NO:195)
Human kappa v1	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC (SEQ ID NO:196)
Human kappa v2	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC (SEQ ID NO:197)

[00340] 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.

[00341] 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 EN2**.

TABLE EN2: Exemplary Human Immunoglobulin Heavy Chain Constant Regions

Ig isotype	Heavy Chain Constant Region Amino Acid Sequence
Human IgG1z	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK (SESQ ID NO:198)
Human IgG1za	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK (SESQ ID NO:199)
Human IgG1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV

Ig isotype	Heavy Chain Constant Region Amino Acid Sequence
	TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK (SESQ ID NO:200)
Human IgG1fa	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK (SESQ ID NO:201)
Human IgG1z aglycosylated v1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK (SESQ ID NO:202)
Human IgG1z aglycosylated v2	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK (SESQ ID NO:203)
Human IgG2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTK VDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPML DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK (SESQ ID NO:204)
Human IgG4	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY

Ig isotype	Heavy Chain Constant Region Amino Acid Sequence
	TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK (SESQ ID NO:205)

[00342] 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.

[00343] 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.

[00344] 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.

[00345] 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.

[00346] 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).

[00347] 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.

[00348] 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.

[00349] 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.

[00350] 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).

[00351] 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.

[00352] 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.

[00353] 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).

[00354] 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).

[00355] 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

[00356] 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

[00357] 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.

[00358] 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.

[00359] 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).

[00360] 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.

[00361] 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).

[00362] 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.

[00363] 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.

[00364] 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

[00365] 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.

[00366] 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

[00367] 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.

[00368] 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

[00369] 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.

[00370] 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.

[00371] 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.

[00372] 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.

[00373] 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.

[00374] 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.

[00375] 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.

[00376] 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.

[00377] 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.

[00378] 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.

[00379] 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

[00380] 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.

[00381] 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.

[00382] 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.

[00383] 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.

[00384] 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

[00385] 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.

[00386] 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.

[00387] 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)).

[00388] 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

[00389] 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.

[00390] 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.

[00391] 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.

[00392] 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.

[00393] 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.

[00394] 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.

[00395] 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).

[00396] 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.

[00397] 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.

[00398] 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.

[00399] 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.

[00400] 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).

[00401] 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).

[00402] 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.

[00403] 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.

[00404] 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.

[00405] 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.

[00406] 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.

[00407] 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.

[00408] In some embodiments, the anti-TREM2 antibody is administered to a human patient via an IV infusion. In some embodiments, an IV infusion of anti-TREM2 antibody is up to about 5 hours, up to about 4 hours, up to about 3 hours, up to about 2 hours, or up to about 60 minutes. In some embodiments, an IV infusion of anti-TREM2 antibody is from about 5 minutes to about 5 hours, from about 5 minutes to about 4 hours, from about 5 minutes to about 3 hours, from about 5 minutes to about 2 hours, or from about 5 minutes to about 60 minutes. In some embodiments, an IV infusion of anti-TREM2 antibody is about 5 minutes, about 10 minutes, about 15 minutes, about 20 minutes, about 25 minutes, about 30 minutes, about 35 minutes, about 40 minutes, about 45 minutes, about 50 minutes, about 55 minutes, about 60 minutes, about 70 minutes, about 80 minutes, or about 90 minutes.

[00409] In some embodiments, anti-TREM2 antibody is administered to a human patient at a dose of up to about 200 mg/kg. In some embodiments, anti-TREM2 antibody is administered to a human patient at a dose of up to about 150 mg/kg. In some embodiments, anti-TREM2 antibody is administered to a human patient at a dose of up to about 100 mg/kg. In some embodiments, anti-TREM2 antibody is administered to a human patient at a dose of from about 1 mg/kg to about 100 mg/kg, from about 1 mg/kg to about 90 mg/kg, from about 1 mg/kg to about 80 mg/kg, from about 1 mg/kg to about 70 mg/kg, or from about 1 mg/kg to about 60 mg/kg. In some embodiments, anti-TREM2 antibody is administered to a human patient at a dose of about 1 mg/kg, about 2 mg/kg, about 3 mg/kg, about 5 mg/kg, about 10 mg/kg, about 15 mg/kg, about 20 mg/kg, about 25 mg/kg, about 30 mg/kg, about 35 mg/kg, about 40 mg/kg, about 45 mg/kg, about 50 mg/kg, about 55 mg/kg, or about 60 mg/kg.

[00410] In some embodiments, anti-TREM2 antibody is administered to a human patient once daily. In some embodiments, anti-TREM2 antibody is administered to a human patient 1, 2, 3 or 4 times weekly. In some embodiments, anti-TREM2 antibody is administered to a human patient 1, 2, 3 or 4 times monthly. In some embodiments, anti-TREM2 antibody is administered to a human patient once every 1, 2, 3, or 4 weeks. In some embodiments, anti-TREM2 antibody is administered to a human patient once every 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, or 14 days. In some embodiments, anti-TREM2 antibody is administered to a human patient once weekly.

[00411] In some embodiments, the present invention provides a liquid formulation, comprising anti-TREM2 antibody at a concentration of up to about 300 mg/mL. In some embodiments, the present invention provides a liquid formulation, comprising anti-TREM2 antibody at a concentration of up to about 250 mg/mL. In some embodiments, the present invention provides a liquid formulation, comprising anti-TREM2 antibody at a concentration of up to about 200 mg/mL. In some embodiments, the present invention provides a liquid formulation, comprising anti-TREM2 antibody at a concentration of up to about 150 mg/mL. In some embodiments, the present invention provides a liquid formulation, comprising anti-TREM2 antibody at a concentration of about 300 mg/mL, about 250 mg/mL, about 200 mg/mL, about 180 mg/mL, about 170 mg/mL, about 160 mg/mL, about 150 mg/mL, about 140 mg/mL, about 130 mg/mL, about 120 mg/mL, about 110 mg/mL, or about 100 mg/mL. In some embodiments, the present invention provides a liquid formulation, comprising anti-TREM2 antibody at a concentration of about 140 mg/mL. In some embodiments, a method of the invention comprises administering to a human patient a liquid formulation as described herein. In some embodiments, a method of the invention comprises administering to a human patient a liquid formulation, comprising anti-TREM2 antibody at a concentration of about 140 mg/mL.

[00412] 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

[00413] In some embodiments, the agonist of TREM2 is a small molecule agonist of TREM2.

[00414] 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.

[00415] In some embodiments, the agonist of TREM2 is a lipopolysaccharide.

[00416] 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.

[00417] 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.

[00418] In some embodiments, the agonist of TREM2 is a small molecule disclosed in PCT Application Publication WO2021/226135 or WO2021/226629.

[00419] In some embodiments, the agonist of TREM2 is a TREM2 agonist compound comprising a bicyclic core. In some embodiments, the bicyclic core is a 10-membered heteroaryl core. In some embodiments, the TREM2 agonist compound comprises a 10-membered heteroaryl core, comprising 1-4 nitrogen atoms as part of the core ring structure. In some embodiments, the TREM2 agonist compound comprises a 10-membered heteroaryl core, comprising 3 or 4 substituent groups.

IV. Other TREM2 Agonists

[00420] In some embodiments, the agonist of TREM2 is heat shock protein 60 (HSP60).

[00421] In some embodiments, the agonist of TREM2 is apopoliprotein E (ApoE).

V. Pharmaceutically Acceptable Compositions

[00422] 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.

[00423] 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.

[00424] 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.

[00425] 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.

[00426] 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.

[00427] 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.

[00428] 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.

[00429] 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.

[00430] 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.

[00431] 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.

[00432] 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.

[00433] 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.

[00434] 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.

[00435] In other embodiments, pharmaceutically acceptable compositions of this invention are formulated for intravenous (IV) administration.

[00436] 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.

[00437] 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.

[00438] 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.

[00439] 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

Microglial Differentiation Protocol

[00440] Pluripotent stem cell (PSC) differentiation is induced with mTeSR Custom medium (STEMCELLTechnologies®) containing 80ng/mL BMP4. At day 4, cells are induced with 25 ng/mL basic fibroblast growth factor, 100 ng/mL stemcell factor (SCF), and 80 ng/mL vascular endothelial growth factor in StemPro-34 SFM (with 2 mM GutaMAX, Life Technologies). Two days later, the medium is supplemented with 50 ng/mL SCF, 50 ng/mL IL-3, 5 ng/mL thrombopoietin, 50 ng/mL macrophage CSF (M-CSF) and 50 ng/mL Flt3l, and from day 14 with 50 ng/mL M-CSF, 50 ng/mL Flt3l, and 25 ng/mL GMCSF. Between days 25 and 50, CD14+ or CD14+CX3CR1+ progenitors are isolated and plated onto tissue culture-treated dishes or Thermanox plastic coverslips (all from Thermo Fisher Scientific) in Microglial Medium (RPMI-1640 [Life Technologies] with 2 mM GlutaMAX-I, 10 ng/mL GM-CSF, and 100 ng/mL IL-34). Medium is replenished every 3–4 days for at least 2 weeks.

Generation of induced pluripotent stem cells (iPSCs) from primary healthy, adrenomyeloneuropathy (AMN) and cerebral childhood ALD (cALD) fibroblasts

[00441] Fibroblast cell cultures from healthy individuals (AG01439, male 3 days old), Adrenomyeloneuropathy (AMN) (GM 07530, male 26 years old) and cALD (GM04934, male 7 years old with VLCFA abnormality and clinical X-ALD disease) patients are obtained. A control human IPSC ATCC-DYR0100 cell line is also obtained. Fibroblasts are cultured in DMEM with 10% FBS, 2mM L-glutamine and 1% penicillin/streptomycin at 37°C with 5% CO_2.

[00442] Fibroblast cells seeded at 0.2 X 106 cells/well of a 6-well plate in fibroblast medium (DMEM + 10% FBS) are transduced with six lentiviral vectors designed to deliver human OCT4, SOX2, c-MYC, KLF4, Nanog and Lin28 cDNA sequences. On the next day, fresh fibroblast media is added to the cells 24 hours after transduction. At 48 hours after transduction the media is changed to half E8 medium and half fibroblast medium. When the cells reach about 60% confluence they are transferred to 10 cm Matrigel-coated plates (one well of a 6-well plate into one 10 cm dish) in E8 medium (StemCell Technologies) and media is replaced daily. Between day 15 and day 30 in culture, individual hiPS clones are manually picked using a Leica stereomicroscope. Each hiPS clone is expanded and characterized by immunofluorescence for the expression of Oct4 and Tra-1-60. IPSCs are cultured on a Matrigel (BD-Biosceicnes) coated plate in IPSC medium (mTeSR media from Stemcell technologies, Vancouver, Canada) and media is changed daily until cells are ready for passage.

Microglia characterization assays and methods

[00443] Microglia are analyzed using flow cytometry, immunohistochemistry and cell quantification procedures such as those disclosed by Masuda et al. (Masuda *et al*., Nature. 2019; 566: 388-394.)

Monocyte derived macrophage isolation protocols

[00444] Monocyte derived macrophages (MDMs) are derived from PBMCs collected from patients with adrenomyeloneuropathy (AMN) or cALD and isolated by magnetic bead separation and differentiation into macrophages as reported in Jin, et al. J Vis Exp. 2016; (112): 54244. CD14+ monocytes are collected for use in the Examples described below.

Example 1. The effects of TREM2 agonists on microglia after VLCFA challenge.

Conceptual basis

[00445] Saturated very long chain fatty acids (VLCFAs; ≥C22:0) accumulate in the microglia of patients suffering from X-linked adrenoleukodystrophy (X-ALD, OMIM 300100), a severe hereditary

neurodegenerative disease, due to peroxisomal impairment. Previous studies analysed the development of X-ALD in humans and gene knockout animal models. However, the toxic effect of VLCFA leading to severe symptoms with progressive and multifocal demyelination, adrenal insufficiency and inflammation still remains unclear. To understand the toxic effects of VLCFA in the brain, neural cells are exposed to VLCFA and the effects are analyzed. Oligodendrocytes and astrocytes challenged with docosanoic- (C22:0), tetracosanoic- (C24:0) and hexacosanoic acids (C26:0) die within 24 h. VLCFA-induced depolarization of mitochondria in situ and increased intracellular Ca21 level in all three brain cell types provides indications about the mechanism of toxicity of VLCFA. VLCFAs affect to the largest degree the myelin-producing oligodendrocytes. In isolated mitochondria, VLCFAs exert a detrimental effect by affecting the inner mitochondrial membrane and promoting the permeability transition. Without intending to be limited to any particular theory, it is reasonable to conclude that there is potent toxic activity of VLCFA due to dramatic cell physiological effects with mitochondrial dysfunction and Ca21 deregulation. This provides evidence for mitochondrial-based cell death mechanisms in neurodegenerative diseases with peroxisomal defects and subsequent VLCFA accumulation. Treatment with a TREM2 agonist rescues at least some of the deleterious effects of VLCFA accumulation in microglia, by preventing apoptosis and activating phagocytic mechanisms to clear myelin debris to lower inflammation in the vicinity of axonopathy.

Experiments

[00446] Healthy patient-derived microglia are plated in 96 well microtiter plates. Each well also contains either a TREM2 agonist (eg. a TREM2 antibody agonist or TREM2 small molecule agonist) or a control compound (eg. an isotype control IgG as a control antibody or DMSO as a control small molecule). An exemplary method uses an immobilized TREM2 antibody agonist in the test wells at 10 μg/well and an isotype control plated in the control wells at 10 μg/well. Another exemplary method uses a solubilized TREM2 antibody agonist or small molecule agonist in the test wells. Cells are maintained in CSF1-containing culture medium (50 ng/mL) for 2 days prior to adding VLCFA (e.g., C26:0, C24:0, C22:0 added at 10-20 uM concentration to culture medium; Hein *et al.*, Human Molecular Genetics. 2008; 17: 1750–176.). After 24 hrs of VLCFA challenge, wells are analyzed microscopically by immunohistochemical staining, e.g., by staining for Iba1, P2YR12 or other myeloid cell surface markers, staining for caspases, which indicate cell apoptosis, and for the number of viable cells as well as for cell morphology. Other microtiter wells can be treated with lysis buffer to collect mRNA for qPCR analysis for markers of myeloid phenotype, such as homeostatic or activated cell states (Keren-Shaul *et al.*, Cell. 2017; 169: 1276–1290; Decskowska *et al.*, Cell. 2018; 173:1073-1081.). Other microtiter wells can be analyzed for total cell death by measuring lactate dehydrogenase levels, a measure of cell lysis, from the

culture supernatant (Hein *et al.*, Human Molecular Genetics. 2008; 17: 1750–176.). This experiment can be modified to measure the kinetics of phenotypic transition following the pilot described above by analyzing changes over time and at various doses of VGL101 to understand the dose dependence of rescue. In addition, the Incucyte method of monitoring cell cultures can be used to monitor for morphological changes in real time.

[00447] The above experiments are also repeated using monocytes derived macrophages, in place of the microglia.

Example 2. The effects of TREM2 agonists on microglia with an ABCD1 dysfunction.

Conceptual basis

[00448] Microglia derived from patients suffering from cALD, such as by differentiating patient iPSC or patient monocytes, have transcriptional and biochemical signatures distinct from healthy donor-derived microglia, e.g., potentially enriched for disease associated microglia (DAM). Treatment of cALD patient-derived microglia with VLCFA in vitro will cause toxic and pro-inflammatory effects due to accumulation of fatty acids from dysfunctional peroxisome-mediated metabolism. cALD microglia may also autonomously accumulate VLCFAs without an extracellular challenge. Rescue of the cytotoxicity and inflammatory state by treating with TREM2 agonists during VLCFA challenge can be characterized through transcriptional and biochemical analyses.

Experiments

[00449] iPSC or monocyte-derived microglia, derived from patients suffering from an ABCD1 dysfunction, such as cALD or AMN, are plated in 96 well microtiter plates. Each well also contains either a TREM2 agonist (eg. a TREM2 antibody agonist or TREM2 small molecule agonist) or a control compound (eg. an isotype control IgG as a control antibody or DMSO as a control small molecule). An exemplary method uses an immobilized TREM2 antibody agonist in the test wells at 10 μg/well and an isotype control plated in the control wells at 10 μg/well. Another exemplary method uses a solubilized TREM2 antibody agonist or small molecule agonist in the test wells. Cells are maintained in a CSF1-containing culture medium (50 ng/mL) for 2 days prior to adding VLCFA (e.g., C26:0, C24:0, C22:0 added at 10-20 uM concentration to culture medium; Hein *et al.*, Human Molecular Genetics. 2008; 17: 1750–176.). Vehicle is added to select wells, in place of the VLCFA. After 24 hrs of challenge, wells are analyzed microscopically by immunohistochemical staining, e.g., by staining for Iba1, PYR12 or other myeloid cell surface markers, staining for caspases, which indicate cell apoptosis, and for the number of viable cells as well as for cell morphology. Other microtiter wells can be treated with lysis buffer to collect mRNA for qPCR analysis for markers of myeloid phenotype, such as homeostatic or activated cell

states (Keren-Shaul *et al*., Cell. 2017; 169: 1276–1290; Decskowska *et al*., Cell. 2018; 173:1073-1081.). Other microtiter wells can be analyzed for total cell death by measuring lactate dehydrogenase levels, a measure of cell lysis, from the culture supernatant (Hein *et al.*, Human Molecular Genetics. 2008; 17: 1750–176.). This experiment can be modified to measure the kinetics of phenotypic transition following the pilot described above by analyzing changes over time and at various doses of VLCFA or VGL101 to understand the dose dependence of rescue. In addition, the Incucyte method of monitoring cell cultures can be used to monitor for morphological changes in real time.

[00450] The above experiments are also repeated using monocytes derived macrophages, in place of the iPSC or microglia. The above experiments may also be repeated, wherein the VLCFA challenge is replaced with alternative additions known to induce increased accumulation of VLCFAs in cALD microglia. For example, myelin debris or lipids can be added to the wells in place of the VLCFA.

Example 3. Neurofilament light chain as a biomarker for tracking x-ALD treatment efficacy

[00451] Monitoring of serum from patients with x-ALD 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.

CLAIMS

We claim:

1. A method of treating a disease or disorder caused by and/or associated with ATP-binding cassette transporter 1 (ABCD1) 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 X-linked adrenoleukodystrophy (x-ALD), Globoid cell leukodystrophy, Metachromatic leukodystrophy (MLD), Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), Alexander disease, fragile X-associated tremor ataxia syndrome (FXTAS), adult-onset autosomal dominant leukodystrophy (ADLD), and X-linked Charcot–Marie–Tooth disease (CMTX).

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), or Parkinson's disease; wherein the patient exhibits ABCD1 dysfunction, and/or has a mutation in a gene affecting the function of ABCD1.

4. The method of claim 1, wherein the disease or disorder is x-ALD.

5. The method of claim 1, wherein the disease or disorder is Addison disease wherein the patient has been found to have a mutation in one or more ABCD1 genes affecting ABCD1 function.

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-4, 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-12 p40, 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;

(k) 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;

(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 levels of one or more of CSF1, CSF2 and IL-34; or

(s) 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 EX1** and **A10**, and a heavy chain variable region having a CDRH1, CDRH2, and CDRH3 selected from **Table EX2** and **A11**.

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 EX1** or **A14**, and a heavy chain variable region selected from **Table EX2** and **A15**.

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).