

ANTI-TAU ANTIBODIES AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Application No. 62/572,910, filed October 16, 2017; U.S. Application No. 62/577,011, filed October 25, 2017; and U.S. Application No. 62/697,034, filed July 12, 2018. Each of these applications is incorporated herein by reference in its entirety.

SEQUENCE LISTING

[0002] This application includes a Sequence Listing submitted electronically as a text file named “104018_001025_SL.txt”, created on September 17, 2018 with a size of 916,053 bytes. The Sequence Listing is incorporated by reference herein.

TECHNICAL FIELD

[0003] The present invention relates to antibodies that specifically bind Tau and methods of using the same.

BACKGROUND

[0004] Human Tau is encoded by the microtubule-associated protein Tau gene, MAPT, located on chromosome 17q21. The adult human brain contains six main Tau isoforms which are generated by alternative splicing of exon 2 (E2), E3, and E10. These isoforms differ depending on the number of 29-residue repeat regions near the N-terminus. Tau isoforms containing 0, 1, or 2 inserts are known as 0N, 1N, and 2N, respectively. Unprocessed Tau isoforms also contain either 3 (“3R”) or 4 (“4R”) microtubule-binding repeat domains. The second of these repeat domains is encoded by E10 and is not included in 3R Tau isoforms (**Figure 1**).

[0005] Although Tau is usually highly soluble, under pathological conditions, it can aggregate into paired helical filaments, neurofibrillary tangles and other structures that define a large spectrum of neurodegenerative diseases termed Tauopathies. Tauopathy thus refers to a

class of neurodegenerative diseases associated with aggregation of the microtubule-associated protein Tau, including Alzheimer's disease (AD), progressive supranuclear palsy (PSP), and frontotemporal dementia (FTD).

[0006] The underlying mechanism of Tau-mediated neurotoxicity is poorly understood and the trigger for Tau aggregation in neurons is yet to be elucidated. Thus, while therapeutic approaches targeting Tau are being explored, there remains a need for specific and effective therapeutic agents that target Tau.

SUMMARY

[0007] Described herein are monoclonal antibodies, or antigen-binding fragments thereof, that specifically bind a human Tau isoform or fragment. In one aspect, the present disclosure refers to a monoclonal antibody comprising a heavy chain and a light chain, or an antigen-binding fragment thereof, that specifically binds a human Tau, wherein: the heavy chain comprises a heavy chain complementarity determining region 1 (HCDR1) comprising SEQ ID NO: 732, a heavy chain complementarity determining region 2 (HCDR2) comprising SEQ ID NO: 734, and a heavy chain complementarity determining region 3 (HCDR3) comprising SEQ ID NO: 736, and the light chain comprises a light chain complementarity determining region 1 (LCDR1) comprising SEQ ID NO: 846, a light chain complementarity determining region 2 (LCDR2) comprising SEQ ID NO: 848, and a light chain complementarity determining region 3 (LCDR3) comprising SEQ ID NO: 850 as defined according to the method of Kabat; or the heavy chain comprises a HCDR1 comprising SEQ ID NO: 1002, a HCDR2 comprising SEQ ID NO: 1004, and a HCDR3 comprising SEQ ID NO: 1006 and the light chain comprises a LCDR1 comprising SEQ ID NO: 1116, a LCDR2 comprising SEQ ID NO: 1118, and a LCDR3 comprising SEQ ID NO: 1120 as defined by IMGT. In some examples, the antibody is murine antibody, a chimeric antibody, or a humanized antibody. In some examples, the antibody isotype is IgG1. In some examples, the antibody comprises: a heavy chain complementarity determining region 1 (HCDR1), a heavy chain complementarity determining region 2 (HCDR2), and a heavy chain complementarity determining region 3 (HCDR3) as set forth in SEQ ID NO: 196 and a light chain complementarity determining region 1 (LCDR1), a light chain complementarity determining region 2 (LCDR2), and a light chain complementarity determining region 3 (LCDR3) as set forth in SEQ ID NO: 411; a HCDR1, a HCDR2, and a HCDR3 as set forth in

SEQ ID NO: 268 and a LCDR1, a LCDR2, and a LCDR3 as set forth in SEQ ID NO: 465; or a HCDR1, a HCDR2, and a HCDR3 as set forth in SEQ ID NO: 402 and a LCDR1, a LCDR2, and a LCDR3 as set forth in SEQ ID NO: 572. In some examples, the monoclonal antibody or antigen-binding fragment thereof comprises a HCDR1 comprising SEQ ID NO: 594, a HCDR2 comprising SEQ ID NO: 596, a HCDR3 comprising SEQ ID NO: 598, a LCDR1 comprising SEQ ID NO: 738, a LCDR2 comprising SEQ ID NO: 740, and a LCDR3 comprising SEQ ID NO: 742 as defined according to the method of Kabat; a HCDR1 comprising SEQ ID NO: 864, a HCDR2 comprising SEQ ID NO: 866, a HCDR3 comprising SEQ ID NO: 868, a LCDR1 comprising SEQ ID NO: 1008, a LCDR2 comprising SEQ ID NO: 1010, and a LCDR3 comprising SEQ ID NO: 1012 as defined by IMGT; a HCDR1 comprising SEQ ID NO: 642, a HCDR2 comprising SEQ ID NO: 644, a HCDR3 comprising SEQ ID NO: 646, a LCDR1 comprising SEQ ID NO: 774, a LCDR2 comprising SEQ ID NO: 776, and a LCDR3 comprising SEQ ID NO: 778 as defined according to the method of Kabat; a HCDR1 comprising SEQ ID NO: 912, a HCDR2 comprising SEQ ID NO: 914, a HCDR3 comprising SEQ ID NO: 916, a LCDR1 comprising SEQ ID NO: 1044, a LCDR2 comprising SEQ ID NO: 1046, and a LCDR3 comprising SEQ ID NO: 1048 as defined by IMGT; a HCDR1 comprising SEQ ID NO: 732, a HCDR2 comprising SEQ ID NO: 734, a HCDR3 comprising SEQ ID NO: 736, a LCDR1 comprising SEQ ID NO: 846, a LCDR2 comprising SEQ ID NO: 848, and a LCDR3 comprising SEQ ID NO: 850 as defined according to the method of Kabat; or a HCDR1 comprising SEQ ID NO: 1002, a HCDR2 comprising SEQ ID NO: 1004, a HCDR3 comprising SEQ ID NO: 1006, a LCDR1 comprising SEQ ID NO: 1116, a LCDR2 comprising SEQ ID NO: 1118, and a LCDR3 comprising SEQ ID NO: 1120 as defined by IMGT.

[0008] According to some examples, the aforementioned monoclonal antibodies or antigen-binding fragments thereof comprise sequence modifications. In some examples, modification(s) is position 49 of the light chain according to the method of Kabat is not cysteine, the residue at position 57 of the heavy chain according to the method of Kabat is not cysteine, the residue at position 34 of the light chain according to the method of Kabat is glutamate, the residue at position 36 of the light chain according to the method of Kabat is not phenylalanine, the residue at position 46 of the light chain according to the method of Kabat is not arginine, the residue at position 94 of the heavy chain according to the method of Kabat is not lysine, the residue at position 71 of the heavy chain according to the method of Kabat is not arginine, or any

combination thereof. In some embodiments in which the residue at position 49 of the light chain according to the method of Kabat is not cysteine, the residue is serine. In some examples in which the residue at position 57 of the heavy chain according to the method of Kabat is not cysteine, the residue is serine. In some examples in which the residue at position 36 of the light chain according to the method of Kabat is not phenylalanine, the residue is tyrosine. In some examples in which the residue at position 46 of the light chain according to the method of Kabat is not arginine, the residue is leucine. In some examples in which the residue at position 71 of the heavy chain according to the method of Kabat is not arginine, the residue is valine.

[0009] In some examples of the monoclonal antibody or antigen-binding fragment that specifically binds human Tau, the antibody comprises: a heavy chain variable domain (HCVD) comprising SEQ ID NO: 268 and a light chain variable domain (LCVD) comprising SEQ ID NO: 465; a HCVD comprising SEQ ID NO: 268 and a LCVD comprising SEQ ID NO: 581; a HCVD comprising SEQ ID NO: 384 and a LCVD comprising SEQ ID NO: 545; a HCVD comprising SEQ ID NO: 393 and a LCVD comprising SEQ ID NO: 545; a HCVD comprising SEQ ID NO: 402 and a LCVD comprising SEQ ID NO: 545; a HCVD comprising SEQ ID NO: 384 and a LCVD comprising SEQ ID NO: 572; a HCVD comprising SEQ ID NO: 393 and a LCVD comprising SEQ ID NO: 572; or a HCVD comprising SEQ ID NO: 402 and a LCVD comprising SEQ ID NO: 572.

[0010] In one aspect, the present disclosure refers to a monoclonal antibody, or an antigen-binding fragment thereof, that specifically binds a human Tau, wherein the antibody is produced by the cell line having ATCC deposit number PTA-124524. In some examples of the monoclonal antibody or antigen-binding fragment that specifically binds human Tau, the antibody is produced by the cell line having ATCC deposit number PTA-124523 or ATCC deposit number PTA-124524.

[0011] In some examples, the antibodies or antigen-binding fragments described herein bind monomeric wild-type human 2N4R Tau with a K_D of less than about 0.5 nM as measured by surface plasmon resonance. In some examples, the antibodies or antigen-binding fragments bind human Tau at an epitope comprising the amino acid sequence HVPG (SEQ ID NO: 1133). Also described are biepitopic antibodies or antigen-binding fragments that bind human Tau at an epitope comprising the amino acid sequence HVPG (SEQ ID NO: 1133) within repeat region 2 or repeat region 4. In certain examples, the antibodies or antigen-binding fragments bind human

Tau at an epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79). Also described are biepitopic antibodies or antigen-binding fragments that bind human Tau at an epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 2 or repeat region 4. In some examples, the monoclonal antibody or antigen-binding fragment binds human Tau at the epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 2 and/or repeat region 4 with a binding preference that is at least about 10-fold greater than binding at an epitope comprising the amino acid sequence HKPGG (SEQ ID NO: 182) within repeat region 3 or at an epitope comprising the amino acid sequence HQPGG (SEQ ID NO: 183) within repeat region 1, as determined by a peptide binding assay. In some examples, the antibodies or antigen-binding fragments described herein do not bind Tau at an epitope comprising the amino acid sequence HVSGG (SEQ ID NO: 184) within repeat region 2 or at an epitope comprising the amino acid sequence HVLGG (SEQ ID NO: 185) within repeat region 2.

[0012] In some examples, the monoclonal antibodies or antigen-binding fragments as described herein are labeled.

[0013] Further described are nucleic acid molecules encoding any of the described monoclonal antibodies or antigen-binding fragments, vectors comprising the nucleic acid molecules, cells that express the nucleic acid molecules, and methods of producing the anti-Tau antibodies or antigen-binding fragments by culturing such cells under conditions suitable for production thereof. The methods of producing may further involve recovery of the antibody or antigen-binding fragment.

[0014] In another aspect, the present disclosure refers to a pharmaceutical composition comprising the antibody or antigen-binding fragment as disclosed herein and a pharmaceutically acceptable carrier. Also disclosed herein are pharmaceutical compositions of any of the described monoclonal antibodies, or antigen-binding fragments thereof, that specifically bind a human Tau and a pharmaceutically acceptable carrier.

[0015] Methods of use of the described monoclonal antibodies, or antigen-binding fragments thereof, that specifically bind a human Tau also are described provided herein. In some embodiments examples, the antibodies or antigen-binding fragments that specifically bind a human Tau are for use as a medicament. In some aspects examples, the antibodies or antigen-binding fragments that specifically bind a human Tau are for use in the treatment of a Tauopathy or in the preparation of a medicament for the treatment of a Tauopathy. Methods of treating a Tauopathy in a subject also are provided. In some embodiments examples, the methods of treating a Tauopathy involve administering to the subject any of the described monoclonal antibodies, or antigen-binding fragments thereof, that specifically bind a human Tau under conditions effective to treat the Tauopathy in the subject. In some aspects examples, the Tauopathy is Alzheimer's disease, frontotemporal dementia, or progressive supranuclear palsy. The frontotemporal dementia may be Pick's Disease, for example.

[0016] Further provided are methods for decreasing sarkosyl-insoluble Tau levels in a subject by administering to the subject any of the described monoclonal antibodies, or antigen-binding fragments thereof, that specifically bind a human Tau. Also provided are methods for inhibiting Tau aggregation in a subject by administering to the subject any of the described

monoclonal antibodies, or antigen-binding fragments thereof, that specifically bind a human Tau. The methods may be performed *in vitro* or *in vivo*.

BRIEF DESCRIPTION OF THE DRAWINGS

[0017] **Figure 1** illustrates the six isoforms of Tau expressed in adult human brain: 2N4R (UniProt Acc. No. P10636-8); 1N4R (UniProt Acc. No. P10636-7); 0N4R (UniProt Acc. No. P10636-6); 2N3R (UniProt Acc. No. P10636-5); 1N3R (UniProt Acc. No. P10636-4); and 0N3R (UniProt Acc. No. P10636-2) (Spillantini & Goedert, *The Lancet*, 2013, 12(6): 609–622).

[0018] **Figure 2** illustrates the region of protein (“Peptide antigen”) selected to generate the anti-Tau antibodies described herein. Figure 2 discloses SEQ ID NOS. 1137, 1138 and 1138, respectively, in order of appearance.

[0019] **Figures 3A and 3B** illustrate the results of the fine epitope mapping of the murine 7G6 (“ms7G6”) anti-Tau antibody. For Figure 3A, translated overlapping peptides (SEQ ID NOS: 1-37, respectively) of the wild-type 2N4R Tau sequence were synthesized and printed onto a glass chip along with a control HA-tag peptide. ms7G6 antibody binding (signal in figure interior) and the control peptide (signal on figure periphery) was detected as described in the methods. Figure 3B shows spot intensity as a result of antibody binding to the peptide chip, quantified by the LI-COR Odyssey™ and Pepslide™ Analyser software packages. Fluorescence intensity was then plotted against peptide sequence to generate the epitope mapping data. Figure 3B discloses SEQ ID NOS 1139-1140 and 1-37, respectively, in order of appearance.

[0020] **Figure 4** illustrates the results of the murine 7G6 antibody epitope substitution scanning of the peptide sequence KDNIKHVPGGGSVQI (SEQ ID NO: 26), corresponding to amino acids 294 to 308 of the human 2N4R Tau protein. Each amino acid position of the peptide was replaced by every naturally occurring amino acid possible, printed onto a glass chip, and probed with the ms7G6 antibody. Figure 4 illustrates the results for select peptides (SEQ ID NOS 38-78, respectively). While ms7G6 antibody binding allows some variation in the second position (valine) of SEQ ID NO: 79, antibody binding is completely dependent on the proline residue of SEQ ID NO: 79. No binding of antibody 7G6 to KDNIKHVS GGGSVQI (SEQ ID NO: 59) was observed. The latter is the sequence present in Tau P301S mutant protein.

[0021] **Figures 5A and 5B** illustrate the degree and rate of heparin-induced aggregation for the wild-type and P301S Tau proteins, respectively, in the presence and absence of ms7G6 (“7G6”) anti-Tau antibody. Mouse IgG that is unable to bind Tau was included as a control antibody.

[0022] **Figures 6A, 6B, 6C, and 6D** illustrate the effects of vehicle control, human IgG1k, murine 7G6 anti-Tau antibody, and humanized 7G6-HCzu25-LCzu18 antibody, respectively, in an *in vitro* cell-based model of Tau seeding and aggregation.

[0023] **Figure 7** illustrates the results of pre-incubation of recombinant human P301S Tau seeds with either vehicle, mouse IgG control antibody, and murine anti-Tau antibodies 1F1, 7G6, or 8E5 in a preclinical *in vivo* Tau seeding model.

[0024] **Figure 8** illustrates the time course of insoluble Tau development in the hippocampus and cortex of P301S transgenic mice that were ICV-injected with recombinant P301S Tau seeds.

[0025] **Figure 9** illustrates the effect of peripheral, single repeat dosing of ms7G6 antibody in the P301S *in vivo* seeding model. ms7G6 caused a reduction in insoluble Tau levels in hippocampus and cortex.

[0026] **Figure 10** illustrates the effect of peripheral multiple repeat dosing of ms7G6 antibody in the P301S *in vivo* seeding model. Reduction of insoluble Tau levels by antibody 7G6 was dose-dependent.

[0027] **Figure 11** illustrates the closest homologous human germline sequences to murine anti-Tau antibody ms7G6. ms7G6 and homologous human germline sequences were aligned. The Vh and VK domains are annotated by the IMGT and Kabat numbering systems. Identical residues are represented as a “.” in the human germline sequences. Figure 11 discloses SEQ ID NOS 1141-1144, 1143, 1145, 1143, 1146-1149, 1148, 1150 and 1148, respectively, in order of appearance.

[0028] **Figure 12** compares the sequences of ms7G6 antibody heavy and light chain to humanized 7G6 Vh1 and Vk2 variants. The murine 7G6 and humanized 7G6 variants were aligned. The Vh and Vk domains are annotated by the IMGT and Kabat numbering systems. Mutations are underlined. Figure 12 discloses SEQ ID NOS 1151-1174, respectively, in order of appearance.

[0029] **Figures 13A, 13B, 13C, 13D, 13E, and 13F** illustrate Tau binding by ELISA with 7G6 LCzu1 humanized variants (Figure 13A), 7G6 LCzu2 humanized variants (Figure 13B), 7G6 LCzu3 humanized variants (Figure 13C), 7G6 LCzu4 humanized variants (Figure 13D), 7G6 LCzu5 humanized variants (Figure 13E), and 7G6 humanized variants with Ser substituted for Cys49 (according to Kabat) on the light chain and Cys57 (according to Kabat) on the heavy chain (Figure 13F).

[0030] **Figure 14** illustrates the results of Tau binding by humanized 7G6 Vh1/Vk2 variants analyzed by a direct ELISA. Samples were incubated for 1 h at room temperature in 96-well plates coated with 2N4R Tau. Plates were washed and then HRP-conjugated anti-mouse or anti-human antibodies were added to the wells. The amount of HRP activity in each well was measured by QuantaBlu™ fluorescent substrate and the relative fluorescence units (RFUs) were detected by a SpectraMax M5 plate reader. The majority of the mAbs showed little difference in Tau binding in a direct ELISA assay. The notable exception was 7G6-LCzu9 which exhibited no binding, even at the highest concentrations. In addition, 7G6-LCzu22 showed reduced binding; Vκ Tyr36 in combination with Arg46 resulted in disruption of the antigen binding site.

[0031] **Figure 15** illustrates results of the SDS-PAGE analysis of heavy chain and light chain stability for the Vh1 and Vκ2 humanized 7G6 variants. Two micrograms of each mAb were mixed with 4x NuPAGE™ LDS Sample Buffer in the absence of reducing agent and loaded onto a 4-12% Bis-Tris SDS-PAGE gel in MOPS buffer. Gels were stained with InstantBlue™ and destained in water. HC-HC-LC trimers (HHL), HC-HC dimers (HH), and free LC (L) are indicated by arrows. The molecular weight of the markers is indicated in kDa.

[0032] **Figure 16** illustrates the BLAST alignment of antibody ms7G6 ("7G6") to the human germline database at <http://www.ncbi.nlm.nih.gov/igblast/>. The Vh and Vκ domains are annotated by the IMGT and Kabat numbering systems. Figure 16 discloses SEQ ID NOS 1175-1178, 1177, 1179, 1180-1183, 1182 and 1184, respectively, in order of appearance.

[0033] **Figure 17** illustrates an alignment of ms7G6 and humanized 7G6 Vh3/Vκ1 variants. The Vh and Vκ domains are annotated by the IMGT and Kabat numbering systems. Mouse and humanized 7G6 variants were aligned. The Vh and Vκ domains are annotated by the IMGT and Kabat numbering systems. Mutations are underlined. Figure 17 discloses SEQ ID NOS 1185-1207, respectively, in order of appearance.

[0034] **Figure 18** demonstrates direct binding of Tau by ms7G6 and humanized 7G6Vh3/V κ 1 variants 7G6-HCzu11-LCzu11 (“HCzu11-LCzu11”), 7G6-HCzu11-LCzu12 (“HCzu11-LCzu12”), 7G6-HCzu12-LCzu11 (“HCzu12-LCzu11”), and 7G6-HCzu12-LCzu12 (“HCzu12-LCzu12”). Samples were incubated for 1 h at room temperature in 96-well plates coated with 2N4R wild-type recombinant Tau protein. After washing, HRP-conjugated anti-mouse or anti-human antibodies were added to the wells. The amount of HRP activity in each well was measured by QuantaBlu™ fluorescent substrate and the RFUs were detected by a SpectraMax M5 plate reader.

[0035] **Figures 19A and 19B** demonstrate direct binding of Tau by ms7G6, non-Tau binding IgG1 control Ab mAb2, and humanized 7G6 Vh3/V κ 1 variants. Figure 19A demonstrates direct binding of Tau by ms7G6, non-Tau binding IgG1 control Ab mAb2, and humanized 7G6 Vh3/V κ 1 variants 7G6-HCzu12-LCzu12 (“HCzu12-LCzu12”), 7G6-HCzu13-LCzu12 (“HCzu13-LCzu12”), 7G6-HCzu14-LCzu12 (“HCzu14-LCzu12”), 7G6-HCzu15-LCzu12 (“HCzu15-LCzu12”), 7G6-HCzu16-LCzu12 (“HCzu16-LCzu12”), 7G6-HCzu17-LCzu12 (“HCzu17-LCzu12”), 7G6-HCzu18-LCzu12 (“HCzu18-LCzu12”), 7G6-HCzu19-LCzu12 (“HCzu19-LCzu12”), and 7G6-HCzu20-LCzu12 (“HCzu20-LCzu12”). Figure 19B demonstrates direct binding of Tau by ms7G6, non-Tau binding IgG1 control Ab mAb2, and humanized 7G6 Vh3/V κ 1 variants 7G6-HCzu12-LCzu12 (“HCzu12-LCzu12”), 7G6-HCzu12-LCzu13 (“HCzu12-LCzu13”), 7G6-HCzu12-LCzu14 (“HCzu12-LCzu14”), 7G6-HCzu12-LCzu15 (“HCzu12-LCzu15”), 7G6-HCzu12-LCzu16 (“HCzu12-LCzu16”), and 7G6-HCzu12-LCzu17 (“HCzu12-LCzu17”). Samples were incubated for 1 hour at room temperature in 96-well plates coated with 2N4R wild-type recombinant Tau protein. After the plates were washed, HRP-conjugated anti-mouse or anti-human detection antibodies were added to the wells. The amount of HRP activity in each well was measured by QuantaBlu™ fluorescent substrate and the RFUs were detected by a SpectraMax M5 plate reader.

[0036] **Figures 20A, 20B, and 20C** illustrate the results of the non-reducing SDS-PAGE analysis of heavy chain/light chain stability for Vh3 and V κ 1 variants of antibody 7G6. **Figure 20A** illustrates the results of the SDS-PAGE analysis of heavy chain/light chain stability for Vh3 and V κ 1 variants 7G6-HCzu11-LCzu11 (“HCzu11-LCzu11”), 7G6-HCzu11-LCzu12 (“HCzu11-LCzu12”), 7G6-HCzu12-LCzu11 (“HCzu12-LCzu11”), and 7G6-HCzu12-LCzu12

("HCzu12-LCzu12"). **Figure 20B** illustrates the results of the SDS-PAGE analysis of heavy chain/light chain stability for Vh3 and Vκ1 variants 7G6-HCzu12-LCzu12 ("HCzu12-LCzu12"), 7G6-HCzu13-LCzu12 ("HCzu13-LCzu12"), 7G6-HCzu14-LCzu12 ("HCzu14-LCzu12"), 7G6-HCzu16-LCzu12 ("HCzu16-LCzu12"), 7G6-HCzu17-LCzu12 ("HCzu17-LCzu12"), and 7G6-HCzu18-LCzu12 ("HCzu18-LCzu12"). **Figure 20C** illustrates the results of the SDS-PAGE analysis of heavy chain/light chain stability for Vh3 and Vκ1 variants 7G6-HCzu12-LCzu19 ("HCzu12-LCzu19"), 7G6-HCzu12-LCzu13 ("HCzu12-LCzu13"), 7G6-HCzu12-LCzu14 ("HCzu12-LCzu14"), 7G6-HCzu12-LCzu15 ("HCzu12-LCzu15"), 7G6-HCzu12-LCzu16 ("HCzu12-LCzu16"), and 7G6-HCzu12-LCzu17 ("HCzu12-LCzu17"). Two micrograms of each mAb were mixed with 4x NuPAGE™ LDS Sample Buffer in the absence of reducing agent and loaded onto a 4-12% Bis-Tris SDS-PAGE gel in MOPS buffer. Gels were stained with InstantBlue™ and destained in water. HC-LC dimers (HL) and free HC are indicated by arrows. The molecular weight markers are indicated in kDa.

[0037] Figures 21A and 21B illustrate the results of SEC-HPLC analysis to assess the homogeneity of antibody 7G6 humanized variants 7G6-HCzu8-LCzu6 (Fig. 21A) and 7G6-HCzu25-LCzu18 (Fig. 21B) in solution. Five micrograms of mAb 7G6 humanized variant were injected into an Agilent 1260 Infinity with an AdvanceBio SEC 300A 2.7um 4.6x50 Guard column, and AdvanceBio SEC 300A 2.7um 4.6x300mm column. Samples were analyzed in 0.1M sodium phosphate buffer, pH 6.5 at a flow rate of 0.35 mL/min, and the absorbance at 280 nm was analyzed. Representative data for mAb 7G6-HCzu8-LCzu6 or 7G6-HCzu25-LCzu18 are shown.

[0038] Figures 22A-L illustrate the thermal melting curves of F(ab')₂ fragments that were analyzed by differential scanning calorimetry (DSC). Figures 22A-L show the thermal melting curves for mAb1 (Figure 22A), mAb2 (Figure 22B), chimeric ("xi") 7G6 ("xi7G6") (Figure 22C), 7G6-HCzu8-LCzu6 (Figure 22D), 7G6-HCzu8-LCzu21 (Figure 22E), 7G6-HCzu23-LCzu15 (Figure 22F), 7G6-HCzu24-LCzu15 (Figure 22G), 7G6-HCzu25-LCzu15 (Figure 22H), 7G6-HCzu23-LCzu18 (Figure 22I), 7G6-HCzu24-LCzu18 (Figure 22J), 7G6-HCzu25-LCzu18 (Figure 22K), and 7G6-HCzu8-LCzu6 (Figure 22L). F(ab')₂ fragments and controls were subjected to thermal analysis ranging from 25-100°C using a scan rate of 100°C/hour. The profiles of the chimeric, 7G6-HCzu8 and 7G6-HCzu25 F(ab')₂ were similar to

non-Tau-binding IgG1 control mAb1 and mAb2. 7G6-HCzu23 and 7G6-HCzu24, however, contained a second peak, indicating instability of the F(ab')₂ fragment, possibly the dissociation of the HC-LC interaction. The transition midpoints of 7G6-HCzu8-LCzu21, 7G6-HCzu25-LCzu15, and 7G6-HCzu25-LCzu18 were similar, ranging from 77.4 to 77.6°C. The midpoint of 7G6-HCzu8-LCzu6 was one degree higher at 78.6°C.

[0039] **Figures 23A and 23B** show results of the immunoreactive T cell epitope analysis, providing putative hotspots (SEQ ID NOs: 80-94 in Fig. 23A; SEQ ID NOs: 95-111 in Fig. 23B) in humanized antibody 7G6 heavy chains. The peptides in the tables were identified as having identity 5% or less identity to human germline sequences. The percent homology of the peptides to variable domain germline sequences was also taken into consideration. Peptides with ~5% or less homology to variable region germline sequences and/or were predicted to bind three or more HLA alleles were identified as higher risk (highlighted in gray).

[0040] **Figures 24A-24D** show results of the immunoreactive T cell epitope analysis, providing putative hotspots in humanized antibody 7G6 light chains (SEQ ID NOs: 112-130 in Fig. 24A; SEQ ID NOs: 131-150 in Fig. 24B; SEQ ID NOs: 151-165 in Fig. 24C; and SEQ ID NOs: 166-180 in Fig. 24D). The peptides in the tables were identified as having identity 5% or less identity to human germline sequences. The percent homology of the peptides to variable domain germline sequences was also taken into consideration. Peptides with ~5% or less homology to variable region germline sequences and/or were predicted to bind three or more HLA alleles were identified as higher risk (highlighted in gray).

[0041] **Figure 25** shows images of immunohistochemical staining of AD, PSP, and PiD tissue samples with antibody 7G6-HCzu25-LCzu18. Antibody 7G6-HCzu25-LCzu18 strongly and specifically recognizes pathological Tau (depicted by black arrows in each image) in human post-mortem diseased brain.

[0042] **Figures 26A and 26B** show the results of fine epitope mapping for humanized antibodies 7G6-HCzu8/LCzu6 and 7G6-HCzu25/LCzu18, respectively. Fluorescent images of the chips and resulting intensity plots show that the 7G6-HCzu8/LCzu6 (Figure 26A) and 7G6-HCzu25/LCzu18 (Figure 26B) antibodies both bind to two major sites on the full length Tau protein. Figure 26A discloses SEQ ID NOS 1-37, respectively, in order of appearance. Figure 26B discloses SEQ ID NOS 1-37, respectively, in order of appearance.

[0043] **Figure 27** illustrates the degree and rate of heparin-induced aggregation for the wild-type 2N4R Tau protein in the presence and absence of antibody 7G6-HCzu25-LCzu18. Recombinant wild-type 2N4R Tau was induced to aggregate under the conditions described in Example 15. Reactions contained either no antibody (buffer only; open triangle), a human IgG1 control antibody (solid diamond), or antibody 7G6-HCzu25-LCzu18 (open circle). Thioflavin S (ThS) fluorescence was measured immediately after heparin addition (day 0) and then on days 1, 2, 5 and 6 thereafter. Data is represented as mean $\pm$ SD from four independent experiments. Statistical analysis (multiple t-tests comparing IgG control and antibody 7G6-HCzu25-LCzu18) was performed for each time point ($p \leq 0.01$ **; $p \leq 0.001$ ***). **Figure 27** shows that 7G6-HCzu25-LCzu18 antibody effectively inhibits Tau aggregation *in vitro*. The effect was statistically significant when comparing the IgG control and 7G6-HCzu25-LCzu18 antibody for days 1, 2, 5 and 6 following incubation at 37 °C. No significance was observed on day 0 just after the reactions were initiated following heparin addition.

[0044] **Figure 28** illustrates the degree and rate of heparin-induced aggregation for the wild-type 2N4R Tau protein in the presence and absence of antibody 7G6 or antibody 7G6-HCzu25-LCzu18. Recombinant wild-type 2N4R Tau was induced to aggregate under the conditions described in the materials and methods. Reactions contained either no antibody (buffer only; open triangle); a human IgG1 control antibody (solid diamond); antibody 7G6 (solid square); or antibody 7G6-HCzu25-LCzu18 (open circle). Thioflavin S (ThS) fluorescence was measured immediately after heparin addition (day 0) and then on days 1, 2, 5 and 6 thereafter. **Figure 28** shows that, when both antibody 7G6 and antibody 7G6-HCzu25-LCzu18 were tested according to the assay conditions provided in Example 5, both antibodies effectively inhibited Tau aggregation *in vitro*. The same effect size was seen between 7G6 and 7G6-HCzu25-LCzu18 antibodies.

[0045] **Figure 29** shows the normalized ThS positive rate in a K18 fibril cell-based seeding assay after immunodepletion of samples with 7G6-HCzu25-LCzu18 antibody. 1.5 and 15 μ g/ml of 7G6-HCzu25-LCzu18 antibody removed seeding effects of K18 fibril (>70% reduction vs human IgG1 kappa control).

[0046] **Figures 30A-30D** illustrate the effect of antibody 7G6 on brain sarkosyl-insoluble Tau induced by intra-hippocampal Tau seed injection in human P301S Tau transgenic

mice. Tau seed or non-seed (100 mmol/L sodium acetate, pH7.0) was stereotactically injected into the left hippocampus. 7G6 or control IgG at 40 mg/kg was intraperitoneally administered once weekly for 3 weeks. Control IgG = Mouse IgG2b isotype control antibody, 7G6 = Anti-human Tau mouse IgG2b monoclonal antibody Data represent the mean $\pm$ SEM (n=6 for Non-Seed, n=11 for Control IgG, 7G6). **** P<0.0001, * P<0.05 versus control IgG (analyzed by 1-way ANOVA followed by Fisher's LSD test). The intraperitoneal administration of 7G6 once weekly for 3 weeks at 40 mg/kg produced significant suppression of the increase of sarkosyl-insoluble Tau in the contralateral hippocampus induced by intra-hippocampal Tau seed injection in P301S Tau transgenic mice.

[0047] **Figures 31A and 31B** show MTBR-Tau in cerebrospinal fluid from cynomolgus monkey treated with 7G6-HCzu25-LCzu18 antibody. Figure 31A shows bound MTBR-Tau. Figure 31B shows free MTBR-Tau. Mean $\pm$ SEM. Male Cynomolgus monkey N=3 (Vehicle, 10 mg/kg, 30 mg/kg, 100 mg/kg).

[0048] **Figure 32** shows bound MTBR-Tau in human cerebrospinal fluid spiked with 7G6-HCzu25-LCzu18 antibody (10, 100, 500, 1000 and 2000 ng/mL).

[0049] **Figures 33A and 33B** show the efficacy of Tau monomer or fibril uptake, respectively, in CHO cells overexpressing CD32A. 7G6-HCzu25-LCzu18 antibody (3 μ g/mL) significantly increased Tau monomer uptake compared to human IgG1 control (3 μ g/mL) (Fig. 33A). Likewise, 7G6-HCzu25-LCzu18 antibody (0.3 and 3 μ g/mL) also significantly increased Tau fibril uptake compared to human IgG1 control (3 μ g/mL) (Fig. 33B). In both cases, FcR inhibitor treatment significantly blocked the effect of 7G6-HCzu25-LCzu18 antibody-induced Tau uptake in this cell assay system.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

[0050] The following description characterizes antibodies, and antigen-binding fragments thereof, that specifically bind to Tau. Also described are related polynucleotides capable of encoding these antibodies and antigen-binding fragments, cells expressing the antibodies and antigen-binding fragments, as well as associated vectors. In addition, methods of using the antibodies and antigen-binding fragments are described. For example, the provided antibodies, and antigen-binding fragments, may be used to treat a Tauopathy in a subject.

[0051] Various terms relating to aspects of the description are used throughout the specification and claims. Such terms are to be given their ordinary meaning in the art unless otherwise indicated. Other specifically defined terms are to be construed in a manner consistent with the definitions provided herein.

[0052] As used in this specification and the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to “a cell” includes a combination of two or more cells, and the like.

[0053] The term “about” as used herein when referring to a measurable value such as an amount, a temporal duration, and the like, is meant to encompass variations of up to $\pm 10\%$ from the specified value, as such variations are appropriate to perform the disclosed methods. Unless otherwise indicated, all numbers expressing quantities of ingredients, properties such as molecular weight, reaction conditions, and so forth used in the specification and claims are to be understood as being modified in all instances by the term “about.” Accordingly, unless indicated to the contrary, the numerical parameters set forth in the following specification and attached claims are approximations that may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of the claims, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques.

[0054] Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the invention are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently contain certain errors necessarily resulting from the standard deviation found in their respective testing measurements.

[0055] “Isolated” means a biological component (such as a nucleic acid, peptide or protein) has been substantially separated, produced apart from, or purified away from other biological components of the organism in which the component naturally occurs, i.e., other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acids, peptides and proteins that have been “isolated” thus include nucleic acids and proteins purified by standard purification methods. “Isolated” nucleic acids, peptides and proteins that can be part of a

composition and still be isolated if such composition is not part of the native environment of the nucleic acid, peptide, or protein. The term also embraces nucleic acids, peptides and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids.

[0056] “Polynucleotide,” synonymously referred to as “nucleic acid molecule” or “nucleic acids,” refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. “Polynucleotides” include, without limitation single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. “Polynucleotide” also embraces relatively short nucleic acid chains, often referred to as oligonucleotides.

[0057] The meaning of “substantially the same” can differ depending on the context in which the term is used. Because of the natural sequence variation likely to exist among heavy and light chains and the genes encoding them, one would expect to find some level of variation within the amino acid sequences or the genes encoding the antibodies or antigen-binding fragments described herein, with little or no impact on their unique binding properties (e.g., specificity and affinity). Such an expectation is due in part to the degeneracy of the genetic code, as well as to the evolutionary success of conservative amino acid sequence variations, which do not appreciably alter the nature of the encoded protein. Accordingly, in the context of nucleic acid sequences, “substantially the same” means at least 65% identity between two or more sequences. Preferably, the term refers to at least 70% identity between two or more sequences, more preferably at least 75% identity, more preferably at least 80% identity, more preferably at least 85% identity, more preferably at least 90% identity, more preferably at least 91% identity, more preferably at least 92% identity, more preferably at least 93% identity, more preferably at least 94% identity, more preferably at least 95% identity, more preferably at least 96% identity, more preferably at least 97% identity, more preferably at least 98% identity, and more preferably at least 99% or greater identity. Such identity may be determined using

nBLAST algorithm (Altschul et al., (1990) Proc. Natl. Acad. Sci. USA 87:2264-8; Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-7).

[0058] The degree of variation that may occur within the amino acid sequence of a protein without having a substantial effect on protein function is much lower than that of a nucleic acid sequence, since the same degeneracy principles do not apply to amino acid sequences. Accordingly, in the context of an antibody or antigen-binding fragment, “substantially the same” means the sequences have “insubstantial differences”. Insubstantial differences are substitutions of 1, 2, 3, 4, 5 or 6 amino acids in an antibody or antibody fragment amino acid sequence. Amino acid sequences substantially the same as the sequences disclosed herein are also part of this application. In some embodiments, the sequence identity can be about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher. Other embodiments include Tau-specific antibodies, or antigen-binding fragments, that have framework, scaffold, or other non-binding regions that do not share significant identity with the antibodies and antigen-binding fragments described herein, but do incorporate one or more CDRs or other sequences needed to confer binding that are 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to such sequences described herein.

[0059] A “vector” is a replicon, such as plasmid, phage, cosmid, or virus in which another nucleic acid segment may be operably inserted so as to bring about the replication or expression of the segment.

[0060] The terms “express” and “produce” are used synonymously herein, and refer to the biosynthesis of a gene product. These terms encompass the transcription of a gene into RNA. These terms also encompass translation of RNA into one or more polypeptides, and further encompass all naturally occurring post-transcriptional and post-translational modifications. The expression or production of an antibody or antigen-binding fragment thereof may be within the cytoplasm of the cell, or into the extracellular milieu such as the growth medium of a cell culture.

[0061] The term “treating” or “treatment” refers to any success or indicia of success in the attenuation or amelioration of an injury, pathology or condition, including any objective or subjective parameter such as abatement, remission, diminishing of a symptom or making the condition more tolerable to the patient, slowing in the rate of degeneration or decline, making the

final point of degeneration less debilitating, improving a subject's physical or mental well-being, or prolonging the length of survival. The treatment may be assessed by objective or subjective parameters; including the results of a physical examination, neurological examination, or psychiatric evaluations. In a particular embodiment, the symptom of a Tauopathy is an impairment in cognition. In a specific embodiment, the symptom of a Tauopathy is an impairment in learning and/or memory. In a specific embodiment, the symptom of a Tauopathy is a long-term memory loss. In a specific embodiment, the symptom of a Tauopathy is dementia. In some embodiments, the symptom of a Tauopathy is confusion, irritability, aggression, mood swings, or a language impairment. In some embodiments, the symptom of a Tauopathy is an impairment or loss of one or more cognitive functions such as reasoning, situational judgment, memory capacity, and/or learning.

[0062] The term “antibody” as used herein is meant in a broad sense and includes immunoglobulin or antibody molecules including polyclonal antibodies, monoclonal antibodies including murine, human, human-adapted, humanized and chimeric monoclonal antibodies and antibody fragments. In general, antibodies are proteins or peptide chains that exhibit binding specificity to a specific antigen. Intact antibodies are heterotetrameric glycoproteins, composed of two identical light chains and two identical heavy chains. Typically, each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (variable region) (VH) followed by a number of constant domains (constant regions). Each light chain has a variable domain at one end (VL) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain and the light chain variable domain is aligned with the variable domain of the heavy chain. Antibody light chains of any vertebrate species can be assigned to one of two clearly distinct types, namely kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

[0063] Immunoglobulins can be assigned to five major classes or isotypes, depending upon the type of constant domain possessed by its heavy chain, namely IgA, IgD, IgE, IgG and IgM, depending on the heavy chain constant domain amino acid sequence. IgA and IgG are

further sub-classified as the isotypes IgA1, IgA2, IgG1, IgG2, IgG3 and IgG4. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α , δ , ϵ , γ , and μ , respectively.

[0064] An immunoglobulin light chain variable region or heavy chain variable region consists of a “framework” region interrupted by three “antigen-binding sites”. The antigen-binding sites are defined using various terms as follows: (i) the term Complementarity Determining Regions (CDRs) is based on sequence variability (Wu and Kabat, J. Exp. Med. 132:211-250, 1970). Generally, the antigen-binding site has six CDRs; three in the VH (HCDR1, HCDR2, HCDR3), and three in the VL (LCDR1, LCDR2, LCDR3) (Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991). The “IMGT-CDRs” as proposed by Lefranc (Lefranc et al., Dev. Comparat. Immunol. 27:55-77, 2003) are based on the comparison of V domains from immunoglobulins and T-cell receptors. The International ImMunoGeneTics (IMGT) database ([http://www_imgt_org](http://www.imgt.org)) provides a standardized numbering and definition of these regions. The correspondence between CDRs and IMGT delineations is described in Lefranc et al., Dev. Comparat. Immunol. 27:55-77, 2003.

[0065] Antigen-binding fragments are any proteinaceous structure that may exhibit binding affinity for a particular antigen. Some antigen-binding fragments are composed of portions of intact antibodies that retain antigen-binding specificity of the parent antibody molecule. For example, antigen-binding fragments may comprise at least one variable region (either a heavy chain or light chain variable region) or one or more CDRs of an antibody known to bind a particular antigen. Examples of suitable antigen-binding fragments include, without limitation diabodies and single-chain molecules as well as Fab, F(ab')₂, Fc, Fabc, and Fv molecules, single chain (Sc) antibodies, individual antibody light chains, individual antibody heavy chains, chimeric fusions between antibody chains or CDRs and other proteins, protein scaffolds, heavy chain monomers or dimers, light chain monomers or dimers, dimers consisting of one heavy and one light chain, and the like. All antibody isotypes may be used to produce antigen-binding fragments. Additionally, antigen-binding fragments may include non-antibody proteinaceous frameworks that may successfully incorporate polypeptide segments in an orientation that confers affinity for a given antigen of interest, such as protein scaffolds.

Antigen-binding fragments may be recombinantly produced or produced by enzymatic or chemical cleavage of intact antibodies. The phrase “an antibody or antigen-binding fragment thereof” may be used to denote that a given antigen-binding fragment incorporates one or more amino acid segments of the antibody referred to in the phrase.

[0066] “Specific binding” or “specifically binds” refers to the binding of an antibody or antigen-binding fragment to an antigen with greater affinity than for other antigens. Typically, the antibody or antigen-binding fragment binds to the antigen with an equilibrium dissociation constant K_D of about 5×10^{-8} M or less, for example about 5×10^{-9} M or less, about 1×10^{-9} M or less, about 1×10^{-10} M or less, or about 1×10^{-11} M or less.

[0067] “Biepitopic” when used in the context of antibodies or antibody fragments refers to the ability of the antibody or fragment to specifically bind to two non-overlapping epitopes on the same target antigen molecule though not necessarily simultaneously.

[0068] The term “subject” refers to human and non-human animals, including all vertebrates, e.g., mammals and non-mammals, such as non-human primates, mice, rabbits, sheep, dogs, cats, horses, cows, chickens, amphibians, and reptiles. In many embodiments of the described methods, the subject is a human.

[0069] The embodiments described herein are not limited to particular methods, reagents, compounds, compositions or biological systems, which can, of course, vary.

[0070] Described herein are isolated monoclonal antibodies and antigen-binding fragments that specifically bind Tau, preferably human Tau (“anti-Tau antibodies”). Human Tau 2N4R (also referred to as Tau441) is set forth herein as SEQ ID NO: 181:

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MAEPRQEFEV MEDHAGTYGL GDRKDQGGYT MHQDQEGDTD AGLKESPLQT
PTEDGSEEPG SETSDAKSTP TAEDVTAPLV DEGAPGKQAA AQPHTIEPEG
TTAEEAGIGD TPSLEDEAAG HVTQARMVSK SKDGTGSDDK KAKGADGKTK
IATPRGAAPP GQKGQANATR IPAKTTPAPK TPPSSGEPPK SGDRSGYSSP
GSPGTPGSRS RTPSLPTPPT REPKKVAVVR TPPKSPSSAK SRLQTAPVPM
PDLKNVSKI GSTENLKHQP GGGKVQIINK KLDLSNVQSK CGSKDNIKHV
PGGGSVQIVY KPDLSKVTS KCGSLGNIHH KPGGGQVEVK SEKLDFKDRV
QSKIGSLDNI THVPGGGNKK IETHKLTFRE NAKAKTDHGA EIVYKSPVVS
GDTSPRHLN VSSTGSIDMV DSPQLATLAD EVSASLAKQG L.
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Human Tau also refers to Tau variants, for example, naturally occurring allelic variants, including those illustrated in Figure 1 [2N4R (UniProt Acc. No. P10636-8); 1N4R (UniProt Acc. No. P10636-7); 0N4R (UniProt Acc. No. P10636-6); 2N3R (UniProt Acc. No. P10636-5); 1N3R (UniProt Acc. No. P10636-4); and 0N3R (UniProt Acc. No. P10636-2)], or sequences containing at least one amino acid substitution relative thereto. In some embodiments, the antibodies or antigen-binding fragments are murine IgG, or derivatives thereof. While the anti-Tau antibodies or antigen-binding fragments may be human, humanized, or chimeric, the antibodies or antigen-binding fragments exemplified herein are murine and humanized antibodies.

[0071] In any of the embodiments described herein, the antibody that specifically binds Tau is preferably IgG1, more preferably human IgG1. The antibodies and antigen-binding fragments that specifically bind Tau as disclosed in the examples section are derived from mice. Similar antibodies may be derived from any species by recombinant means. For example, the antibodies or antigen-binding fragments may be chimeric rat, goat, horse, swine, bovine, chicken, rabbit, camelid, donkey, human, and the like. For use in administration to humans, non-human derived antibodies or antigen-binding fragments may be genetically or structurally altered to be less antigenic upon administration to a human patient.

[0072] In some embodiments, the anti-Tau antibodies or antigen-binding fragments are chimeric. As used herein, the term “chimeric” refers to an antibody, or antigen-binding fragment thereof, having at least some portion of at least one variable domain derived from the antibody amino acid sequence of a non-human mammal, a rodent, or a reptile, while the remaining portions of the antibody, or antigen-binding fragment thereof, are derived from a human. For example, a chimeric antibody may comprise a mouse antigen binding domain with a human Fc or other such structural domain. Chimeric antibodies are denoted by the term “xi”. In some embodiments, the antibodies or antigen-binding fragments that specifically bind Tau are humanized antibodies or fragments. Humanized antibodies may be chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary-determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as

mouse, rat or rabbit having the desired specificity, affinity, and capacity. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin sequence. The humanized antibody may include at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanized antibody heavy or light chains are denoted herein by the term “zu”.

[0073] The antibodies or antigen-binding fragments described herein can occur in a variety of forms, but will include one or more of the antibody variable domain segments or CDRs shown in Table 1.

Table 1. Antibody segments of the described antibodies and antigen-binding fragments thereof 7G6 VH sequences

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
mouse 7G6-Vh	With leader [SEQ ID NO: 190]: ATGGGATGGAGCTGTATCATCTCTCA TTTTGGTAGCAGCAGCTACAGGTGT CCACTCCAGGTCCTGCTGCAG CCTGGGCTGAGCTTGTGAAGCCTG GGGCTTCAGTAATAATGTCTGCAA GGCTTCTGGCTACACCTTCACCAC TACTGGATAACCTGGGTGAAGCAGA GGCTGGACAAAGCCTTGAGTGGAT TGGAGATAATTTATCCTGGTAGTAGT ATTGTAACACAAATGAGAAGTTCA AGAGCAAGCCACACACTGACTGAGA CACATCCTCCAGCACAGCCTACATG CAGCTCAACAGCCTGACATCTGAGG ACTCTGCGGTCTATTACTGTGCAAG GGAGGATGGTTACGACGCCTGGTTT GCTTACTGGGGCCAAAGGACTCTGG TCACTGTCTCCGACAGCCAAACAC ACCCCATCAGTCTATCCACTGGCC CCTGGGTGTGGAGATACAACTGGTT CCTCTGTGACTCTGGGATGCCTGGT CAAGGGCTA	With leader [SEQ ID NO: 192] MGWSCIIILILVAAATGVHSQVQ LLQPGAELVKPGASVIMSKAS GYTFTTYWITWVKQRPQGQLEW IGDIYPGSSICNYNEKFKSKAT LTVDTSSSTAYMQLNSLTSEDS AVYYCAREDDGYDAWFAYWGQGT LVTVSAAKTTTPPSVYPLAPGCG DTTSSVTLGCLVKG	ATGGGATG GAGTGTA TCATCCTC ATTTTGGT AGCAGCAG CTACAGGT GTCCACTC C (Nucleotides 1-57 of SEQ ID NO: 190) [SEQ ID NO: 194]	CAGGTCCAACTGCTGCAG CCTGGGCTGAGCTTGTG AAGCCTGGGCTTCAGTA ATAATGCTCTGCAAGGCT TCTGGCTACACCTTCACC ACCTACTGGATAACCTGG GTGAAGCAGAGGCCTGGA CAAGCCTTGAGTGGATT GGAGATATTATCTCTGGT AGTAGATTTGTAACTAC AATGAGAACTCAAGAGC AAGCCACACTGACTGTA GACACATCCTCCAGCACA GCCTACATGCAGCTCAAC AGCCTGACATCTGAGGAC TCTGCGGTCTATTACTGT GCAAGGAGGATGGTTAC GACGCTGGTTTGTCTTAC TGGGGCCAAAGGACTCTG GTCACCTGCTCCGCA (Nucleotides 58 to 414 of SEQ ID NO: 190) [SEQ ID NO: 195]	GCCAAAACAAACACCCCA TCAGTCTATCCACTGGCC CCTGGGTGGAGATACA ACTGGTCTCTGTGACT CTGGGATGCCTGGTCAAG GGCTA (Nucleotides 415 to 509 of SEQ ID NO: 190) [SEQ ID NO: 197] AKTTPPSVYPLAPGCGDT TGSSVTLGCLVKG [SEQ ID NO: 198]
	Without leader [SEQ ID NO: 191]: CAGGTCCAAGTCTGCAGCCTGGGG CTGAGCTTGTGAAGCCTGGGGCTTC AGTAATAATGTCTGCAAGGCTTCT GGCTACACCTTCACCACCTACTGGA TAACCTGGGTGAAGCAGAGGCCTGG	Without leader [SEQ ID NO: 193]: QVQLLPGAELVKPGASVIMSC KASGYTFTTYWITWVKQRPQGQ LEWIGDIYPGSSICNYNEKFKS KATLTVDTSSSTAYMQLNSLT EDSAVYYCAREDDGYDAWFAYWG		QVQLLPGAELVKPGASV IMSKASGYTFTTYWITW VKQRPQGQLEWIGDIYPG SSICNYNEKFKSKATLTV DTSSSTAYMQLNSLTSED SAVYYCAREDDGYDAWFAY	

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ACAAGGCCCTTGAGTGGATTGGAGAT ATTATCCTGGTAGTAGTATTGTA ACTACAATGAGAAGTTCAAGAGCAA GGCCACACTGACTGTAGACACATCC TCCAGCACAGCCTACATGCAGCTCA ACAGCCTGACATCTGAGGACTCTGC GGTCTATTACTGTGCAAGGAGGAT GGTTACGACGCCCTGGTTGCTTACT GGGGCAAGGACTCTGGTCACTGT CTCCGACGCCAAACACACCCCA TCAGTCTATCCACTGCCCTGGGT GTGAGATACAACTGGTTCCTCTGT GACTCTGGGATGCCTGGTCAAGGGC TA	QGTLVTVSAAKTTPPSVYPLAP GCGDTTGSSVTLGCLVKG		WGQGLVTVSA [SEQ ID NO: 196]	
7G6-HCzu1	With leader [SEQ ID NO: 199]: ATGGGCTGGTCTCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCCAGGTGCAGCTGGTGCA TCTGGCGCCGAAAGTGAAGAACCTG GCGCCTCCGTGAAGGTGCTCTGCA GGCTCCGGCTACACCTTTACCACC TACTGGATCACCTGGGTGCGACAGG CTCCTGGACAGGGCCTGGAATGGAT GGCGACATCTACCCCGGCTCCTCC ATCTGCAACTACAAACAGAGATTCA AGTCCCGCGTGACCATGACCCGGGA CAGCTCCACAGCACCGGTGTACATG GAAGTCTCCTCCCTGCGGAGCGAGG ACACCGCGGTGACTACTCGGCTAG AGAGACGGCTACGACGCTTGGTTT	With leader [SEQ ID NO: 201]: MGWSCIIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVSKAS GYTFITYWITWVRQAPGQGLEW MGDIYPGSSICNYNEKFKSRVT MTRDTSTVYMEISSLRSED AVYICAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSSVWTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELGGPSVFLF PPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSLTIVL	ATGGGCTG GTCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 199) [SEQ ID NO: 203]	ATGGGCTGGTCTCTGCATC ATCCTGTTTCTGGTGGCC ACCGCCACCGGCGTGAC AGCCAGGTGCAGCTGGTG CAGTCTGGCGCCGAAAGTG AAGAACTGGCGCCTCC GTGAAGGTGCTCTGCAAG GCTTCCGGCTACACCTTT ACCACTACTGGATCAC TGGGTGCGACAGGCTCCT GGACAGGGCTGGAATGG ATGGCGACATCTACCCC GGTCTCCATCTGCAAC TACACAGAGAAATTCAAG TCCCGGTGACCATGACC CGGGACACCTCCACGAC ACCGTGTACATGGAATG	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCAC TCTGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCGAACCG GTGACGGTGTCTGGGAAC TCAGGCGCCTGACCAGC GGCGTGACACCTTCCC GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCCAAG AACACCAAGGTGGACAAG AAAGTTGAGCCCAATCT

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GCCTACTGGGGCCAGGGCACCCTCG TGACCGTGTCACTGCATCCACCAA GGGCCATCGGTCTTCCCTCGGCA CCCTCCTCCAAGAGCACCTCTGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCGAACCGGTG ACGGTGTCTGTGGAACCTCAGGCGCC TGACAGCGGGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCCTACCCGTCTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG	HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGFFLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 202]: QVQLVQSGAEVKKPGASVKVSC KASGYTFITTYMITWVRQAPGQG LEWMGDIYPGSSICNYNEKFKS RVTMTRDSTSTVYMELSLRS EDTAVYICAREDDYDAWFAYWG QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAAALGCLVKDYFPE PVTVSNWNGALTSGVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPK SCDKHTCPCPAPELLGGPSV FLFPPKPKDTLIMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIETKISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK		TCCTCCCTGGGGAGCGAG GACACCGCGTGTACTAC TGCGCTAGAGAGGACGGC TACGACGCTTGGTTTGCC TACTGGGGCCAGGGCACCC CTCGTGACCGTGTCACTCT (Nucleotides 58 to 414 of SEQ ID NO: 199) [SEQ ID NO: 204] QVQLVQSGAEVKKPGASV KVSQKASGYTFITYWITW VRQAPGGLEWMGDIYPG SSICNYNEKFKSRVMTTR DTSTSTVYMELSLRS TAVYICAREDDYDAWFAY WGQGLTVTVSS [SEQ ID NO: 205]	TGTGACAAAACCTCACACA TGCCACACCGTGCCACGA CCTGAACCTCTGGGGGA CCGTCACTCTTCTCTTC CCCCAAAACCCCAAGGAC ACCTCATGATCTCCCG ACCCCTGAGGTACATG GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGT AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAAGCCG CGGGAGGAGCAGTACAAAC AGCACGTACCGTGTGGT AGCTCTCACCGTCTCTG CACCAGGACTGGTGAAT GGCAAGGAGTACAAAGCC AAGGTCTCAACAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCAAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCCAGGT AGCCTGACCTGCCTGGT AAAGGCTTCTATCCAGC GACATCGCGTGGAGTGG GAGAGCAATGGGACGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCTCTCTC TTATATTCAAAGCTCACC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	<p>CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAACGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA</p> <p>Without leader [SEQ ID NO: 200]</p> <p>CAGGTGCAGCTGGTGCACTGTGGCG CCGAAGTGAAGAAACCTGGCGCCTC CGTGAAGGTGCTCTGCAAGGCTTC GGCTACACCTTTACCACCTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGGCCTGGAATGGATGGCGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAACGAGAAAGTTCAAGTCCCG CGTGACCATGACCCGGACACCTCC ACCAGCACCGTGATCATGGAAGTGT CCTCCCTGCGGAGCGAGGACACCGC CGTGACTACTGCGCTAGAGAGGAC GGCTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC</p>				<p>GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401 of SEQ ID NO: 199) [SEQ ID NO: 206]</p> <p>ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTVF SSSLGTQTYICNVNHKPS NTKVDKKEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMISRTPEVTC VVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCS [SEQ ID NO: 207]</p>

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGCGTGACACCTTCCCGGTGTC CTACAGTCTCTCAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCCAAATCTTGTGACAAAAT CACACATGCCCCACCGTGCCCGACAC CTGAACTCCTGGGGGACCGTCAGT CTTCTCTTCCCCCCCCAAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGGTGGTCAAGCTCCTCA CCGTCTGCAACCAAGACTGGGTGAA TGGCAAGGAGTACAAGTGCAAGTTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCACAGGTG TACACCTTGCCCCCATCCCGGGATG AGCTGACCAAGAACCAGGTACGCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAA CTACAAGACCCACGCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAGAG				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAGGTGGCAGCAGGGGAAGTCTTC TCATGCTCCGTGATGCATGAGGTC TGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCCGGGAATGA				
7G6-HC _{2u2}	With leader [SEQ ID NO: 208]: ATGGGTGGTCTCGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCCAGGTGCAGCTGGTGCG TCTGGCGCCGAAGTGAAGAAACCTG GCGCTCCGTGAAGGTGCTCTGCAA GGCTTCGGGTACACCTTTACCAAC TACTGGATCACCTGGGTGCGACAG CTCTGGACAGGGCCTGGAATGGAT GGCGACATCTACCCCGGCTCCTCC ATCTGCAACTACAACGAGAAGTTCA AGTCCCGCGTGACCATGACCGTGA CACCTCCACAGCACCGGTGACATG GAACTGTCTCTCCCTGCGGAGCGAG ACACCGCGGTACTACTGCGCTAG AGAGGACGGCTACGACGCTTGGTTT GCCTACTGGGGCCAGGCAACCTCG TGACCGTGTCTATCTGCATCCACCAA GGGCCATCGGTCTTCCCGCTGGCA CCCTCTCCAAGAGCACCTCTGGG GCACAGGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACTCAGGCGCCC TGACGAGCGGCGTGACACCTTCCC GGCTGTCTACAGTCTCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCAACCCA	With leader [SEQ ID NO: 210]: MGWSCIIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVSKAS GYFTTYWITWVRQAPGQGLEW MGDIYPGSSICNYNEKFKSRVT MTVDTSTSTVYMEISLSRSED AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGTAALGLVLDYFPEPVT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGFSFLYSLKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK Without leader [SEQ ID NO: 211]: QVQLVQSGAEVKKPGASVKVSC	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57) [SEQ ID NO: 212]	CAGGTGCAGCTGGTGCAG TCTGGCGCGAAGTGAAG AAACCTGGCGCTCCGTG AAGGTGCTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCGACAGGCTCCTGGA CAGGCGCTGGAATGGATG GGGACATCTACCCCGGC TCCTCCATCTGCAACTAC AACGAGAACTCAAGTCC CGGTGACCATGACCGTG GACACCTCCACCGACACC GTGTACATGGAATGTCC TCCCTGCGGAGCGAGGAC GCTAGAGAGGACGGCTAC GACGCTGGTTTGGCTTAC TGGGGCCAGGCAACCTC GTGACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 208) [SEQ ID NO: 213] QVQLVQSGAEVKKPGASV KVSCKASGYFTTYWITW VRQAPGQGLEWMGDIYPG	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACC TCTGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGCGCTTGAACGAC GGGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTACTCCCTCAGC AGCGTGGTACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAAGCCACG AACACCAAGTGGACAAG AAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCACGCA CCTGAACCTCTGGGGGA CCGTGAGTCTTCTCTTC CCCCAAAACCAAGGAC ACCCTCATGATCTCCCG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GACCTACATCTGCAACGCTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAAACCTCACACATGCCACCGTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCAA ACCAAGGACACCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGCGGAGGAGCAGTA CAACGACACGTACCGTGTGGTCAGC GTCTCACCCTCTGACACAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAAC ACAGGTGTACACCCCTGCCCCATCC CGGGATGAGCTGACCAAGAACAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAACGCTCC CGTGTGACTCCGACGGCTCCTTC TTCTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA	KASGYTFTTYWITWVRQAPGQG LEWMGDIYPGSSICNYNEKFKS RVTMTVDTSTSTVYMELESLRS EDTAVYVCAREDDGYDAWFAYWG QGTIVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTQ TYICNVNHPKSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTIISKAKGPPEPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK		SSICN'YNEKFKSRVTMTV DTSTSTVYMELESLRSED TAVYVCAREDDGYDAWFAY WGQGLIVTVSS [SEQ ID NO: 214]	AATGCCAAGACAAAAGCCG CGGGAGGAGCAGTACAAAC AGCAGTACCGTGTGGTC AGCGTCTCACCGTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAAGTGC AAGGTCTCAACAAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCCCTG CCCCCTCCCGGATGAG CTGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACC GTGGACAAGACAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGG (Nucleotide 415 to 1401 of SEQ ID NO: 208) [SEQ ID NO: 215]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	Without leader [SEQ ID NO: 209]: CAGGTGCAGCTGGTGCAGTCTGGCG CCGAAGTGAAGAAACCTGGCGCCTC CGTGAAGGTGTCCTGCAAGGCTCC GGCTACACCTTTACCACTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGGCCTGGAATGGATGGCGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAACGAGAAGTTCAAGTCCCG CGTGACCATGACCGTGACACCTCC ACCAGCACCGGTACATGGAACGT CCTCCCTGCGGAGCGAGGACACCGC CGTGTACTACTGCGCTAGAGGAC GGTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACCTTCCCGGCTGTC CTACAGTCTCTCAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCAAGGCCA GCAACACCAAGTGGACAGAAAGT TGAGCCCCAAATCTTGTGACAAAAT CACACATGCCCCACCGTGCCCGACAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCCCCAAAACCCAG				ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVEVHNAKTKPREEQYN STYRVVSVLTVQLHQLDNLN GKEYCKKVSNNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 216]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GACACCCCTCATGATCTCCGGACCC CTGAGGTCACATGCGTGGTGGGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAAGCTCCTCA CCGTCTCTGCACCAAGGACTGGTGAA TGGCAAGGAGTACAAAGTGAAGGTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGCGAGCCCCGAGAACCCACAGGTG TACACCCCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGCGGAGAACAA CTACAAGACCCACGCCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCCGGGAAATGA				
7G6-HC2u3	With leader [SEQ ID NO: 217]: ATGGGTGGTCTGTCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCCAGGTGCAGCTGGTGAG TCTGGCGCCGAAGTGAAGAAACCTG GCGCCTCCGTGAAGGTGCTCTGCAA GGCTTCCGGCTACACCTTTACCACC	With leader [SEQ ID NO: 219]: MGWSCIIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVSKAS GYFTTYWITWVRQAPGQGLEW MGDIYPGSSICNYNEKFKSRVT MTVDTSTSTAYMELSLRSED AVYYCAREDDGYDAWFAYWGQGT	ATGGGCTG GTCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C	CAGGTGCAGCTGGTGCAG TCTGGCGCCGAAGTGAAG AAACCTGGCGCTCCCGTG AAGGTGTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCGACAGGCTCCTGGA CAGGGCCTGGAATGGATG	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGGCGCCCTGACCAGC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TACTGGATCACCTGGTGCACAGG	LVTVSSASTKGPSVFPLAPSSK	(Nucleotide 1 to 57 of SEQ ID O: 217) [SEQ ID NO: 221] VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSISKAKGQPREPOVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK Without leader [SEQ ID NO: 220]: QVQLVQSGAEVKKPGASVKVCSKASGYTFTTYITWVRQAPGQG LEWMGDIYPGSSICNYNEKFKSRVTMTVDTSTSTAYMELSSRLSEDTAVYYCAREDDGYDAWFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSVTVSPSSSLGTQYICNVNHKPSNTKVDKKVEPKSCDKTHRTCPCPAPELGGPSVFLFGAGGCGGTGTAATACTGCGCTAGAGAGACGGCTACGACGCTTGTTTGCCTACTGGGGCCAGGCCCTCGTGACCGTGTCACTGCATCCACCAA GGGCCCATCGGTCTTCCCCCTGCCACCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAATCAAGCGCCC TGACACGGCGGTGCACACCTTCCC GGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGTGACA AGAAAGTTGAGCCCAATCTGTGA CAAAACTCACACATGCCCCACCGTC CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCAAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGCTACATCGGTGG TGGTGACGTGAGCCACGAAGCCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA	GGCGACATCTACCCCGGC TCCTCCATCTGCAACTAC AACGAGAAAGTTCAGGTCC CGGTGACCATGACCGTG GACACCTCCACCAGCACCC GCCTACATGGAAGTGTCC TCCCTGCGGAGCGAGGAC ACCGCGGTGTAATACTGC GCTAGAGAGGACGGCTAC GACGCTTGTTTGCCTAC TGGGGCCAGGGCACCCCTC GTGACCGTGTCACT (Nucleotides 58 to 414 of SEQ ID NO: 217) [SEQ ID NO: 222] QVQLVQSGAEVKKPGASV KVSCKASGYTFTTYITW VRQAPGQGLEWMGDIYPG SSICNYNEKFKSRVTMTV DTSTSTAYMELSSRLSED TAVYYCAREDDGYDAWFAY WGQGLTVTVSS [SEQ ID NO: 223] GGAAGGAGTACAAGTGC AAGGTCTCCAACAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTGT CCCCCATCCCGGATGAG	

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAACAGCACGTACCGTGTGGTCAGC GTCCTCACCGTCCTGCACCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCAAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAACGCTCC CGTGTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTACCCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 218]: CAGGTGCAGCTGGTGCACTCTGGCG CCGAAGTGAAGAAACCTGGCGCCTC CGTGAAGGTGTCTCTGCAAGGCTCC GGCTACACACCTTTACCACCTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGGCCTGGAATGGATGGCGGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAACGAGAAAGTTCAAGTCCCG CGTGACCATGACCGTGACACCTCC ACCAGCACCGCCTACATGGAACTGT	HNAKTPREEQYNSTYRVVSVL TVLHQDWINGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYIT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK			CTGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCACAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC AGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCAAC TACACGAGAAAGAGCCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401 of SEQ ID NO: 217) [SEQ ID NO: 224] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVAVTP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTIMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVEVHNAKTKPREEQYN STYRVVSVLTVTLHQDWLN

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CCTCCCTGCGGAGCGAGGACACCGC CGGTACTACTGCGCTAGAGAGGAC GGCTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAAGAAAGT TGAGCCCCAAATCTTGTGACAAAAT CACACATGCCCCACCGTGCCCCAGCAC CTGAACTCCTGGGGGACCGTCAGT CTTCTCTTCCCCCCCCAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGTCAATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCCGGGAGGAGCAGTACAAACAGC ACGTACCGTGTGGTACGCTCCTCA CCGTCTCTGCACCAAGGACTGGCTGAA TGGCAAGGAGTACAAAGTCAAGGTC TCCAAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCCGAGAACCCACAGGTG				GKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 225]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TACACCCCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCCGTGGAGTGGG AGAGCAATGGCGAGCCCGGAGAACAA CTACAAGACCACGCGCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCCGG GAAATGA				
7G6-HCzu4	With leader [SEQ ID NO: 226]: <u>ATGGGCTGGTCTCTGCATCATCTCTGT</u> <u>TTCTGGTGGCCACCGCCACCGGCGT</u> <u>GCACAGCCAGGTGCAGCTGGTGCGAG</u> <u>TCTGGCGCCGAAAGTGAAGAACCTG</u> GCGCCTCCGTGAAGGTGCTCTGCAA GGCTTCCGGCTACACCTTTACCACC TACTGGATCACCTGGGTGCGACAGG CTCCTGGACAGGGCCTGGAATGGAT GGCGACATCTACCCCGGCTCCTCC ATCTGCAACTACGCCAGAAATTC AGGCGAGAGTGACCATGACCGTGGA CACCTCCACCGACCGCCTACATG GAAGTGTCTCCCTGCGGAGCGAGG ACACCGCGGTGTACTACTGCGCTAG AGAGGACGGCTACGACGCTTGGTTT	With leader [SEQ ID NO: 228]: <u>MGWSCIIILFLVATATGVHSQVQ</u> <u>LVQSGAEVKKPGASVKVSKAS</u> <u>GYTFTTYWITWVRQAPGQGLEW</u> MGDIYPGSSICNYAQKFQGRVT MTVDTSTSTAYMELSSLRSEDT AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSSVWTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCD KTHICTPPCPAPELLGPSVFLF PPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSLTIVL	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCACCG CCACCGGC GTGCACAG C (Nucleotide 1 to 57 of SEQ ID NO: 226) [SEQ ID NO: 230]	CAGGTGCAGCTGGTGCGAG TCTGGCGCCGAAAGTGAAG AAACCTGGCGCCTCCGTG AAGGTGTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCACAGGCTCCTGGA CAGGGCTGGAATGGATG GGCGACATCTACCCCGGC TCCTCCATCTGCAACTAC GCCCAGAAATTCAGGGC AGAGTGACCATGACCGTG GACACTCCACCGACACC GCCTACATGGAACGTGCC TCCCCTGGGAGCGAGGAC ACCGCGGTGTACTACTGC GCTAGAGAGGACGGCTAC	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGGCCCTGACCCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCCCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAAGCCAGC AACACCAAGGTGGACAAG AAAGTTGAGCCCAAACTCT

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GCCTACTGGGGCCAGGGCACCCTCG TGACCGTGTGATCTGCATCCACCAA GGGCCCATCGGTCTTCCCTCTGGCA CCCTCCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCGAACCGGTG ACGGTGTGCTGGAACCTCAGGCGCC TGACAGCGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAACTCACACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCCTCACCGTCTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCAGG TCAGCCTGACCTGCTGCTGCTCAAGG	HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGFFLYSKLTVDKSRWQQ GNVFSQVMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 229]: QVQLVQSGAEVKKPGASVKVSC KASGYFTFTYITWVRQAPGQG LEWMGDIYPGSSICNYAQKFQG RVTMTVDTSSTAYMELSSLRS EDTAVYICAREDDGYDAWFAYWG QGTILTVSSASTKGPSVFPLAP SSKSTSGGTAALGLVCKDYFPE PVTVSNWNSGALTSVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYTCNVNHPKSNTKVDKKVEPK SCDKHTCTPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSQVMHEALHNHYTQ KSLSLSPGK		GACGCTGGTTTGGCTTAC TGGGGCCAGGGCACCCCTC GTGACCGTGTGATCT (Nucleotides 58 to 414 of SEQ ID NO: 226) [SEQ ID NO: 231] QVQLVQSGAEVKKPGASV KVSCKASGYFTFTYITW VRQAPGQGLEWMGDIYPG SSICNYAQKFQGRVTMTV DTSTSTAYMELSSLRS TAVYICAREDDGYDAWFAY WGQILTVTVSS [SEQ ID NO: 232]	TGTGACAAAACACTCACACA TGCCACACCGTGCCACGA CCTGAACCTCTGGGGGA CCGTGAGTCTTCTCTTC CCCCAAAACCCCAAGGAC ACCTCATGATCTCCCG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAAGCCG CGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTC AGCGTCTCACCGTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAAGCC CTCCAGCCCCCATCGAG AAAAACCATCTCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGCAGCCG GAGAACAACTACAAGACC ACGCTCTCCCGTGTGGAC TCCGACGGCTCTCTCTC TTATATTCAAAGCTCACC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CTTCTATCCAGCGACATCGCCGTG GAGTGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAAGCCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 227]: CAGGTGCAGCTGGTGCACTGTGGCG CCGAAGTGAAGAAACCTGGCGCCTC CGTGAAGTGTCTGCAAGGCTTCC GGCTACACCTTTACCACTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGCTGGAATGGATGGCGGAC ATCTACCCCGCTCCTCCATCTGCA ACTACGCCCAGAAATTCAGGGCAG AGTGACCATGACCGTGGACACCTCC ACCAGCACCGCTACATGGAATGT CCTCCCTGCGAGCGAGGACACCGC CGTGTACTACTGCGCTAGAGAGGAC GGCTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCCGAACCCGGTGACGGTGT				GTGGACAAGACGAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCA TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401) [SEQ ID NO: 233] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPS NTKVDKKEPKSCDKHTT CPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAAKTKPREEQYN STYRVVSVLTVHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 234]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CGTGGAACCTCAGGGGCCCTGACCAG CGGCGTGACACCTTCCCGGCTGTC CTACAGTCTCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCA GCAACACCAAGTGGACAAGAAAGT TGAGCCCAAACTTTGTGACAAAAC CACACATGCCCCACCGTGCCCGAGCAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGTCCTCA CCGTCTCTGCACCAGGACTGGTGAA TGGCAAGGAGTACAAAGTGAAGGTC TCCAAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCCGAGAACCCACAGGTG TACACCTTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCCGGAGACAA CTACAAGACCCAGCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TCATGCTCCGTGATGCATGAGGCTC TGACAAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCCGGGAAATGA				
7G6-HC _{2u5}	With leader [SEQ ID NO: 235]: ATGGGCTGGTCTCGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCCAGGTGCAGCTGGTGCG TCTGGCGCCGAAGTGAAGAAACCTG GCGCTCCGTGAAGGTGTCCTGCAA GGCTTCCGGTACACCTTTACCACC TACTGGATCACCTGGTGGCAGAG CTCTGGACAGGGCCTGGAATGGAT GGCGACATCTACCCCGCTCCTCC ATCTCAAACATAACAGAGAGTTCA AGTCCCGCGTGACCATGACCGTGA CACCTCCACAGCACCGCTACATG GAACTGTCTCTCCCTGCGGAGCGAG ACACCGCGGTACTACTGCGCTAG AGAGGACGGCTACGACGCTTGGTTT GCCTACTGGGGCCAGGCAACCTCG TGACCGTGTCTATCTGCATCCACCAA GGGCCATCGGTCTTCCCGCTGGCA CCCTCTCCAAGAGCACCTCTGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACCTCAGGCGCCC TGACGAGCGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCCA	With leader [SEQ ID NO: 237]: MGWSCIIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVSKAS GYFTTYWITWVRQAPGQGLEW MGDIYPGSSISNYNEKFKSRVT MTVDTSTSTAYMELSSLRSEDT AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFLAPSSK STSGTAALGLVDYFPEPVT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGFSFLYSLKLTVDKSRWQQ GNVFSCVSMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID NO: 238]: QVQLVQSGAEVKKPGASVKVSC	ATGGGCTG GTCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 235) [SEQ ID NO: 239]	CAGGTGCAGCTGGTGCGAG TCTGGCGCCGAAAGTGAAG AAACCTGGCGCTCCGTG AAGGTGCTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCGACAGGCTCCTGGA CAGGCGCTGGAATGGATG GGGACATCTACCCCGGC TCCTCCATCTCAAATAC AACGAGAAATTCAAGTCC CGGTGACCATGACCGTG GACACCTCCACCGACACC GCCTACATGGAATGTCC TCCCTGCGGAGCGAGGAC ACCGCGGTACTACTGC GCTAGAGAGGACGGCTAC GACGCTGGTTTGGCTTAC TGGGGCCAGGCAACCTC GTGACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 235) [SEQ ID NO: 240] QVQLVQSGAEVKKPGASV KVSCKASGYFTTYWITW VRQAPGQGLEWMGDIYPG	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACC TCTGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGCGCTGACACGAGC GGGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTACTCCCTCAGC AGCGTGGTGACCGTGCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAAGCCACG AACACCAAGTGGACAAG AAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCACGCA CCTGAACCTCTGGGGGA CCGTGAGTCTTCTCTTC CCCCAAAACCAAGGAC ACCCTCATGATCTCCCG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GACCTACATCTGCAACGCTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGG TGGTGACGCTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGCGGAGGAGCAGTA CAACGACACGTACCGTGTGGTCAGC GTCTCACCCTCTGTGACACGAGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACCC ACAGGTGTACACCCCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACCTACAAGACCAACGCTCC CGTGTGACTCCGACGCGTCTCTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA	KASGYTFTTYWITWVRQAPGQG LEWMGDIYPGSSISNYNEKFKS RVTMTVDVTSTAYMELSSLRS EDTAVYVCAREDDGYDAWFAYWG QGTIVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTQ TYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPISRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK		SSISNYNEKFKSRVTMTV DTSTSTAYMELSSLRSED TAVYVCAREDDGYDAWFAY WGQGLIVTVSS [SEQ ID NO: 241]	AATGCCAAGACAAAAGCCG CGGGAGGAGCAGTACAAAC AGCAGTACCGTGTGGTC AGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAAGTGC AAGGTCTCAACAAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCCCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGG (Nucleotides 415 to 1401 of SEQ ID NO: 235) [SEQ ID NO: 242]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	Without leader [SEQ ID NO: 236]: CAGGTGCAGCTGGTGCAGTCTGGCG CCGAAGTGAAGAAACCTGGCGCCTC CGTGAAGGTGTCCTGCAAGGCTCC GGCTACACCTTTACCACTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGGCCTGGAATGGATGGCGAC ATCTACCCCGGCTCCTCCATCTCCA ACTACAACGAGAAGTTCAAGTCCCG CGTGACCATGACCGTGACACCTCC ACCAGCACCGCCTACATGGAACGT CCTCCCTGCGGAGCGAGGACACCGC CGTGTACTACTGCGCTAGAGGAC GGCTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACCTTCCCGGCTGTC CTACAGTCTCTCAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCAAGGCCA GCAACACCAAGTGGACAGAAAGT TGAGCCCAAAATCTTGTGACAAAAT CACACATGCCCCACCGTGCCCGACAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCCCCAAACCCCAAG				ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYN STYRVVSVLTVQLHQLDNLN GKEYCKKVSNNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSL SLSPGK [SEQ ID NO: 243]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GACACCCCTCATGATCTCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAAGCTCCTCA CCGTCTCTGCACCAAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGAAGGTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCACAGGTG TACACCCCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCAAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCGCGGAGAACAA CTACAAGACCAACGCCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCCGGGAAATGA				
7G6-HC2u6	With leader [SEQ ID NO: 244]: ATGGCTGGTCTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCCAGGTGCAGCTGGTGCAG TCTGGCGCCGAAGTGAAGAAACCTG GCGCCTCCGTGAAGGTGTCCTGCAA	With leader [SEQ ID NO: 246]: MGWSCIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVSKAS GYFTTYWITWVRQAPGQGLEW MGDIYPGSSISNYNEKFSRVT MTVDTSTSTVYMEISLSRSED	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG	CAGGTGCAGCTGGTGCAG TCTGGCGCCGAAGTGAAG AAACCTGGCGCCTCCGTG AAGGTGTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCGACAGGCTCCTGGA	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACC TCTGGGGCACACGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCGCAACCG GTGACGGTGTCTGTGGAAC

[illegible]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AGACAAAGCCGGGGAGGAGCAGTA CAACAGCAGTACCGTGTGGTCAGC GTCCTCACCGTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGTGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGCGAGCCGG AGAACAACTACAAGACCCAGCCTCC CGTCTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 245]: CAGGTGCAGCTGGTGCAGTCTGGCG CCGAAGTGAAGAAACCTGGCGCCTC CGTGAAGGTGTCCTGCAAGGCTTCC GGCTACACCTTTACCACCTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGGCCTGGAATGGATGGCGGAC ATCTACCCCGGCTCCTCCATCTCCA ACTACAACGAGAAAGTTCAAGTCCCG CGTGACCATGACCGTGGACACCTCC	VVDVSHEDPEVKFNWYVDGVEV HNAKTPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYF LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK			CCCCCATCCCGGGATGAG CTGACCAAGAACCCAGGTC AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGCGAGCCG GAGAACAACTACAAGACC AGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401) [SEQ ID NO: 251] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYN STYRVVSVLTVHLQDWLN GKEYCKVSNKALPAPIE

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ACCAGCACCGTGATGGAACGTG CCTCCCTGCGGAGCGAGGACACCGC CGTGACTACTGCGCTAGAGAGGAC GGCTACGACGCTTGGTTGCCTACT GGGGCCAGGCGACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCGGCTGTC CTACAGTCTCTCAGGACTCTACTCC TCAGACGCTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAAAT CACACATGCCCCACCGTGCCCGAGCAC CTGAACTCTGGGGGACCGTCACT CTTCTCTTCCCCCCCCAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGCGGAGGAGCAGTA CAACAGCAGTACCGTGTGGTCAGC GTCTCACCGTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA				KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 252]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AAGCCAAAGGGCAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGAGAGCAATGGCAGCCGG AGAACAACTACAAGACCAAGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA				
7G6- HCzu7	With leader [SEQ ID NO: 253]: ATGGGCTGGTCTCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCCAGGTGCAGTGGTGCGAG TCTGGCGCCGAAGTGAAGAAACCTG CGCCTCCGTGAAGGTGCTCTGCAA GGCTCCGGCTACACCTTTACCACC TACTGGATCACCTGGGTGCGACAGG CTCCTGGACAGGGCCTGGAATGGAT GGCGACATCTACCCCGGCTCCTCC ATCTCCAACCTACGCCCAAGAGTCC AGGGCGCGGTGACCATGACCGTGG CACCTCCACAGCACCGGTGTACATG GAACTGTCTCCTCCCTGCGGAGCGAGG ACACGCGCGTGTACTACTGCGCTAG	With leader [SEQ ID NO: 255]: MGWSCIIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVCKAS GYTFITYWITWVRQAPGQGLEW MGDIYPGSSISNYAQKFQGRVT MTVDTSTSTVYMEISSLRSEDT AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSSVWTVPPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELGGPSVFLF PPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVSVLTIVL	ATGGGCTG GTCTGCA TCATCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleot ides 1 to 57 of SEQ ID NO: 253) [SEQ ID NO: 257]	CAGTGGAGCTGGTGCGAG TCTGGCGCCGAAGTGAAG AAACCTGGCGCTCCGTG AAGGTGTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCAGAGGCTCCTGGA CAGGGCTGGAATGGATG GGCGACATCTACCCCGGC TCCTCCATCTCCAATAC GCCCAGAAAGTTCCAGGGC CGCGTGGTACACCTGCGT GACACTCCACAGCACCC GTGTACATGGAATGTCC TCCCTCGGAGCGAGGAC ACCGCGGTGTACTACTGC GCTAGAGAGGACGGCTAC	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGGCCCTGACCCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCAGC AACACCAAGGTGGACAAG AAAGTTAGGCCCAATCT

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AGAGGACGGCTACGACGGCTTGGTTT GCCTACTGGGGCCAGGGCACCCCTCG TGACCGTGTCTCATCTGCATCCACCAA GGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGTGCCTGGT CAAGGACTACTTCCCGAACCGGTG ACGGTGTCTGGAACTCAGGGCCCC TGACCAAGCGCGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCGTGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCCAAATCTTGTGA CAAAAGTCAACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCTCACCCTCCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG	HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 256]: QVQLVQSGAEVKKPGASVKVSC KASGYFTFTYITWVRQAPGQG LEWMGDIYPGSSISNYAQKFQ RVTMDVDTSTVYMELSSLR EDTAVYICAREDDYDAWFAYWG QGTILTVSSASTKGPSVFPLAP SSKTSSTGTAALGLVCKDYFPE PVTVSNWNSGALTSVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYTCNVNHPKSNPKVDKKVEPK SCDKHTCTCPCPAPELGGPSV FLFPPKPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVY LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSQSVMEALHNHYTQ KSLSLSPGK		GACGCTTGGTTTGCCCTAC TGGGGCCAGGGCACCCCTC GTGACCGTGTCTCATCT Nucleotides 58 to 414 of SEQ ID NO: 253) [SEQ ID NO: 258] QVQLVQSGAEVKKPGASV KVSCKASGYFTFTYITW VRQAPGQGLEWMGDIYPG SSISNYAQKFQGRVTMTV DTSTSTVYMELSSLRSED TAVYICAREDDYDAWFAY WGQGITLVTVSS [SEQ ID NO: 259]	TGTGACAAAACACTCACACA TGCCACACCGTGCCACGA CCTGAACCTCTGGGGGA CCGTCACTCTTCTCTTC CCCCAAAACCCCAAGGAC ACCTCATGATCTCCCG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAAGCCG CGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTC AGCGTCTCACCGTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAGCC CTCCAGCCCCCATCGAG AAAAACATCTCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCTCTCCCGTGTGGAC TCCGACGGCTCTCTCTTC TTATATTCAAAGCTCACC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TCAGCCTGACCTGCCTGGTCAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAACGCTCC CGTGCTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGTCTCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 254]: CAGGTGCAGCTGGTGCACTGTGGCG CCGAAGTGAAGAAACCTGGCGCCTC CGTGAAGGTGCTCTGCAAGGCTTC GGCTACACCTTTACCACCTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGGCCTGGAATGGATGGCGAC ATCTACCCCGGCTCCTCCATCTCCA ACTACGCCCCAGAGTTCCAGGGCCG CGTGACCATGACCGTGGACACCTCC ACCAGACCCGTGTACATGGAAGTGT CCTCCCTGCGAGCGAGGACACCCG CGTGTAAGTGTGCTAGAGGAC GGCTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC				GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401 of SEQ ID NO: 253) [SEQ ID NO: 260] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVTVTP SSSLTGTQYICNVNHKPS NTKVDKKEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSGDSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKS LSLSPGK [SEQ ID NO: 261]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGCGTGACACCTTCCCGGTGTC CTACAGTCTCTCAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCA GCAACACCAAGTGGACAAGAAAGT TGAGCCCCAAATCTTGTGACAAAAT CACACATGCCCCACCGTGCCCGACAC CTGAACCTCTGGGGGACCGTCACT CTTCTCTTCCCCCCCCAAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGGTGGTCAAGCTCCTCA CCGTCTGCACCAAGACTGGCTGAA TGGCAAGGAGTACAAGTGCAAGTCT TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCACAGGTG TACACCTTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTCAACCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAA CTACAAGACCCAGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCCGTGGACAAGAG				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGGGAATGA				
7G6-HCzu8	With leader [SEQ ID NO: 262]: ATGGGTGCTGCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCCAGGTGCAGCTGGTGCG TCTGGCGCCGAAGTGAAGAACCTG GCGCTCCGTGAAGTGTCTGCAA GGCTTCGGGTACACCTTTACCAC TACTGGATCACCTGGTGGCAGAG CTCTGGACAGGGCTGGAATGGAT GGCGACATCTACCCCGGCTCCTCC ATCTCCAACCTACGCCCAGAGTTC AGGGCCGCGTGACCATGACCCGGA CACTCCACAGCACCGTGTACATG GAACTGCTCCCTCCCTGGGAGCGAG ACACCGCGGTACTACTACGCTTGGTT AGAGGACGGCTACGACGCTTGGTT GCCTACTGGGGCAGGGCACCTCG TGACCGTGTCTATCTGCATCCACCA GGGCCCATCGGTCTCCCGCTGGCA CCCTCTCCAAGAGCACCTCTGGG GCACAGGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACCTCAGGCGCC TGACAGCGGGCTGCACACCTTCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG	With leader [SEQ ID NO: 264]: MGWSCILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVSKAS GYFTTYWITWVRQAPGQGLEW MGDIYPGSSISNYAQKFQGRVT MTRDTSTSTVYMEISLSRSED AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGTAALGLVLDYFPEPT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGGSFFLYSKLTVDKSRWQQ GNVFCSVMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID NO: 265]: QVQLVQSGAEVKKPGASVKVSC	ATGGGTG GTCTGCA TCATCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 262) [SEQ ID NO: 266]	CAGGTGCAGCTGGTGCGAG TCTGGCGCCGAAGTGAAG AAACCTGGCGCTCCGTG AAGGTGCTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCGACAGGCTCCTGGA CAGGCGCTGGAATGGATG GGGACATCTACCCCGGC TCCTCATCTCCAACTAC GCCCAGAAGTTCAGGGC CGGTGACCATGACCCGG GACACCTCCACAGCACCC GTGTACATGGAATGTCC TCCCTGGCGAGCGAGGAC ACCGCGTGTACTACTGC GCTAGAGAGGACGGCTAC GACGCTGGTTTGGCTTAC TGGGGCAGGGCACCTC GTGACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 262) [SEQ ID NO: 267] QVQLVQSGAEVKKPGASV KVSCKASGYFTTYWITW VRQAPGQGLEWMGDIYPG	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCC TCTGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGCGCTGACACAGC GGGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTACTCCCTCAGC AGCGTGTGACCGTGCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAAGCCACG AACACCAAGTGGACAAG AAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCACGCA CCTGAACCTCTGGGGGA CCGTGAGTCTTCTCTTC CCCCAAAACCCAAAGAC ACCCTCATGATCTCCCG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGCCCTCCAGCAGCTTGGGCACCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCAA ACCAAGGACACCTCATGATCTCC CGACCCCTGAGGTACATGCGTGG TGGTGACGTGAGCCACGAAGACC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGAGGTGCATAATGCCA AGACAAAGCCGCGGAGGAGCAGTA CAACAGCACGTACCGTGTGTCAGC GTCTCACCGTCTGACCCAGGACT GGCTGAATGGCAAGGAGTACAAGT CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAACCATCTCCA AAGCCAAAGGCGAGCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACAGG TCAGCTGACCTGCCTGGTCAAAG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGACGCCG AGAACAACACTACAAGACCAACGCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA	KASGYTFTTYWITWVRQAPGQG LEWMGDIYPGSSISNYAQKFQG RVTMTTRDTSTVYMELSLRS EDTAVYCCAREDDGYDAWFAYWG QGTIVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTQ TYICNVNHPKSTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK		SSISNYAQKFQGRVTMTTR DTSTSTVYMELSLRS TAVYCCAREDDGYDAWFAY WGQGLIVTVSS [SEQ ID NO: 268]	AATGCCAAGACAAAAGCCG CGGGAGGAGCAGTACAAAC AGCAGTACCGTGTGGTC AGCGTCTCACCGTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAAGTGC AAGGTCTCAACAAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAAGTGC AGCCTGACCTGCCTGGTC AAAGGTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACC GTGGACAAGACAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCTCCCGG (Nucleotides 415 to 1401 of SEQ ID NO: 262) [SEQ ID NO: 269]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	Without leader [SEQ ID NO: 263]: CAGGTGCAGCTGGTGCAGTCTGGCG CCGAAGTGAAGAAACCTGGCGCTC CGTGAAGGTGTCCTGCAAGGCTCC GGCTACACCTTTACCACTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGCCCTGGAATGGATGGCGAC ATCTACCCCGGCTCCTCCATCTCCA ACTAGCCCCAGAAAGTCCAGGGCCG CGTGACCATGACCCGGACACCTCC ACCAGACCCGTGTACATGGAACGT CCTCCCTGCGGAGCGAGGACACCGC CGTGACTACTGCGCTAGAGAGGAC GGCTACGACGCTTGGTTGCCTACT GGGGCCAGGGCACCCCTCGTGACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCGGCTGTC CTACAGTCCCTCAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGACCCAGACCTAC ATCTGCAACGTGAATCACAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAAACCT CACACATGCCCCACCGTGCCCCAGCAC CTGAACTCCTGGGGGACCCGTCACT				ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYN STYRVVSVLTVQLHQLDNLN GKEYCKKVSNNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 270]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CTTCTCTTCCCCCCCCAAACCCAG GACACCCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGGTCCTCA CCGTCTGCAACAGGACTGGTGAA TGGCAAGGAGTACAAGTGCAAGGTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCACAGGTG TACACCCTGCCCCCATCCCCGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCCGGAGAACAA CTACAAGACCACGCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCCGGGAATGA				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
7G6-HC2u9	With leader [SEQ ID NO: 271]: ATGGGTGGTCTGTCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCCAGGTGCAGCTGGTGCG TCTGGCGCCGAAGTGAAGAACCTG GCGCTCCGTGAAGGTGCTCTGCAA GGCTTCGGGTACACCTTTACCACC TACTGGATCACCTGGTGGACAGG CTCCTGGACAGGCCCTGGAATGGAT GGCGACATCTACCCCGGCTCCTCC ATCTGCAACTACGCCCCAGAAGTTC AGGCCCGCTGACCATGACCGTGA CACTCCACACGACCGGTGATG GAACTGTCTCCCTCGGAGCGAGG ACACCGCGGTACTACTACGCTGCTAG AGAGGACGGCTACGACGCTTGTTT GCCTACTGGGGCCAGGCCACCTCG TGACCGTGTCTATCTGATCCACCAA GGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGACACCTCTGGG GCACAGCGCCCTGGGCTGCCTGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACCTCAGGCGCC TGACAGCGCGGTGCACACCTTCC GGCTGTCTACAGTCTCAGGACTC TACTCCTCAGACGCTTGGACCG TGCCCTCCAGACGCTTGGGACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAAACTCACACATGCCACCGTGC	With leader [SEQ ID NO: 273]: MGWSCIIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVCKAS GYFTTYITWVRQAPGQGLEW MGDIYPGSSICNYAQKFQGRVT MTVDTSTSTVYMEISLRSRSDT AVYICAREDDYDAWFAYWGQT LVTYSSASTKPSVFPLAPSSK STSGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTPVPSSSLGTQYI CNVNHPKNTKVDKKVEPKSCD KTHCTPPCPAPELGGPSVFLF PPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVSVLTIVL HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSLKLTVDKSRWQQ GNVFPSCVMHEALHNYTQKSL SLSPGK Without leader [SEQ ID NO: 274]: QVQLVQSGAEVKKPGASVKVSC KASGYFTTYITWVRQAPGQG LEWMGDIYPGSSICNYAQKFQ RVMTVDTSTSTVYMEISLRS EDTAVYICAREDDYDAWFAYWG	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 271) [SEQ ID NO: 275]	CAGTGCAGCTGGTGACG TCTGGCGCCGAAGTGAAG AAACCTGGCGCCTCCGTG AAGGTGCTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGACAGAGCTCCTGGA CAGGCTTGAATGGATG GGGACATCTACCCCGGC TCCTCCATCTGCAACTAC GCCCAGAAGTTCAGGGC CGCGTACCATGACCGTG GACCTCCACGACACCC GTGATACATGGAATGTCC TCCCTGGGAGCGAGGAC ACCGCGTGTACTACTG GCTAGAGAGGACGGCTAC GACGCTGTGTTTGCTTAC TGGGCGCAGGCGACCCCTC GTGACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 271) [SEQ ID NO: 276] QVQLVQSGAEVKKPGASV KVSCKASGYFTTYITW VRQAPGQGLEWMGDIYPG SSICNYAQKFQGRVTMTV DTSTSTVYMEISLRSRSD TAVYICAREDDYDAWFAY WGQGLTVSS	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCC TCTGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGCGCCTGACACGAC GGCGTGCACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCACGAC AACACCAAGGTGGACAAG AAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCCGAGCA CCTGAACCTCCTGGGGGA CCGTACGTCTTCTCTTTC CCCCAAAACCAAGGAC ACCTCATGATCTCCCGG ACCCCTGAGGTACATGC GTGGTGGTGACGTGAGC CACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGAGGAGCAGTACCAAC AGCACGTACCGTGTGGTC AGCGTCTCTACCGTCTCTG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)	
	CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCAAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGTCAGC GTCCTCACCGTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGCGAGCCGG AGAACAACTACAAGACCAACGCTCC CGTGTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA	QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTQ TYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMEALHNHYTQ KSLSLSPGK		[SEQ ID NO: 277]	CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCCGAGAA CCACAGGTGTACACCTG CCCCATCCCGGATGAG CTGACCAAGAACCCAGGT AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGCGAGCCG GAGAACAACTACAAGACC AGCCTCCCGTGTCTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGG (Nucleotides 415 to 1401 of SEQ ID NO: 271) [SEQ ID NO: 278]	ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVTVTP
	Without leader [SEQ ID NO: 272]: CAGGTGCAGCTGGTGCAGTCTGGCG CCGAAGTGAAGAAACCTGGCGCCTC					

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CGTGAAGGTGTCCTGCAAGGCTTCC GGTACACCTTTTACCACCTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGGCCTGGAATGGATGGGCGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACGCCCCAGAAAGTTCCAGGGCG CGTGACCATGACCGTGGACACCTCC ACCAGACCGGTGTACATGGAAGTGT CCTCCCTGCGGAGCGAGGACACCCG CGTGACTACTGCGCTAGAGAGGAC GGCTACGACGCTTGGTTGCCTACT GGGGCAGGGCACCCCTCGTGACCGT GTGATCTGCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCGGTGTC CTACAGTCTCTAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAAATCTTGTACAAAAT CACACATGCCCCACCGTGCCCGAC CTGAACCTCTGGGGGACCCGTGAGT CTTCTCTTCCCCCCCCAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG				SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VWVDVSHEDPEVKFNWYV DGEVHNAAKTKPREEQYN STYRVSVLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPDSIAVEWESNGQP ENNYKTTTPPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 279]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGAGAGTGCATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTCTGCACAGGACTGGCTGAA TGGCAAGGAGTACAAGTGCAAGGTC TCCAACAAAAGCCCTCCAGCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGAGCCCCCGAGAACACAGGTG TACACCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAA CTACAAGACACGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGGGAAATGA				
7G6-HCzu10	With leader [SEQ ID NO: 280]: ATGGGCTGGTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCCAGGTGCAGCTGGTGCAG TCTGGCGCCGAAGTGAAGAAACCTG CGCCTCCGTGAAGGTGCTCTGCAA GGCTCCGGCTACACCTTTACCACC TACTGGATCACCTGGGTGCGACAGG CTCTGGACAGGGCCTGGAATGGAT GGGCGACATCTACCCCGGCTCCTCC	With leader [SEQ ID NO: 282]: MGWSCIIILFLVATATGVHSQVQ LVQSGAEVKKPGASVKVSKAS GYFTTYWITWVRQAPGQGLEW MGDIYPGSSICNYAQKFQGRVT MTRDTSSTVYMEISLSRSED AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS	ATGGGCTG GTCCTGCA TCATCTGT TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of	CAGTGCAGCTGGTGCAG TCTGGCGCCGAAGTGAAG AAACCTGGCGCCTCCGTG AAGGTGTCTGCAAGGCT TCCGGCTACACCTTTACC ACCTACTGGATCACCTGG GTGCACAGGCTCTGGGA CAGGGCTGGAATGGATG GGCGACATCTACCCCGGC TCCTCCATCTGCAACTAC GCCCAAGAGTTCCAGGGC	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGGCCCTGACCAGC GGCGTGCACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ATCTGCAACTACGCCAGAGTTCC AGGGCCGCGTGACCATGACCCGGGA CACCTCCACCAGACCGGTGACATG GAACTGTCTCTCCCTGCGGAGCGAGG ACACCGCGGTGTAATACTGCGCTAG AGAGACGGCTACGACGCTTGTTT GCCTACTGGGGCCAGGCAACCTCG TGACCGGTGTCATCTGCATCCACCAA GGGCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGTGGAACCTCAGCGGCC TGACAGCGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCTTGGGCACCCA TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAAACTTTGTGA CAAACTCACACATGCCACCGTGC CCAGCACCTGAATCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTCAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCAACTGGTACGTG GACGGGTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAG GTCTCACCGTCTGCACCAAGACT GGCTGAATGGCAAGGAGTACAAGTG	GLYSSSVVTVPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRWVSLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSKLTVDKSRWQQ GNVFCFSVMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 283]: QVQLVQSGAEVKKPGASVKVSC KASGYFTTYITWVRQAPGQG LEWMGDIYPGSSICNYAQKFQ RVTMRDTSSTVYMEISLRS EDTAVYFCAREDDYDAWFAYWG QGTLLTVSSASTKGPSVFLAP SSKSTSGGTAALGLVVDYFPE PVTVSNWSGALTSVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPK SCDKHTCTCPPAPELLGGPSV FLPPTPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRWVSL TVLHQDWLNGKEYKCKVSNKAL PAPIETISKAKGQPREPQVYT	SEQ ID No: 280) [SEQ ID No: 284]	CGGTGACCATGACCCGGG GACACCTCCACAGCACCC GTGTACATGGAACGTGCC TCCCTGCGGAGCGAGGAC ACCGCGGTGTAATACTGC GCTAGAGGACGGCTAC GACGCTGGTTTGCCTAC TGGGGCCAGGCAACCTC GTGACCGGTGTCATCT (Nucleotides 58 to 414 of SEQ ID No: 280) [SEQ ID No: 285] QVQLVQSGAEVKKPGASV KVSCKASGYFTTYITW VRQAPGGLEWMGDIYPG SSICNYAQKFQGRVTMTTR DTSTSYMEISLRS TAVYFCAREDDYDAWFAY WGQGLTVTVSS [SEQ ID No: 286]	AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCGACG AACACCAAGGTGGACAAG AAAGTTGAGCCCAAACTCT TGTGACAAAACCTCACACA TGCCACCGTGCCCGAGCA CCTGAACCTCTGGGGGA CCGTGAGTCTTCTCTTC CCCCCAAAACCAAGGAC ACCCCTCATGATCTCCCG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CAGGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGAGGAGCAGTACAAAC AGCACGTACCGTGTGGTC AGCGTCTTACCGTCTTG CACCAGGACTGGTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCAACAAGCC CTCCAGCCCGCCATCGAG AAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCGAC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGCGAGCCGG AGAACAACTACAAGACCACGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 281]: CAGGTGCAGCTGGTGCACTGGCG CCGAAGTGAAGAAACCTGGCGCTC CGTGAAGGTGCTCTGCAAGGCTCC GGCTACACCTTTACCACCTACTGGA TCACCTGGGTGCGACAGGCTCCTGG ACAGGCTGGAATGGATGGCGGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACGCCACAGAAATCCAGGCGCG CGTGACCATGACCCGGGACACCTCC ACCAGACCGGTACATGGAAGTGT CCTCCCTGCGGAGCGAGGACACCGC CGTGTACTACTGCGCTAGAGAGGAC GGCTACGACGCTTGGTTTGCCTACT	LPSPRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK			GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGG (Nucleotides 415 to 1401 of SEQ ID NO: 280) [SEQ ID NO: 287] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTVF SSSLGTQTYICNVNHKPS NTKVDKKEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVVSVLTVHLQDNLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GGGGCCAGGGCACCCCTCGTGACCGT GTCACTGTCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGGGTGCACACCTTCCCGGTGTC CTACAGTCCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAAATCTTGTGACAAAAT CACACATGCCCCACCGTGCCCGAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCAAAACCCCAAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTTGACCAAGGACTGGCTGAA TGGCAAGGAGTACAAAGTCAAGGTC TCCAAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCAGGTG TACACCCCTGCCCCCATCCCCGGATG AGCTGACCAAGAACCCAGGTCAAGCT GACCTGCCTGGTCAAGAGGCTTCTAT				KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMEALHNHHTQKSL SLSPGK [SEQ ID NO: 288]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGAACAA CTACAAGACACGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGGGAATGA				
7G6-HC2u1	With leader [SEQ ID NO: 289]: ATGGGCTGGTCTGTCATCATCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCGAAGTGACGCTGCTGGAA TCTGGCGGGGAGTGGTGACGCTG GCGGCTCTCTGAGACTGTCTTGTG CGCCTCCGGCTACACCTTCACCACC TACTGGATCACCTGGGTCGGACAGG CTCCCGGCAAGGACTGGAATGGGT GTCCGACATCTACCCGGCTCCTCC ATCTGCAACTACAACGAGAAGTTCA AGTCCCGGTTACCATCTCCCGGA CAACTCAAAGAACACCTGTACCTC CAGATGAACCTCCCTGCGGGCCGAG ACACCGCGGTACTACTGTGCCAA AGAGACGGCTACGACGCTTGGTT GCCTACTGGGGCAGGCAACCTCG TCACCGTGTCTATCTGCATCCACCA GGGCCCATCGTCTTCCCGCTGGCA CCCTCCTCCAAGAGCACCTCTGGGG GCACAGCGGCTGGGCTGCCTGGT CAAGGACTACTTCCCGCAACCGGTG	With leader [SEQ ID NO: 291]: MGWSCIIILFLVATATGVHSEVQ LLESGGLVQPGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VSDIYPGSSICNYNEKFSRFT ISRDNSKNTLYLQMNSLRAEDT AVYCAKEDGYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVFSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHCTCPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYCKVKVSNKALPAP IEKTI SAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LQSDGSFFLYSKLTVDKSRWQQ	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 289) [SEQ ID NO: 293]	GAAGTGACGCTGCTGGAA TCTGGCGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGCTGTGTGCCGCC TCCGGGTACACCTTCACC ACCTACTGGATCACCTGG TCCGACAGGCTCCCGG AAGGACTGGAATGGGTG TCCGACATCTACCCCGGC TCCTCCATCTGCAACTAC AACGAGAAAGTTCAAGTCC CGGTTACCATCTCCCGG GACAACTCAAAGAACACC CTGTACTCCAGATGAAC TCCCTGGGGCCGAGGAC ACCGCCGTGTACTACTGT GCCAAAGAGACGGCTAC TACGCTGGTTTGCCTAC TGGGCGCAGGCAACCTG GTCACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 289)	GCATCCACCAAGGGCCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTACGGTGTCTGTGAAC TCAGGCGCCTGACCAGC GCGGTGCACACCTTCCCG GGTCTACTCCCTCAGC GGACTTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCACG AACACCAAGGTGGACAAG AAAAGTTGAGCCCAAAATCT TGTGACAAAACTCACACA TGCCCCACCGTGCCAGCA CCTGAACCTCTGGGGGA CCGTCAGTCTTCTCTTC CCCCCAAAACCAAGGAC ACCCTCATGATCTCCCGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ACGGTGTGCTGGAACCTCAGGGGCCC TGACCAGCGGGCTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCGTGTGACCG TGCCCTCCAGCAGCTTGGCACCCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCCGTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCACA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGCCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCCTCACCGTCTCTGCACCGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACACTACAAGACCACGCCTC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA	GNVFSCVMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 292]: EVQLLESGGGLVQPGGSLRLSC AASGYTFTTYITWVRQAPGKG LEWVSDIYPGSSICNYNEKFKS PFTISRDNKNTLYLQMNSLRA EDTAVYYCAKEDGYDAWFAYWG QGLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTQ TYICNVNHPKNTKVDKKVEPK SCDKTHTCPPCPAPELGGPSV FLPPPKKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQDGNVFSCSVMHEALHNHYTQ KSLSLSPGK		[SEQ ID No: 294] EVQLLESGGGLVQPGGSL RLSCAASGYTFTTYITW VRQAPGKLEWVSDIYPG SSICNYNEKFKSRFTISR DNSKNTLYLQMNSLRAED TAVYYCAKEDGYDAWFAY WGQGLVTVSS [SEQ ID No: 295]	ACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGC CACGAAGACCCCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAAGCCG CGGAGGAGCAGTACAAC AGCAGTACCGTGTGGTC AGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCCCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CGTCTTCTCATGTCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 290]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGGTGCCGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAACGAGAAGTTCAAGTCCCG GTTCACCATCTCCCGGGACAACTCC AAGAACACCCCTGTACCTCCAGATGA ACTCCCTGCGGGCCGAGGACACCGC CGTGTAATACTGTGCCAAAGAGGAC GGCTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTGGTCAACGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGCGGTGCACACCTTCCCCGGCTGC CTACAGTCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTTGAATCACAAAGCCCA				(Nucleotides 415 to 1401 of SEQ ID NO: 289) [SEQ ID NO: 296] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVVSVLTVHLQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFPYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 297]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACT CACACATGCCCACCGTGCCAGCAC CTGAATCTCTGGGGGACCGTCAGT CTTCTCTTCCCCCAAAACCCAG GACACCCTCATGATCTCCCGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCTGAGTTC AAGTTCAACTGGTACGTGGACGGC TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTGTCACCAAGGACTGGCTGAA TGGCAAGGAGTACAAGTGCAAGTTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCAACAGGTG TACACCCCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCCGGAGAACAA CTACAAGACCAACGCTCCCGTGTG GACTCCGACGGCTCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGGGAAATGA				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
7G6-HC2u1	With leader [SEQ ID NO: 298]: ATGGGTGGTCTGTCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGAAGTGACGCTGCTGGAA TCTGGCGGCGGACTGGTGACGCTG GCGGCTCTCTGAGACTGCTTGTGC CGCTCCGGCTACACCTTCAACACC TACTGGATCACCTGGTCCGACAGG CTCCCGCAAGGACTGGAATGGGT CGGAGACATCTACCCCGGCTCCTCC ATCTGCAACTACACGAGAGTTCA AGTCCCGGTTACCATCTCCGTGGA CAACTCAAAGTCCACCGCTACCTC CAGATGAACCTCCCTGAGAGCCGAGG ACACCGCCGTGACTACTGCGCCAG AGAGGACGGCTACGACGCTTGTTT GCTTACTGGGCGGAGGCAACCTGG TCACCGTGTCTATCTGATCCACCAA GGGCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGACACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACTCAGGCGCC TGACAGCGGCGTGACACCTTCCC GGTGTCTCTACAGTCTCAGGACTC TACTCCTCAGACGCTTGGGACCG TGCCCTCCAGACTTGGGACCCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAAACTCACACATGCCCAACCGTGC	With leader [SEQ ID NO: 300] MGWSCIIILFLVATATGVHSEVQ LLESGLLVQPGGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VGDIYPGSSICNYNEKFKSRFT ISVDNSKSTAYLQMNSLRAEDT AVYICAREDDYDAWFAYWGQT LVTSSASTKPSVFPLAPSSK STSGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSVTVTPSSSLGTQYI CNVNHKPSNTKVDKKEPKSCD KTHCTPPCPAPELGGPSVFLF PPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFELYSLKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK Without leader [SEQ ID NO: 301]: EVQLLESGGGLVQPGGSLRLSC AASGYTFITYWITWVRQAPGK LEWVGDIYPGSSICNYNEKFKS RFTISVDNSKSTAYLQMNSLRA EDTAVYICAREDDYDAWFAYWG	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 298) [SEQ ID NO: 302]	GAAGTGACAGTGTGGAA TCTGGCGGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTTGTGCCGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGGC AAGGACTGGAATGGGTC GGAGACATCTACCCCGGC TCCTCCATCTGCAACTAC AACGAGAAGTTCAGTCC CGGTACCACATCTCCGTG GACAACTCCAAAGTCCACC GCCTACTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCGTGTACTACTGC GCCAGAGAGGACGGCTAC GACGCTGTGTTTGTCTTAC TGGGGCAGGGCACCCCTG GTCACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 298) [SEQ ID NO: 303] EVQLLESGGGLVQPGGSL RLSCAASGYTFITYWITW VRQAPGKLEWVVDIYPG SSICNYNEKFKSRFTISV DNSKSTAYLQMNSLRAED TAVYICAREDDYDAWFAY WGQGLTVTVSS	GCATCCACCAAGGGCCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAAACCG GTGACGGTGTCTGTGAAC TCAGGCGGCTGACCAAGC GGCGTGCACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCCAAGC AACACCAAGGTGGACAAG AAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCCAACCGTGCCCAAGCA CCTGAACCTCTGGGGGA CCGTACAGTCTTCTCTTTC CCCCAAAACCAAGGAC ACCTCATGATCTCCCGG ACCCCTGAGGTACATGC GTGGTGGTGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGGAGGAGCAGTACAA AGCACGTACCGTGTGGT AGCGTCTCTACCGTCTCTG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCAAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCCTCACCGTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCGAGAACCC ACAGGTGTACACCCCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCCTGGTCAAAGG CTTCTATCCCGAGCATCGCCGTG GAGTGGGAGAGCAATGGGCGCCGG AGAACAACTACAAGACCAACGCTCC CGTGTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 299]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC	QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTQ TYICNVNHPKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMEALHNHYTQ KSLSLSPGK		[SEQ ID NO: 304]	CACCAGGACTGGTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCGGGATGAG CTGACCAAGAACCCAGGT AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCGAGCCG GAGAACAACTACAAGACC AGCCTCCCGTGTCTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGACAAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGG (Nucleotides 415 to 1401) [SEQ ID NO: 305] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVTVTP SSSLGTQTYICNVNHPKPS

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TCTGAGACTGTCTTGTGCGGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGTCCGACAGGCTCCCG CAAGGACTGGAATGGTCGGAGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAACGAGAAAGTTCAAGTCCG GTTACCATCTCCGTGGACAACTCC AAGTCCACCGCTACCTCCAGATGA ACTCCCTGAGAGCCGAGACACCCG CGTGTACTACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTACT GGGGCAGGGCACCCCTGGTCACCGT GTCTATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCGGTGTC CTACAGTCTCTAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAAATCTTGTACAAAAT CACACATGCCCCACCGTGCCGAGCAC CTGAACCTCTGGGGGACCCGTAGT CTTCTCTTCCCCCCCCAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG				NTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLF PPKPKDTIMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVFNHNAKTKPREEQYN STYRVSVLTVQLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 306]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGAGAGTGCATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGTCTCTCA CCGTCTCTGCACAGGACTGGCTGAA TGGCAAGGAGTACAAGTGCAAGGTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACACACAGGTG TACACCTGCCCCCATCCCCGGGATG AGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGACGCCGGAGAACAA CTACAAGACACAGCCTCCCCGTGTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGGGAATGA				
7G6- HC2u1 3	With leader [SEQ ID NO: 307]: ATGGCTGGTCTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGAAGTGCAGCTGCTGGAA TCTGGCGGCGGACTGGTGCAGCCTG GCGGCTCTCTGAGACTGTCTTGTC CGCTCCGGCTACACCTTCACCAAC TACTGGATCACCTGGTCCGACAGG CTCCCGGCAAGGACTGGAATGGGT CGGAGACATCTACCCCGGCTCCTCC ATCTGCAACTACGCCGACTCCGTCA	With leader [SEQ ID NO: 309]: MGWSCIIILFLVATATGVHSEVQ LLESGGILVQPGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VGDYIPGSSICNYADSVKGRFT ISVDNSKSTAYLQMNSLRAEDT AVYYCAREDDGYDAWFAYWGQT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSSVWTVPSSSLGTQYI	ATGGGCTG GTCCTGCA TCATCTGT TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID	GAAGTGCAAGCTGCTGGAA TCTGGCGGGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTTGTGCCGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACACGGCTCCCGGC AAGGACTGGAATGGGTC GGAGACATCTACCCCGGC TCCTCCATCTGCAACTAC GCCGACTCCGTCAAGGGC CGGTTACCATCTCCGTG	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAAACCG GTGACGGTGTCTGTGAAC TCAGGCGCCCTGACCCAGC GGCTGCACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AGGGCCGGTTACACATCTCCGTGGA CAACTCCAAAGTCCACCGCTACCTC CAGATGAACCTCCCTGAGAGCCGAGG ACACCGCCGTGTACTACTGCGCCAG AGAGACGGCTACGACGCTTGTTT GCTTACTGGGCCAGGCCACCTGG TCACCGTGTATCTGCATCCACCAA GGGCCATCGGTCTTCCCTCGGCA CCCTCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTGCTGGAACCTCAGGCGCC TGACAGCGCGGTGCACACCTTCCC GGTGTCTTACAGTCTCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTCAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAGCCCGGGAGGAGCAGTA CAACAGCAGTACCGTGTGGTCAGC GTCCTCACCGTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA	CNVNHPKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRWVSVLTVL HQDWINGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSKLTVDKSRWQQ GNVPSCSVMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 310]: EVQLLESGGGLVQPGGSLRLSC AASGYSFRTTYWITWVRQAPGK LEWVGDIYPGSSICNYADSVK RFTISVDNSKSTAYLQMNSLRA EDTAVYYCAREDDGYDAWFAYWG QGTLLVTVSSASTKGPSVFPLAP SKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYICNVNHPKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRWVSVL TVLHQDWINGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF	No: 307) [SEQ ID No: 311]	GACAACTCCAAAGTCCACC GCCTACCTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCCGTGTACTACTGC GCCAGAGAGGACGGCTAC GACGCTGGTTTGTCTTAC TGGGGCCAGGACACCTG GTACCGGTGCATCT (Nucleotides 58 to 414 of SEQ ID NO: 307) [SEQ ID NO: 312] EVQLLESGGGLVQPGGSL RLSAAAGSYFTTYWITW VRQAPGKLEWVVDIYPG SSICNYADSVKGRFTISV DNSKSTAYLQMNSLRAED TAVYYCAREDDGYDAWFAY WGQGLTVTVSS [SEQ ID NO: 313]	TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCGAGC AACACCAAGGTGGACAAG AAAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCACACCGTGCCGAGCA CCTGAACCTCTGGGGGA CCGTAGTCTTCTCTTC CCCCAAAACCCCAAGGAC ACCTCATGATCTCCCG ACCCCTGAGGTACATGTC GTGGTGGTGGACGTGAGC CAGAAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTC AGCGTCTTACCGTCTCTG CACCAGGACTGGCTGAAT GGCAAGGATACAAGTGC AAGGTCTCAACAAGGAC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCGAGC GACATCGCCGTGGAGTGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGAGCCGG AGAACAACTACAAGACCACGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 308]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCCGAGAC ATCTACCCCGCTCCTCCATCTGCA ACTACGCCGACTCCGTCAAGGCCG GTTACCATCTCCGTGGACAACTCC AAGTCCACCCGCTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCCG CGTGTACTACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTCTACT GGGGCCAGGGCACCCCTGGTCAACCGT	YPSDIAVEWESNGQPENNYKTT PPVLDSGDSFFLYSKLTVDKSR WQQGNVFSQVMHEALHNHYTQ KSLSLSPGK			GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACC GTGACAAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGG (Nucleotides 415 to 1401 of SEQ ID NO: 307) [SEQ ID NO: 314] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNNAKT KPREEQYN STYRVSVSLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPDSIAVEWESNGQP ENNYKTTTPPVLDSDGSFF

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGCGTGACACACCTTCCCGGTGTC CTACAGTCCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCCAAATCTTGTGACAAAAC CACACATGCCCCACCGTGCCCGAGCAC CTGAACCTCCTGGGGGACCGTCAGT CTTCTCTTCCCCCCCCAAACCCCAAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACACACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTGCAACAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAGGTC TCCAACAAAAGCCCTCCAGCCCCCA TCGAGAAAAACCATCTCCAAAGCCAA AGGGCAGCCCCCGAGAACACACAGGTG TACACCCCTGCCCCCATCCCCGGGATG AGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCCGTGGAGTGGG				LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 315]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AGAGCAATGGGCAGCGGGAGACAA CTACAAGACCACGCTCCCGTGCTG GACTCCGACGGCTCCTTCTTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTC TCATGCTCCGTGATGATGAGGCTC TGCACAACCACTACACGCAAGAGAG CCTCTCCCTGTCTCCCGGGAATGA				
7G6- HCzu1 4	With leader [SEQ ID NO: 316]: ATGGGCTGGTCTGTCATCATCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCGAAGTGACGCTGCTGGAA TCTGGCGCGGACTGGTGCAGCCTG CGGGCTCTGTGAGACTGTCTTGTC GCGCTCCGGCTACACCTTCAACACC TACTGGATCACCTGGTCCGACAGG CTCCCGCAAGGACTGGAATGGT CGGAGACATCTACCCCGCTCCTCC ATCTGCAACTACGCCGACAAAGTTCA AGGCCGGTTACCATCTCCGTGGA CAACTCAAAGTCCACCGCTACCTC CAGATGAACCTCCCTGAGAGCCGAG ACACCGCGGTACTACTCGGCCAG AGAGACGGCTACGACGCTTGGTT GCTTACTGGGCCAGGCCACCTGG TCACCGTGTCTGTCATCCACCAA GGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGTGAACCTCAGGCGCC	With leader [SEQ ID NO: 317]: MGWSCIIILFLVATATGVHSEVQ LLESGGLVQPGGSLRLSCAAS GYTFYTWITWVRQAPGKGLEW VGDIYPGSSICNYADKFKGRFT ISVDNSKSTAYLQMNLSRAEDT AVYYCAREDDYDAWFAYWQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGLVVDYFPEPT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCD KTHICTPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL	ATGGGCTG GTCTGCA TCATCTG TTTCTGGT GGCACCG CCACCGG GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 316) [SEQ ID NO: 319]	GAAGTGCAGCTGCTGGAA TCTGGCGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTGTGCGCGC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGG AAGGACTGGAATGGGTC GGAGACATCTACCCCGG TCCTCCATCTGCAACTAC GCCGACAAGTTCAAGGGC CGGTTACCATCTCCGTG GACAACTCAAAGTCCACC GCCTACCTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCGGTACTACTGC GCCAGAGAGGACGGCTAC GACGCTGGTTGCTTAC TGGGGCAGGACACCTGT GTACCGGTGCATCT (Nucleotides 58 to 414 of SEQ ID NO: 316) [SEQ ID NO: 320]	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCAC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCAGAACCG GTGACGGTGTCTGGAAC TCAGGCGCTGACCCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCCCAGC AACACCAAGGTGGACAAG AAAAGTTAGCCCAATCT TGTGACAAAACCTCACACA TGCCACACCGTGCCAGCA CCGTGAGTCTTCTCTTC CCCCCAAAACCAAGGAC ACCTCATGATCTCCCG ACCCCTGAGGTACATGC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGACGAGCGCGGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAAAATCTTGTA CAAAACCTACACATGCCACCGTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCAACTGTTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCCTCACCGTCTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCGCCTCC CGTGTGGAATCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAAT	SLSPGK Without leader [SEQ ID NO: 318]: EVQLLESGGGLVQPGGSLRLSC AASGYTFITYWITWVRQAPGKG LEWVDIYPGSSICNYADKFKG RFTISVDNSKSTAYLQMNSLRA EDTAVYYCAREDDGYDAWFAYWG QGTLVTVSSASTKGPSVFPLAP SSKTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYICNVNHPKSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLIMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYIT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK		EVQLLESGGGLVQPGGSL RLSCAASGYTFITYWITW VRQAPGKLEWVVDIYPG SSICNYADKFKGRFTISV DNSKSTAYLQMNSLRAED TAVYYCAREDDGYDAWFAY WGQTLVTVSS [SEQ ID NO: 321]	GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTC AGCGTCTCACCGTCCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCAACAAGGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCGAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG (Nucleotides 415)

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	<p>GAGGCTCTGCACAAACCCTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA</p> <p>Without leader [SEQ ID NO: 1134]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCGGAGAC ATCTACCCCGGCTCCTCCATCTGCA ACTAGCCGACAAAGTTCAAGGCGCG GTTACCATCTCCGTGGACAACTCC AAGTCCACCCCTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCGC CGTGTAATACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTTACT GGGGCCAGGGCACCCCTGGTCACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCTGCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCCTCAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTTGAATCACAAGCCCA GCAACACCAAGGTGGACAAAGAAAGT</p>				<p>to 1401 of SEQ ID NO: 316) [SEQ ID NO: 322]</p> <p>ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPS NTKVDKKEPKSCDKKTH CPPCPAPPELLGGPSVFLF PPKPKDTLMISRTPEVTC VVDVSHEDPEVKFNWYV DGEVHNAAKTKPREEQYN STYRVVSVLTVHLQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSL SLSPGK [SEQ ID NO: 323]</p>

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGAGCCCCAAATCTTGTGACAAACT CACACATGCCCCACCGTGCCCCAGCAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCCCCAAACCCCAAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTCTGACCAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAGGTC TCCAACAAAGCCCTCCCAAGCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCCGAGAACACACAGTG TACACCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAA CTACAAGACCAAGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGGGAAATGA				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
7G6-HC2u1 5	With leader [SEQ ID NO: 324]: <u>ATGGGCTGGTCTCTGCATCATCTCTGT</u> <u>TTCTGGTGGCCACCGCCACCGGCGT</u> <u>GCACAGCGAAGTGCAGCTGCTGGAA</u> <u>TCTGGCGGCGGACTGGTGACGCTG</u> <u>GCGGCTCTCTGAGACTGCTTGTGC</u> <u>CGCTCCGGCTACACCTTCACCACC</u> <u>TACTGGATCACCTGGTCCGACAGG</u> <u>CTCCCGGCAAGGACTGGAATGGT</u> <u>CGGAGACATCTACCCCGGCTCCTCC</u> <u>ATCTGCAACTACAACAGAGATTCA</u> <u>AGTCCCGGTTACCATCTCCGTGGA</u> <u>CAACTCCAAGAACACCGCTACCTC</u> <u>CAGATGAACCTCCCTGAGAGCCGAG</u> <u>ACACCGCGGTGTACTACTGCGCCAG</u> <u>AGAGGACGGCTACGACGCTTGGTTT</u> <u>GCTTACTGGGCGCAGGCCCTCTG</u> <u>TCACCGTGTCTATCTGCATCCACAA</u> <u>GGGCCCATCGGTCTTCCCCCTGGCA</u> <u>CCCTCTCCAAGACACCTCTGGGG</u> <u>GCACAGCGCCCTGGGCTGCCTGGT</u> <u>CAAGGACTACTTCCCCGAACCGGTG</u> <u>ACGGTGTCTGGAACCTCAGGCGCC</u> <u>TGACAGCGCGCTGCACACCTTCCC</u> <u>GGCTGTCTACAGTCTCTCAGGACTC</u> <u>TACTCCCTCAGACGCTGGTACCG</u> <u>TGCCCCTCAGCAGCTTGGGCACCCA</u> <u>GACCTACATCTGCAACGTGAATCAC</u> <u>AAGCCCAGCAACACCAAGGTGGACA</u> <u>AGAAAGTTGAGCCCCAAATCTTGTA</u>	With leader [SEQ ID NO: 326]: MGWSCIIILFLVATATGVHSEVQ LLESGLLVQPPGSLRLSCAAS GYTFTTYWITWVRQAPGKLEW VGDIYPGSSICNYNEKFSRFT ISVDNSKNTAYLQMNLSRAEDT AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSVVTVTPSSSLGTQTYI CNYNHKPSNTKVDKKVEPKSCD KTHCTCPPCPAPELGGPSVFLF PPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRWVSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGFSFLYSLKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK Without leader [SEQ ID NO: 327]: EVQLLESGLLVQPPGSLRLSC AASGYTFTTYWITWVRQAPGK LEWVGDIYPGSSICNYNEKFS RFTISVDNSKNTAYLQMNLSRA	ATGGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 324) [SEQ ID NO: 328]	GAAGTGACAGCTGCTGGAA TCTGGCGGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTTGTGCCGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGGC AAGGACTGGAATGGGTC GGAGACATCTACCCCGGC TCCTCCATCTGCAACTAC AACGAGAAGTTCAGATCC CGGTTCACCATCTCCGTG GACAACTCCAAGAACACC GCCTACTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCGTGTACTACTAGC GCCAGAGAGACGGCTAC GACGCTTGGTTGCTTAC TGGGCGCAGGCGACCCCTG GTCACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 324) [SEQ ID NO: 329] EVQLLESGLLVQPPGSL RLSCAASGYTFTTYWITW VRQAPGKLEWVGDIYPG SSICNYNEKFSRFTISV DNSKNTAYLQMNLSRAED TAVYYCAREDDYDAWFAY WGQGLTVTVSS [SEQ	ATGGGCTGGTCTCTGCATC ATCTGTTTCTGGTGGCC ACCGCCACCGGCGTGCAC AGCGAAGTGCAGCTGCTG GAATCTGGCGGCGGACTG GTGCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCC GCCTCCGGCTACACCTTC ACCACCTACTGGATCAC TGGGTCCGACAGGCTCCC GGCAAGGACTGGAATGG GTCGAGACATCTACCCC GGCTCTCTCATCTGCAAC TACAACGAGAAGTTCAAG TCCCGGTTACCATCTCC GTGGACAACCTCCAAGAAC ACCGCTACCTCCAGATG AACTCCCTGAGAGCCGAG GACACCGCGCTGTACTAC TGCGCCAGAGAGGACGGC TACGACGCTTGGTTGTCT TACTGGGCGCAGGCGCAC CTGGTCACCGTGTCTATCT GCATCCACCAAGGCCCCA TCGGTCTTCCCCCTGGCA CCCTCTCTCAAGAGCACCC TCTGGGCGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGCGGCTGTGACCGC GGCGTGCACACCTTCCCC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAAAACACACATGCCACCGTGC CCAGACCTGAATCCTGGGGGAC CGTCAGTCTTCTCTCCCGCCAAA ACCCAAGGACACCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGG TGGTGACGTGAGCCACGAAGACC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCTCACCGTCTGCACCGAGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCGAGAAC ACAGGTGTACACCTGCCCGCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGAGCCGG AGAACAACTACAAGACCGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 325]: GAAGTGCAGCTGCTGGAATCTGGCG	EDTAVYYCAREDDGYDAWFAYWG QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVWTPSSSLGTQ TYICNVNHPKPSNTKVDKKVEPK SCDKHTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTI SKAGQPPEPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFCFVSMHEALHNHYTQ KSLSLSPGK		ID NO: 330]	GCTGTCTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAAGCCCCAGC AACACCAAGGTGGACAAG AAAGTTGAGCCCCAAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCCAGCA CCTGAACCTCTGGGGGA CCGTCAGTCTTCTCTTTC CCCCACAAACCCAAAGGAC ACCCTCATGATCTCCCGG ACCCTGAGGTCACATGC GTGGTGGTGACGTGAGC CACGAAGACCTGAGGTC AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGGAGGAGCAGTACAAC AGCAGTACCGTGTGGTC AGCGTCTCACCGTCTTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCAACAAAGGCC CTCCCAGCCCCCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTTG CCCCCTATCCCGGATGAG CTGACCAAGAACCAGGTC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCCGAGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAACGAGAAGTCAAGTCCCG GTTACCATCTCCGTGGACAACCTCC AAGAACACCCCTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCGC CGTGTAATACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTACT GGGCCAGGGCACCCCTGGTCAACGT GTCACTGTCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCC TCAGCAGCTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAAATCTTGTACAAAAT CACACATGCCCCACCGTGCCAGCAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCCCCAACCCAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC				AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTG GAGAGCAATGGGAGCCG GAGAACAACTACAAGACC ACGCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGAT GAGGCTCTGCACAACCAC TACACGAGAAGAGCCCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401 of SEQ ID NO: 324) [SEQ ID NO: 331] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVIQSSGLYSLSVVTVP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVSVLTVHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACACACGC ACGTACCGTGTGGTCAGCGTCCTCA CCGTCTGTCACACGAGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAGTC TCCAAACAAAGCCCTCCACGCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGCAGCCCCCGAGAACACACAGGTG TACACCTGCCCCCATCCCGGGATG AGCTGACCAAGAACACAGGTACGCT GACCTGCCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGACGCCGGAGAACAA CTACAAGACACGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGATGAGGCTC TGCACAACCACTACACGCAAGAGAG CCTCTCCCTGTCTCCCGGAAATGA				PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 332]
7G6-HCzu16	With leader [SEQ ID NO: 333]: ATGGGCTGGTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGAAGTGCAGCTGCTGGAA TCTGGCGCGGACTGGTGCACCGCTG GCGGCTCTCTGAGACTGTCTTGTGC CGCTCCGGCTACACCTTCACCACC TACTGGATCACCTGGGTCCGACAGG CTCCCGGCAAGGACTGGAATGGGT CTCCGACATCTACCCCGGCTCCTCC	With leader [SEQ ID NO: 335]: MGWSCIILFLVATATGVHSEVQ LLESGGGLVQPGGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VSDIYPGSSICNYNEKFKSRFT ISVDNSKNTAYLQMNLSRAEDT AVYICAREGDYDAWFAYWQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSS	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of	GAAGTGCAGCTGCTGGAA TCTGGCGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTGTGCCGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGGC AAGGACTGGAATGGGT TCCGACATCTACCCCGGC TCCTCCATCTGCAACTAC AACGAGAAAGTTCAAGTCC	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCTCCTCCAAGAGCACCC TCTGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGGGAAC TCAGGCGCCTGACCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCA GGACTCTACTCCCTCAGC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ATCTGCAACTACAACGAGAGTTCA AGTCCCGGTTACCATCTCCGTGGA CAACTCAAAGAACACCGCCTACCTC CAGATGAACCTCCCTGAGAGCCGAGG ACACGCCGTGTACTACTGCGCCAG AGAGACGGCTACGACGCTTGTTT GCTTACTGGGGCCAGGGCACCTGG TCACCGTGTATCTGCATCCACCAA GGGCCATCGGTCTTCCCTCTGGCA CCCTCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCGAACCCGGTG ACGGTGTCTGGAACCTCAGCGGCC TGACAGCGCGGTGCACACCTTCCC GGCTGCTCAGTCTCAGGACTC TACTCCCTCAGCAGCTTGGGCACCCA TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTCAA ACCAAGGACACCCCTCATGATCTC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCACTGGTACGTG GACGGGTGGAGTGCATAATGCCA AGACAAAGCCGGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAG GTCCTCACCGTCTGCACCGAGACT GGCTGAATGGCAAGGAGTACAAGTG	GLYSSSVTVPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHCTPPCPAPELIGPVSFLF PPKPKDTLMI SRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRWVSLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFELYSLKLTVDKSRWQ GNVFCSTMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 336]: EVQLLESGGGLVQPGGSLRLSC AASGYSFSTYITWVRQAPGK LEWVSDIYPGSSICNYNEKFKS RFTISVDNSKNTAYLQMNSLRA EDTAVYYCAREDDGYDAWFAYWG QGTLLTVSSASTKGPSVFLAP SSKSTSGGTAALGLVLDYFPE PVTVSNWNGALTSVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPK SCDKHTKCPPELIGPVS FLPFPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRWVSL TVLHQDWLNGKEYKCKVSNKAL PAPIETISKAKGQPREPQVYT	SEQ ID No: 333) [SEQ ID No: 337]	CGGTTACCATCTCCGTG GACAACTCAAAGAACACC GCCTACTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCCGTGTACTACTGC GCCAGAGGACGGCTAC GACGCTGGTTTGTCTTAC TGGGGCCAGGGCACCCCTG GTACCCGTGTCTCT (Nucleotides 58 to 414 of SEQ ID NO: 333) [SEQ ID No: 338] EVQLLESGGGLVQPGGSL RLSCAASGYSFTTYITW VRQAPGKLEWVSDIYPG SSICNYNEKFKSRFTISV DNSKNTAYLQMNSLRAED TAVYYCAREDDGYDAWFAY WGQGLVTVSS [SEQ ID No: 339]	AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCGACG AACACCAAGGTGGACAAG AAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCGACGA CCTGAACCTCTGGGGGA CCGTCACTCTTCTCTTC CCCCCAAAACCAAGGAC ACCCCTCATGATCTCCCG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CAGGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGAGGAGCAGTACAAAC AGCACGTACCGTGTGGTC AGCGTCTTACCGTCTTG CACCAGGACTGGTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCAACAAGACC CTCCAGCCCCCATCGAG AAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCGACG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGAGAGCAATGGGAGCCGG AGAACAACTACAAGACCACGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACG AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 334]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCTCCGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAAACGAGAAGTTCAAGTCCCG GTTCACCATCTCCGTGGACAACCTCC AAGAACACCCGCTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCCG CGTGTAATACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTCTTACT	LPSPRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMEALHNHYTQ KSLSLSPGK			GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGGAAA TGA (Nucleotides 415 to 1401 of SEQ ID NO: 333) [SEQ ID NO: 340] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTVF SSSLGTQTYICNVNHKPS NTKVDKKEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVVSVLTVHLQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GGGGCCAGGGCACCCCTGGTCACCGT GTCACTGTCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGGGTGCACACCTTCCCGGTGTC CTACAGTCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAACTTGTGACAAAACCT CACACATGCCCCACCGTGCCCCAGCAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCCCCAAACCCCAAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTGTCACCAAGGACTGGCTGAA TGGCAAGGAGTACAAAGTCAAGGTC TCCAAACAAAGCCCTCCCAAGCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCACAGGTG TACACCCCTGCCCCCATCCCCGGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAGAGGCTTCTAT				KGFPSPDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMEALHNHHTQKSL SLSPGK [SEQ ID NO: 341]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CCGAGCGACATCGCCGCTGGAGTGGG AGAGCAATGGGAGCCGGAGAACAA CTACAAGACACGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGAGAGAGAG CCTCTCCCTGTCTCCCGGGAATGA				
7G6-HC2u1	With leader [SEQ ID NO: 342]: ATGGCTGGTCTGTCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGGAAGTGCAGCTGCTGGAA TCTGGCGCGGACTGGTGCAGCCTG GCGGCTCTCTGAGACTGTCTTGTG CGCTCCGGCTACACCTTCACCCACC TACTGGATCACCTGGGTCGACACAGG CTCCCGCAAGGACTGGAATGGGT CTCCGACATCTACCCCGGCTCCTCC ATCTGCAACTACACGAGAGATCA AGTCCCGGTTACCATCTCCGTGGA CAACTCCAAGAACACCTGTACCTC CAGATGAACCTCCCTGAGAGCCGAGG ACACCGCGGTGACTACTGCGCCAG AGAGACGGCTACGACGCTTGTTT GCTTACTGGGCGGAGGACCCCTGG TCACCTGTGATCTGCATCCACCAA GGGCCCCATCGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGG GCACAGCGGCCCTGGGCTGCCTGGT	With leader [SEQ ID NO: 344]: MGWSCIIILFLVATATGVHSEVQ LLESGGLVQPGGSLRLSCAAS GYFTTYITWVRQAPGKLEW VSDIYPGSSICNYNEKFSRFT ISVDNSKNTLYLQMSLRAEDT AVYYCAREDDYDAWFAYWQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLIMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGDSFFLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCCGG GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 342) [SEQ ID NO: 346]	GAAGTGCACTGCTGGAA TCTGGCGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTGTGCGGCC TCCGGCTACACCTTCACC ACCTACTGGATCACTGG TCCGACAGGCTCCCGGC AAGGACTGGAATGGGTC TCCGACATCTACCCCGGC TCCTCCATCTGCAACTAC AACGAGAAATCAAGTCC CGGTTACCATCTCCGTG GACAACCTCAAGAACACC CTGTACTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCCGTGACTACTGC GCCAGAGAGACGGCTAC TGGGCTGGTTGCTTAC TGGGCGGAGGACCCCTG GTACCCGTGCATCT (Nucleotides 58 to 414 of SEQ ID NO: 342)	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTACGGTGTCTGTGGAAC TCAGGCGCCTGACCCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAAGCCACG AACACCAAGGTGGACAAG AAAGTTGAGCCCAAAATCT TGTGACAAAACTCACACA TGCCCAACCGTGCCACGA CCTGAACCTCTGGGGGGA CCGTAGTCTTCTCTTC CCCCCAAAACCAAGGAC ACCTCATGATCTCCCGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACCTCAGGCGCCC TGACCAGCGCGGTGCACACCTTCCC GGCTGTCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGTGACCG TGCCCTCCAGCAGCTTGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCACCCGTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGCGGTGAGGTGCATAATGCCA AGACAAAGCCCGCGGAGGAGCAGTA CAACAGCACGTACCGTGTGTCAGC GTCTCACCCTCTGCAACCAAGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCCCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCTGTGACCTGCCTGGTCAAAGG CTTCTATCCCAGGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCCG AGAACAACACTACAAGACCAACCCCTC CGTGTGGAATCCGACGGCTCCTTC TTCTTATATTTCAAAGCTCACCGTGG	SLSPGK Without leader [SEQ ID NO: 345]: EVQLLESGGGLVQPGGSLRLSC AASGYTFTTYWITWVRQAPGKG LEWVSDIYPGSSICNYNEKFKS RFTISVDNSKNTLYLQMNSLRA EDTAVYYCAREDDGYDAWFAYWG QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTWSNSGALTSGVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYICNVNHPKSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLIMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYIT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK		[SEQ ID NO: 347] EVQLLESGGGLVQPGGSL RLSCAASGYTFTTYWITW VRQAPGKLEWVSDIYPG SSICNYNEKFKSRFTISV DNSKNTLYLQMNSLRAED TAVYYCAREDDGYDAWFAY WGQGLTVTVSS [SEQ ID NO: 348]	ACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGC CACGAAGACCCCTGAGGTG AAGTTCAAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAAGCCG CGGAGGAGCAGTACAAC AGCAGTACCGTGTGGTC AGCGTCTCACCGTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAGGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCCCTG CCCCCATCCCGGATGAG CTGACCAAGAACCAAGTGC AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 343]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTACCACTACTGGA TCACCTGGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCTCCGAC ATCTACCCCGGCTCTCCATCTGCA ACTACAACGAGAAGTTCAAGTCCCG GTTCACCATCTCCGTGGACAACCTCC AAGAACACCCCTGTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCGC CGTGTAATACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTACT GGGCCAGGGCACCCCTGGTCACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACTCAGGCGCCCTGACCAG CGGCGTGACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC				(Nucleotides 415 to 1401 of SEQ ID NO: 342) [SEQ ID NO: 349] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFPYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 350]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ATCTGCAACGTTGAATCACAAGCCCA GCAACACCAAGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAAAGT CACACATGCCACCGTGCCACAGCAC CTGAACTCCTGGGGGACCGTCAGT CTTCTCTTCCCCCCCCAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTACGCTCCTCA CCGTCTGTGACACAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAGGTC TCCAAACAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCACAGGTG TACACCCCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCCGGAGAACAA CTACAAGACCAAGCCCTCCCGTGCTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCCGGGAAATGA				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
7G6-HC2u18	With leader [SEQ ID NO: 351]: ATGGGCTGGTCTGTCATCATCTCTGT TTCTGGTGGCCACCGCCACCGCGGT GCACAGCGAAGTGACGCTGCTGGAA TCTGGCGGCGGACTGGTGACGCTG GCGGCTCTCTGAGACTGCTTGTGC CGCTCCGGCTACACCTTCACCAC TACTGGATCACCTGGTCCGACAGG CTCCCGGCAAGGACTGGAATGGGT CTCGACATCTACCCCGGCTCCTCC ATCTGCAACTACACAGAGAGTTCA AGTCCCGGTTACCATCTCCCGGA CAACTCCAAGAACACCTGTACCTC CAGATGAACCTCCCTGAGAGCCGAG ACACCGCGGTGTACTACTGCGCCAG AGAGGACGGCTACGACGCTTGGTT GCTTACTGGGCGGACGACCTG TCACCGTGTCTATCTGCATCCACCA GGGCCCATCGGTCTTCCCGCTGGCA CCCTCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCGAACCGGTG ACGGTGTGCTGGAACCTAGGCGCC TGACAGCGCGGTGCACACCTTCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGTGGACA AGAAAGTTGAGCCCAAACTTGTGA	With leader [SEQ ID NO: 353]: MGWSCIIILFLVATATGVHSEVQ LLESGGGLVQPGGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VSDIYPGSSICNYNEKFKSRFT ISRDNKNTLYLQMNSLRAEDT AVYYCAREDDGYDAWFAYWGQT LVTSSASTKPSVFPLAPSSK STSGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSVTVTPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHCTPPCPAPELIGLSPVFLF PPKPDITLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK Without leader [SEQ ID NO: 354] EVQLLESGGGLVQPGGSLRLSC AASGYTFITYWITWVRQAPGK LEWVSDIYPGSSICNYNEKFKS RFTISRDNKNTLYLQMNSLRA EDTAVYYCAREDDGYDAWFAYWG	ATGGGCTG GTCCTGCA TCATCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 351) [SEQ ID NO: 355]	GAAGTGACAGTGTGGAA TCTGGCGGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTTGTGCCGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGGC AAGGACTGGAATGGGT TCCGACATCTACCCCGC TCCTCCATCTGCAACTAC AACGAGAAGTTCAGTCC CGGTACCATCTCCCGG GACAACTCCAAACACAC CTGTACTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCGTGTACTACTGC GCCAGAGAGGACGGCTAC GACGCTGTGTTGCTTAC TGGGCGCAGGCGACCTG GTCACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 351) [SEQ ID NO: 356] EVQLLESGGGLVQPGGSL RLSCAASGYTFITYWITW VRQAPGKLEWVSDIYPG SSICNYNEKFKSRFTISR DNKNTLYLQMNSLRAED TAVYYCAREDDGYDAWFAY WGQGLTVSS	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCC TCTGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAAACCG GTGACGGTGTCTGTGAAC TCAGGCGGCTGACCAAGC GGCGTGCACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCCAAGC AACACCAAGGTGGACAAG AAAGTTGAGCCCAAACTCT TGTGACAAAACCTCACACA TGCCACCGTGCCCGAGCA CCTGAACCTCTGGGGGA CCGTACAGTCTTCTCTTC CCCCAAAACCAAGGAC ACCTCATGATCTCCCGG ACCCCTGAGGTACATGC GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGGAGGAGCAGTACAC AGCACGTACCGTGTGGTC AGCGTCTCTACCGTCTCTG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAAAACATCACACATGCCACCCGCTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGG TGGTGACGCTGAGCCACGAAGACC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCTCACCGTCTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCGGAGAAC ACAGGTGTACACCCCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAAGCCTCC CGTGTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCA GAGGCTCTGCACAACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 352]: GAAGTGCAGCTGCTGGAATCTGGCG	QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTQ TYICNVNHPKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMEALHNHYTQ KSLSLSPGK		[SEQ ID NO: 357]	CACCAGGACTGGTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAGCC CTCCAGCCCTCATCGAG AAAACCATCTCCAAAGCC AAAGGGCAGCCCCCGAGAA CCACAGGTGTACACCTG CCCCCTCCCGGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGCAGCCG GAGAACAACTACAAGACC AGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401 of SEQ ID NO: 351) [SEQ ID NO: 358] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVTVTP

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCTCCGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACAACGAGAAATTCAAGTCCCG GTTACCATCTCCGGGACAACTCC AAGAACACCTGTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCGC CGTGTAATACTGCGCCAGAGAGGAC GGCTACGACGCTTGTTTGCTTACT GGGCCAGGGCACCCCTGGTCACCGT GTCACTGTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGACACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTC CTACAGTCTCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAAATCTTGACAAAAGT CACACATGCCCCACCGTCCCGACAC CTGAACCTCTGGGGGACCGTCAGT CTTCTCTTCCCCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC				SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMISRTPEVTC VWVDVSHEDPEVKFNWYV DGEVHNAAKTKPREEQYN STYRVSVLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 359]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACACACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTGCACACAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAGTC TCCAAACAAAGCCCTCCACGCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGCGAGCCCCGAGAACACACAGGTG TACACCTGCCCCCATCCCGGGATG AGCTGACCAAGAACACAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCGAGCCGGAGAACAA CTACAAGACACAGCCTCCCGTGTG GACTCCGACGGCTCCTCTTCTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGATGAGGCTC TGCACAACTACTACACGACAGAGAG CCTCTCCCTGTCTCCCGGAAATGA				
7G6-HCzu1 9	With leader [SEQ ID NO: 360]: ATGGGCTGGTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGAAGTGCAGCTGCTGGAA TCTGGCGCGGACTGGTGCAGCCTG GCGGCTCTCTGAGACTGTCTTGTGC CGCTCCGGCTACACCTTCACCAC TACTGGATCACCTGGGTCCGACAGG CTCCCGCAAGGACTGGAATGGGT CTCCGACATCTACCCCGGCTCCTCC	With leader [SEQ ID NO: 362]: MGWSCIIILFLVATATGVHSEVQ LLESGGGLVQPGGSLRLSCAAS GYTFTTYWITWVRQAPGKGLEW VSDIYPGSSICNYADKFKGRFT ISRDNSKNTLYLQMNSLRAEDT AVYYCAREDDYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPV	ATGGGCTG GTCCTGCA TCATCTGT TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of	GAAGTGCAGCTGCTGGAA TCTGGCGGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTGTGCGCGC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCACAGGCTCCCGGC AAGGACAGGAAATGGGT TCCGACATCTACCCCGG TCCTCCATCTGCACTAC GCCGACAAAGTTCAAGGGC	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGGAAC TCAGGCGGCTGACCCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ATCTGCAACTACGCCGACAAAGTTCA AGGGCCGGTTACCATCTCCCGGA CAACTCCAAGAACACCTGTACCTC CAGATGAACCTCCCTGAGAGCCGAGG ACACGCCGTGTACTACTGCGCCAG AGAGACGGCTACGACGCTTGTTT GCTTACTGGGGCCAGGCCACCTGG TCACCGTGTATCTGCATCCACCAA GGGCCATCGTCTTCCCTCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCGAACCCGGTG ACGGTGTCTGGAACCTCAGCGCCC TGACAGCGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTC TACTCCCTCAGCAGCTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTCAA ACCAAGGACACCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCAACTGGTACGTG GACGGCTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAG GTCCTCACCGTCTGCACCAAGGACT GGCTGAATGGCAAGGAGTACAAGTG	VSWNSGALTSVHTFPAVLQSS GLYSLSSVTVPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHCTPPCPAPELLGGPSVFLF PPKPKDTLIMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK Without leader [SEQ ID NO: 363]: EVQLLESGGGGLVQPGGSLRLSC AASGYSFTTITWVRQAPGKG LEWVSDIYPGSSICNYADKFKG RFTISRDNSKNTLYLQMNSLRA EDTAVYYCAREDDYDAWFAYWG QGTLLTVSSASTKGPSVFPLAP SSKSTSGGTAALGLVQDYFPE PVTVSWNSGALTSVHTFPAVL QSSGLYSLSVWTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLPPKPKDTLIMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL	SEQ ID NO: 360) [SEQ ID NO: 364]	CGGTTACCATCTCCCGG GACAACTCCAAGAACACACC CTGTACTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCCGTGTACTACTGC GCCAGAGGACGGCTAC GACGCTGGTTTGTCTTAC TGGGGCCAGGGCACCCCTG GTACCCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 360) [SEQ ID NO: 365] EVQLLESGGGGLVQPGGSL RLSCAASGYSFTTITW VRQAPGKLEWVSDIYPG SSICNYADKFKGRFTISR DNSKNTLYLQMNSLRAED TAVYYCAREDDYDAWFAY WGQGLVTVSS [SEQ ID NO: 366]	AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCGACG AACACCAAGGTGGACAAG AAAGTTGAGCCCAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCCGAGCA CCTGAACCTCTGGGGGA CCGTCACTTCTCTCTTC CCCCCAAAACCAAGGAC ACCCCTCATGATCTCCCG ACCCCTGAGGTACATGTC GTGGTGGTGGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGAGGAGCAGTACAAAC AGCACGTACCGTGTGGTC AGCGTCTTACCGTCTCTG CACCAAGGAGTACAAGTGC GAGGTCTCAACAAGGCC CTCCAGCCCGCCATCGAG AAAACCATCTCCAAAGCC AAAGGCGAGCCCGAGAA CCACAGGTGTACACCTGT CCCCCATCCCGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCGAC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCAGCCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGAGCCGG AGAACAACTACAAGACCACGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 361]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCTCCGAC ATCTACCCCGGCTCCTCCATCTGCA ACTACGCCGACAAAGTTCAAGGCCG GTTCACCATCTCCCGGACAACTCC AAGAACACCCCTGTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCCG CGTGTAATACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTCTTACT	PAPIEKTISKAKGQPREPQVYTT LPFSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK			GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGG (Nucleotides 415 to 1401 of SEQ ID NO: 360) [SEQ ID NO: 367] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH CPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAAKTKPREEQYN STYRVSVLTFLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GGGGCCAGGGCACCCCTGGTCACCGT GTCACTGTCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGAACTCAGGCGCCCTGACCAG CGGCGTGACACCTTCCCGGTGTC CTACAGTCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAACTTGTGACAAACT CACACATGCCCCACCGTGCCCGAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCAAAACCCCAAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGTGCATAATGCCAAGACAAA GCCCGGGAGGAGCAGTACACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTTGACACGAGACTGGCTGAA TGGCAAGGAGTACAAAGTCAAGGTC TCCAAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACACAGGTG TACACCTTGCCCCCATCCCCGGGATG AGCTGACCAAGAACACAGGTACGCT GACCTGCCTGGTCAAGGGCTTCTAT				ENNYKTTTPVLDSGSGFF LYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSL SLSPGK [SEQ ID NO: 368]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CCGAGCGACATCGCCGCTGGAGTGGG AGAGCAATGGGAGCCGGAGAACAA CTACAAGACACAGCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGACAAACCACTACACGACAGAGAG CCTCTCCCTGTCTCCCGGGAATGA				
7G6-HCzu20	With leader [SEQ ID NO: 369]: ATGGCTGGTCTGTCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGGAAGTGAGCTGCTGGAA TCTGGCGCGGAGTGGTGCAGCCTG CGGCTCTCTGAGACTGTCTTGTG CGCTCCGGCTACACCTTCACCA TACTGGATCACCTGGTCCGACAGG CTCCCGCAAGGAGTGAATGGGT CTCCGACATCTACCCGGCTCCTCC ATCTGCAACTACCGCGACAAGTCA AGGCGCGTTACCATCTCCCGGA CAACTCAAAGAACACCTGTACCTC CAGATGAACCTCCCTGAGAGCCGAG ACACCGCGTGTACTACTGCGCCAA AGAGACGGCTACGACGCTTGTTT GCTTACTGGGCGAGGACACCTGG TCACCGTGTCTGATGCATCCACCA GGGCCCCATCGTCTTCCCGCTGGCA CCCTCCTCCAAGAGCACCTCTGGG GCACAGCGGCCCTGGGCTGCCTGGT	With leader [SEQ ID NO: 371]: MGWSCIIILFLVATATGVHSEVQ LLESGGLVQPGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VSDIYPGSSICNYADKFGRT ISRDNSKNTLYLQMSLRAEDT AVYYCAKEDGYDAWFAYWGQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGLVKDYFPEPT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVFSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYCKVSNKALPAP IEKTIKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LSDSGSFYLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCACCG CCACCGG GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 369) [SEQ ID NO: 373]	GAAGTGACAGTGTGGAA TCTGGCGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTGTGCGGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG TCCGACAGGCTCCCGG AAGGACTGGAATGGGTC TCCGACATCTACCCCGG TCCTCCATCTGCAACTAC GCCGACAAGTTCAAGGG CGGTTACCATCTCCCGG GACAACCTCAAAGAACAC CTGTACTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCGCTGTACTACTGC GCCAAGAGAGCGGCTAC GAGGCTGGTTGTCTTAC TGGGCGGAGGACACCTG GTCCCGGTGCATCT (Nucleotides 58 to 414 of SEQ ID NO: 369)	GCATCCACCAAGGGCCCA TCGGTCTTCCCGCTGGCA CCCTCCTCCAAAGAGCAC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCGGAACCG GTACGGTGTCTGTGGAC TCAGGCGCCTGACCCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCACG AACACCAAGGTGGACAAG AAAGTTGAGCCCAAAATCT TGTGACAAAACCTCACACA TGCCCAACCGTGCCAGCA CCTGAACCTCTGGGGGA CCGTAGTCTTCTCTTC CCCCCAAAACCAAGGAC ACCTCATGATCTCCCGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACTCAGGGCCCC TGACCAGCGCGTGCACACCTTCCC GGCTGTCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCCAAATCTTGTA CAAAACTCACACATGCCACCCGTGC CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCTCACCCTCTGCAACCAAGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAAC ACAGGTGTACACCCCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCTGTGACCTGCCTGGTCAAAGG CTTCTATCCCAGGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCCG AGAACAACACTACAAGACCAACGCTCC CGTGTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG	SLSPGK Without leader [SEQ ID NO: 372]: EVQLLESGGGLVQPGGSLRLSC AASGYTFITYWITWVRQAPGKG LEWVSDIYPGSSICNYADKFKG RFTISRDN SKNTLYLQMN SLRA EDTAVYYCAKEDGYDAWFAYWG QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTWSN SGALTSVHTFPAVL QSSGLYSLSSVWTVPSSSLGTQ TYICNVN HKPSNTKVDKKVEPK SCDKTHTCPPCPAPEL LGGPSV FLFPPKPKDTLIMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYIT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCVMHEALHNHYTQ KSLSLSPGK		[SEQ ID NO: 374] EVQLLESGGGLVQPGGSL RLSCAASGYTFITYWITW VRQAPGKGLEWVSDIYPG SSICNYADKFKGRFTISR DNSKNTLYLQMN SLRAED TAVYYCAKEDGYDAWFAY WGQGLVTVSS [SEQ ID NO: 375]	ACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGC CACGAAGACCCCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAAGCCG CGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTC AGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAGGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCCGTG CCCCCATCCCGGGATGAG CTGACCAAGAACCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCTCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAGAGCCTC TCCCTGTCTCCCGGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 370]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTACCACTACTGGA TCACCTGGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGTCTCCGAC ATCTACCCCGGCTCTCCATCTGCA ACTACGCCGACAAAGTTCAAGGCCG GTTCACCATCTCCGGGACAACTCC AAGAACACCCCTGTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCGC CGTGTACTACTGCGCCAAAGAGGAC GGCTACGACGCTTGGTTTGTACT GGGCCAGGGCACCCCTGGTCACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCT CCAAGAGCACCTCTGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACTCAGGCGCCCTGACCAG CGGCGTGACACCTTCCCGGCTGTC CTACAGTCCCTCAGGACTCTACTCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC				(Nucleotide 415 to 1401 of SEQ ID NO: 369) [SEQ ID NO: 376] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTVTP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVVSVLTVHLQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFPSPDIAVEWESNGQP ENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 377]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	ATCTGCAACGTTGAATCACAAGCCCA GCAACACCAAGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAAAGT CACACATGCCACCGTGCCACGAC CTGAACTCCTGGGGGACCGTCAGT CTTCTCTTCCCCCCCCAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCGTGAGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTACGCTCCTCA CCGTCTGTGACACAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAGGTC TCCAAACAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCCACAGGTG TACACCCCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTACGCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAA CTACAAGACCAAGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTAT ATTCAAAGCTCACCGTGGACAAAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGGGAAATGA				

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
7G6-HC2u2 3	With leader [SEQ ID NO: 378]: ATGGGTGGTCTGTCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCGAAGTGACGCTGCTGGAA TCTGGCGGCGGACTGGTGACGCTG GCGGCTCTCTGAGACTGCTTGTGC CGCTCCGGCTACACCTTCAACACC TACTGGATCACCTGGTCCGACAGG CTCCCGCAAGGACTGGAATGGGT GTCCGACATCTACCCCGCTCCTCC ATCTCCAATACGCCGACTCCGTCA AGGCCGGTTACCATCTCCCGGA CAACTCAAAGAACCCCTGTACCTC CAGATGAACCTCCCTGGGGCCGAGG ACACCGCCGTACTACTCGGCCAG AGAGGACGGCTACGACGCTTGGTT GCCTACTGGGGCCAGGCCACCTGG TCACCGTGTCTATCGCTCCACCAA GGGCCCATCGGTCTTCCCGCTGGCA CCCTCCTCCAAGACACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACTCAGGCGCC TGACAGCGGCGTGCACACCTCCC GGTGTCTCTACAGTCTCAGGACTC TACTCCTCAGACGCTGGTACCG TGCCCTCCAGACTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGA CAAAACTCACACATGCCACCGTGC	With leader [SEQ ID NO: 380]: MGWSCIIILFLVATATGVHSEVQ LLESGGGLVQPGGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VSDIYPGSSISNYADSVKGRFT ISRDNKNTLYLQMNSLRAEDT AVYFCAREDDGYDAWFAYWGQT LVTSSASTKPSVFPLAPSSK STSGTAALGCLVKDYFPEPTV VSWNSGALTSGVHTFPAVLQSS GLYSLSVTVTPSSSLGTQYI CNVNHKPSNTKVDKKVEPKSCD KTHCTPPCPAPELGGPSVFLF PPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNYTQKSL SLSPGK Without leader [SEQ ID NO: 381]: EVQLLESGGGLVQPGGSLRLSC AASGYTFITYWITWVRQAPGK LEWVSDIYPGSSISNYADSVK RFTISRDNKNTLYLQMNSLRA EDTAVYFCAREDDGYDAWFAYWG	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 378) [SEQ ID NO: 382]	GAAGTGACAGTGTGGAA TCTGGCGGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTTGTGCCGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGGC AAGGACTGGAATGGGTG TCCGACATACCCCGGC TCCTCCATCTCAACTAC GCCGACTCCGTCAAGGGC CGGTACCATCTCCCG GACAACTCCAAACACAC CTGTACTCAGATGAAC TCCCTGGCGGCGGAGGAC ACCCGCTGTACTACTGC GCCAGAGAGGACGGCTAC GACGCTGTGTTCCTTAC TGGGGCCAGGCGACCTG GTCACCTGTCTATCT (Nucleotides 58 to 414 of SEQ ID NO: 378) [SEQ ID NO: 383] EVQLLESGGGLVQPGGSL RLSCAASGYTFITYWITW VRQAPGKLEWVSDIYPG SSISNYADSVKGRFTISR DNKNTLYLQMNSLRAED TAVYFCAREDDGYDAWFAY WGQGLTVTSS	GCCTCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAAACCG GTGACGGTGTCTGTGAAC TCAGGCGGCTGACACAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCCCAGC AACACCAAGGTGGACAAG AAAGTTGAGCCCCAAATCT TGTGACAAAACCTCACACA TGCCACCGTGCCCGAGCA CCTGAACCTCTGGGGGA CCGTCAAGTCTTCTCTTC CCCCAAAACCAAGGAC ACCTCATGATCTCCCGG ACCCCTGAGGTACATGC GTGGTGGTGACGTGAGC CACGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGGAGGAGCAGTACAC AGCACGTACCGTGTGGTC AGCGTCTCTACCGTCTCTG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)	
	CCAGCACCTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCCGGGAGGAGCAGTA CAACAGCACGTACCGTGTGGTCAGC GTCTCACCGTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCGAGAACCC ACAGGTGTACACCTGCCCCCATCC CGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCCGTG GAGTGGGAGAGCAATGGGCGAGCGG AGAACAACTACAAGACCAACGCTCC CGTGTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGC AGAAGAGCCTCTCCCTGTCTCCCGG GAAATGA	QGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVVTPSSSLGTQ TYICNVNHKPSNTKVDKKVEPK SCDKTHCTCPPELLEGPSV FLFPPKDTLMI SRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMEALHNHYTQ KSLSLSPGK		[SEQ ID NO: 384]	CACCAGGACTGGCTGAAT GGCAAGGAGTACAAAGTGC AAGGTCTCCAACAAAGCC CTCCAGCCCCCATCGAG AAAAACCATCTCCAAAGCC AAAGGGCAGCCCCCGAGAA CCACAGGTGTACACCCCTG CCCCATCCCGGATGAG CTGACCAAGAACCCAGGTCT AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCGAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCGAGCCG GAGAACAACTACAAGACC AGCCTCCCGTGTCTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAGAGACCTC TCCCTGTCTCCCGGG (Nucleotides 415 to 1401 of SEQ ID NO: 378) [SEQ ID NO: 385]	ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTVTP
	Without leader [SEQ ID NO: 379]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC					

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TCTGAGACTGTCTTGTGCGGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGGTCCGACAGGCTCCCG CAAGGACTGGAATGGGTGTCGGAC ATCTACCCCGGCTCCTCCATCTCCA ACTACGCCGACTCCGTCAAGGCCG GTTACCATCTCCCGGACAACTCC AAGAACACCTGTACCTCCAGATGA ACTCCCTGCGGCGGAGACACCCG CGTGTACTACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTGCCTACT GGGGCAGGACACCTGGTCAACCGT GTCTATCTGCCTCCACCAGGGCCCA TCGGTCTTCCCCCTGGACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCGGCTGTC CTACAGTCTCTAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAAATCTTGTACAAAATCT CACACATGCCCCACCGTGCCCGAGCAC CTGAACCTCTGGGGGACCCGTCAGT CTTCTCTTCCCCCCCCAAACCCAG GACACCTCATGATCTCCCGGACCC CTGAGGTACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG				SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VWVDVSHEDPEVKFNWYV DGEVHNAKTKPREEQYN STYRVSVLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPDSIAVEWESNGQP ENNYKTTTPPVLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSL SLSPGK [SEQ ID NO: 386]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGAGAGTGCAATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTTGACACGAGACTGGCTGAA TGGCAAGGAGTACAAGTGCAAGGTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGAGCCCCCGAGAACACAGGTG TACACCTGCCCTCATCCCGGGATG AGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCCGGAGAACAA CTACAAGACCAAGCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGATGAGGCTC TGCACAACCACTACACGACGAGAG CCTCTCCCTGTCTCCCGGAAATGA				
7G6- HCzu2 4	With leader [SEQ ID NO: 387]: ATGGCTGGTCTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGAAGTGACAGCTGCTGGAA TCTGGCGCGGACTGGTGCAGCCTG GCGGCTCTCTGAGACTGTCTTGTGC CGCTCCGGCTACACCTTCACCAAC TACTGGATCACCTGGTCCGACAGG TCTCCCGCAAGGACTGGAATGGGT GTCCGACATCTACCCCGGCTCCTCC ATCTCCAACACTACAACGAGAAGTTCA	With leader [SEQ ID NO: 389]: MGWSCIIILFLVATATGVHSEVQ LLESGGIVQPGSLRLSCAAS GYFTTYWITWVRQAPGKLEW VSDIYPGSSISNYNEKFSRFT ISRDNKNTLYLQMNSLRAEDT AVYYCAREDDGYDAWFAYWGQT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSS GLYSLSSVWTVPPSSSLGTQYI	ATGGGCTG GTCCTGCA TCATCTGT TTTCTGGT GGCACCG CCACCGGC GTGCACAG C (Nucleotide 1 to 57 of SEQ ID	GAAGTGCAAGCTGCTGGAA TCTGGCGGGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTTGTGCCGCC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGGC AAGGACTGGAATGGGTG TCCGACATCTACCCCGGC TCCTCCATCTCCAATAC AACGAGAAGTTCAAGTCC CGGTTACCATCTCCCGG	GCCTCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGCGCCCTGACACAGC GGGTGCACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AGTCCCGGTTACACATCTCCGGGA CAACTCAAAGAACACCTGTACCTC CAGATGAACCTCCCTGCGGGCCGAGG ACACCGCCGTGTACTACTGCGCCAG AGAGACGGCTACGACGCTTGGTTT GCCTACTGGGGCCAGGCCACCTGG TCACCGTGTATCTGCCTCCACCAA GGGCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGG GCACAGCGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTGCTGGAACCTCAGGCGCC TGACAGCGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCTCAGGACTC TACTCCCTCAGCAGCGTGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCCAAATCTTGTA CAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTCAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCA AGACAAGCCCGGGAGGAGCAGTA CAACAGCAGTACCGTGTGGTCAGC GTCCTCACCGTCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA	CNVNHPKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLF PPKPKDTLIMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRWVSVLTVL HQDWINGKEYKCKVSNKALPAP IEKTSKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGSEFELYSLTVDKSRWQQ GNVFPSCVMHEALHNHYTQKSL SLSPGK Without leader [SEQ ID No: 390]: EVQLLESGGGLVQPGGSLRLSC AASGYTFITYWITWVRQAPGK LEWVSDIYPGSSISNYNEKFKS RFTISRDN SKNTLYLQMNSLRA EDTAVYYCAREDDGYDAWFAYWG QGTLLVTVSSASTKGPSVFPLAP SKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSVHTFPAVL QSSGLYSLSSVTVTPSSSLGTQ TYICNVNHPKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLIMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRWVSVL TVLHQDWINGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGF	No: 387) [SEQ ID No: 391]	GACAACTCCAAAGAACACC CTGTACCTCCAGATGAAC TCCCTGCGGGCCGAGGAC ACCGCCGTGTACTACTGC GCCAGAGAGGACGGCTAC GACGCTGGTTTGCCTAC TGGGGCCAGGACACCTG GTACCGGTGCATCT (Nucleotides 58 to 414 of SEQ ID No: 387) [SEQ ID No: 392] EVQLLESGGGLVQPGGSL RLSAAAGSYTFITYWITW VRQAPGKLEWVSDIYPG SSISNYNEKFKSRFTISR DNSKNTLYLQMNSLRAED TAVYYCAREDDGYDAWFAY WGQGLTVTVSS [SEQ ID No: 393]	TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCCGAC AACACCAAGGTGGACAAG AAAGTTGAGCCCAAAATCT TGTGACAAAACCTCACACA TGCCACACCGTGCCACGCA CCTGAACCTCTGGGGGA CCGTAGTCTTCTCTTC CCCCAAAACCCAAAGAC ACCTCATGATCTCCCGG ACCCCTGAGGTACACATGC GTGGTGGTGGACGTGAGC CAGAAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTC AGCGTCTTACCGTCTCTG CACCAGGACTGGCTGAAT GGCAAGGATACAAGTGC AAGGTCTCAACAAAGCC CTCCAGCCCCCATCGAG AAAACCATCTCCAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCGAC GACATCGCCGTGGAGTGG

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCCCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGAGCCGG AGAACAACTACAAGACCAAGCCTCC CGTGTGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGTCCGTGATGCAT GAGGCTCTGCACAACTACACGC AGAAAGAGCCTCTCCCTGTCTCCCGG GAAATGA Without leader [SEQ ID NO: 388]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGTCCGACAGGCTCCCGG CAAGGACTGGAATGGGTGTCGGAC ATCTACCCCGGCTCCTCCATCTCCA ACTACAACGAGAAAGTTCAAGTCCCG GTTTACCATCTCCCGGACAACTCC AAGAACACCTGTACCTCCAGATGA ACTCCCTGCGGGCCGAGGACACCCG CGTGTACTACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGCCTACT GGGGCCAGGGCACCCCTGGTCAACCGT	YPSDIAVEWESNGQPENNYKTT PPVLDSGSEFFLYSKLTVDKSR WQQGNVFSQVMHEALHNHYTQ KSLSLSPGK			GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCACCC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGGAAA TGA (Nucleotides 415 to 1401 of SEQ ID NO: 387) [SEQ ID NO: 394] ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTVF SSSLGTQTYICNVNHKPS NTKVDKKEPKSCDKTH CPPCPAPPELLGGPSVFLF PPKPKDTLMISRTPEVTC VVDVSHEDPEVKFNWYV DGEVHNAAKTPREEQYN STYRVSVLTFLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFYPSDIAVEWESNGQP

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	GTCATCTGCCTCCACCAAGGCCCA TCGGTCTTCCCCCTGGCACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGAACTCAGGCGCCCTGACCAG CGGCGTGACACACCTTCCCGGTGTC CTACAGTCCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCA GCAACACCAAGGTGGACAAGAAAGT TGAGCCCCAAATCTTGTGACAAAAC CACACATGCCCAACCGTGCCAGCAC CTGAACCTCTGGGGGACCGTCAGT CTTCTCTTCCCCCCCCAAACCCAAAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGGGGAGGAGCAGTACACACAGC ACGTACCGTGTGGTCAGCGTCTCA CCGTCTGCAACAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAGGTC TCCAACAAAGCCCTCCAGCCCCCA TCGAGAAAAACCATCTCCAAAGCCAA AGGGCAGCCCCCGAGAACACACAGGTG TACACCCCTGCCCCCATCCCCGGGATG AGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCCGTGGAGTGGG				ENNYKTTTPVLDSGGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSL SLSPGK [SEQ ID NO: 395]

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	AGAGCAATGGGCAGCGGGAGACAA CTACAAGACCACGCCTCCCGTGTG GACTCCGACGGCTCCTTCTTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTC TCATGCTCCGTGATGCATGAGGTC TGCACAACCACTACACGCAAGAG CCTCTCCCTGTCTCCCGGAAATGA				
7G6- HC α 2 5	With leader [SEQ ID NO: 396]: ATGGGCTGGTCTGTCATCATCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAAGTGCAGCTGCTGGAA TCTGGCGCGGACTGGTGCAGCCTG CGGGCTCTGTGAGACTGTCTTGTG CGCTCCGGCTACACCTTCAACACC TACTGGATCACCTGGTCCGACAGG CTCCCGCAAGGACTGGAATGGT CTCCGACATCTACCCCGCTCCTCC ATCTCCAACACAAACGAGAGTTCA AGTCCCGGTTACCATCTCCGTGGA CAACTCCAAGAACACCTGTACCTC CAGATGAACCTCCCTGAGAGCCGAG ACACCGCGGTACTACTCGGCCAG AGAGACGGCTACGACGCTTGGTT GCTTACTGGGCGCAGGCAACCTGG TCACCGTGTCTGTCATCCACCAA GGGCCCATCGGTCTTCCCTCGGCA CCCTCTCCAAGAGCACTCTGGGG GCACAGCGGCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGGAACCTCAGGCGCC	With leader [SEQ ID No: 398]: MGWSCIIILFLVATATGVHSEVQ LLESGGLVQPGGSLRLSCAAS GYFTTYITWVRQAPGKGLEW VSDIYPGSSISYNEKFSRFT ISVDNSKNTLYLQMNLSRAEDT AVYVCAREDDYDAFWAYWQGT LVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPT VSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCD KTHCTCPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYKCKVSNKALPAP IEKTSKAGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPV LDSGDSFFLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSL SLSPGK	ATGGGCTG GTCTGCA TCATCTG TTTCTGGT GGCACCG CCACCGG GTGCACAG C (Nucleotides 1 to 57 of SEQ ID No: 396) [SEQ ID No: 400]	GAAGTGCAGCTGCTGGAA TCTGGCGCGGACTGGTG CAGCCTGGCGGCTCTCTG AGACTGTCTGTGCGCGC TCCGGCTACACCTTCACC ACCTACTGGATCACCTGG GTCCGACAGGCTCCCGG AAGGACTGGAATGGGTC TCCGACATCTACCCCGG TCCTCCATCTCCAACCTAC AACGAGAAAGTTCAAGTCC CGGTTACCATCTCCGTG GACAACTCCAAGAACACC CTGTACCTCCAGATGAAC TCCCTGAGAGCCGAGGAC ACCGCGGTACTACTGTC GCCAGAGAGGACGGCTAC GACGCTGGTTGCTTAC TGGGCGCAGGCAACCTG GTACCGTGTCTATCT (Nucleotides 58 to 414 of SEQ ID No: 396) [SEQ ID No: 401]	GCATCCACCAAGGGCCCA TCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCAC TCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCG GTGACGGTGTCTGTGAAC TCAGGCGGCTGACCCAGC GGCGTGACACCTTCCCG GCTGTCTACAGTCTCTCA GGACTCTACTCCCTCAGC AGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACC CAGACCTACATCTGCAAC GTGAATCACAAGCCCCAGC AACACCAAGGTGGACAAG AAAAGTTAGCCCAATCT TGTGACAAAACCTCACACA TGCCACACCGTGCCAGCA CCGTCACTCTTCTCTTC CCCCCAAAACCAAGGAC ACCTCATGATCTCCCG ACCCCTGAGGTACATGC

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGACCAGGGCGGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTC TACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTA CAAACTCACACATGCCACCGTGC CCAGCACTGAACCTCCTGGGGGAC CGTCAGTCTTCTCTTCCCCCCTAAA ACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGG TGGTGGACGTGAGCCACGAAGACC TGAGGTCAAGTTCACTGTGACGTG GACGGCGTGGAGTGCATAATGCCA AGACAAAGCCGCGGAGGAGCAGTA CAACAGCACGTACCGTGTGTCAGC GTCCTCACCGTCCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCCGAGAAC ACAGGTGTACACCTGCCCCCATCC CGGGATGAGCTGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGG CTTCTATCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGG AGAACAACACTACAAGACCGCTCC CGTGTGGACTCCGACGGCTCCTTC TTCTTATATTCAAAGCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGCAI	Without leader [SEQ ID NO: 399]: EVQLLESGGGGLVQPGGSLRLSC AASGFTFTTYITWVRQAPGKG LEWVSDIYPGSSISNINEKFKS RFTISVDNSKNTLYLQMNSLRA EDTAVYYCAREDDGYDAWFAYWG QGTLLTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVWTPSSSLGTQ TYICNVNHNKPSNTKVDKKVEPK SCDKHTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPISRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMEALHNHYTQ KSLSLSPGK		EVQLLESGGGGLVQPGGSL RLSCAASGFTFTTYITW VRQAPGKLEWVSDIYPG SSISNINEKFKSRFTISV DNSKNTLYLQMNSLRAED TAVYYCAREDDGYDAWFAY WGQTLVTVSS [SEQ ID NO: 402]	GTGGTGGTGGACGTGAGC CAGGAAGACCTGAGGTG AAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCAT AATGCCAAGACAAAGCCG CGGAGGAGCAGTACAAAC AGCACGTACCGTGTGGTC AGCGTCTCACCGTCCTG CACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGC AAGGTCTCAACAAGAGCC CTCCAGCCCCCATCGAG AAAAACCATCTCAAAAGCC AAAGGGCAGCCCCGAGAA CCACAGGTGTACACCTG CCCCCATCCCGGATGAG CTGACCAAGAACCCAGGTG AGCCTGACCTGCCTGGTC AAAGGCTTCTATCCAGC GACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCG GAGAACAACTACAAGACC ACGCCCTCCCGTGTGGAC TCCGACGGCTCCTTCTTC TTATATTCAAAGCTCAC GTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCAT GAGGCTCTGCACAACCCAC TACACGCAGAAAGAGCCTC TCCCTGTCTCCCGGAAA TGA

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	<p>GAGGCTCTGCACAAACCCTACACGC AGAAAGAGCCTCTCCCTGTCTCCCCG GAAATGA</p> <p>Without leader [SEQ ID NO: 397]: GAAGTGCAGCTGCTGGAATCTGGCG GCGGACTGGTGCAGCCTGGCGGCTC TCTGAGACTGTCTTGTGCCGCTCC GGCTACACCTTCACCACCTACTGGA TCACCTGGGTCGACAGGCTCCCGG CAAGGACTGGAATGGTCTCCGAC ATCTACCCCGGCTCCTCCATCTCCA ACTACACGAGAAAGTTCAAGTCCCG GTTACCATCTCCGTGGACAACTCC AAGAACACCTGTACCTCCAGATGA ACTCCCTGAGAGCCGAGGACACCGC CGTGTACTACTGCGCCAGAGAGGAC GGCTACGACGCTTGGTTTGTTACT GGGCCAGGGCACCCCTGGTCACCGT GTCATCTGCATCCACCAAGGCCCA TCGGTCTTCCCCCTGGACCCCTCCT CCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGT CGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCC TCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTTGAATCACAAGCCCA GCAACACCAAGGTGGACAAAGAAAGT</p>				<p>(Nucleotides 415 to 1401 of SEQ ID NO: 396) [SEQ ID NO: 403]</p> <p>ASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLSVVTVP SSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT CPPCPAPPELLGGPSVFLF PPKPKDTLMI SRTPEVTC VVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLN GKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLV KGFPYSDIAVEWESNGQP ENNYKTTTPVLDSGDSFF LYSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPGK [SEQ ID NO: 404]</p>

Clone Name (Species & Isotype)	Heavy Chain DNA Sequence	Heavy Chain Amino Acid Sequence	cDNA Leader	Variable Domain (DNA) (amino acid)	Constant Domain (DNA) (amino acid)
	TGAGCCCCAAATCTTGTGACAAACT CACACATGCCCCACCGTGCCCCAGCAC CTGAACCTCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCCCCAAACCCCAAG GACACCCCTCATGATCTCCCGGACCC CTGAGGTCACATGCGTGGTGGTGA CGTGAGCCACGAAGACCCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCG TGGAGGTGCATAATGCCAAGACAAA GCCGCGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGTCCTCA CCGTCTCTGACCAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAGGTC TCCAAACAAAGCCCTCCCAAGCCCCA TCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCCGAGAACACACAGTG TACACCCCTGCCCCCATCCCGGGATG AGCTGACCAAGAACCCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAA CTACAAGACCAAGCCCTCCCGTGTG GACTCCGACGGCTCCTTCTTCTTAT ATTCAAAGCTCACCGTGGACAAGAG CAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAGAG CCTCTCCCTGTCTCCCGG GAAATGA				

Table 1 (cont.): 7G6 VL sequences

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
mouse 7G6-V _κ	With leader [SEQ ID NO: 405]: ATGAAGTTGCCTGTTAGGCTGTTGG TGATGATGTTCTGGATTCTGCTTC CAGCAGTGATGTTTGTGATGACCCAA ACTCCACTCTCCCTGCCTGTCAGTC TTGGAGATCAAGCCTCCATCTCTTG CAGATCTAGTCAGAGCATTTTACAT AGTAATGGAACACCTATTAGAAAT GGTACCTGCAGAAACAGGCCAGTC TCCAAAGCTCCTGATTTGCCAAGTT TCCAAACCGATTTCTGGGTCCTCAG ACAGGTTCAAGTGGCAGTGGATCAGG GACAGATTTCACTCAAGATCAGC AGAGTGGAGGCTGAGGATCTGGAG TTTATTACTGCTTTCAAGGTTTACA TGTTCCATTACAGTTCCGGCTCGGG ACAAAGTTGGAATAAAACGGGCTG ATGCTGCACCAACTGTATCCATCTT CCCACCTTC	With leader [SEQ ID NO: 407]: MKLPVRLILVMMFWIPASSDVL MTQTPLSLPVSLGDAQSISCRS SQSILHSNGNTYLEWYLQKPGQ SPKLLICKVSNRFSGVDPDRFSG SGSGTDFTLKISRVEAEDLGVY YCFQGSHPVPTFGSGTKLEIKR ADAAPTVSIFPPS	ATGAAGTT GCCTGTTA GGCTGTTG GTGATGAT GTTCTGGA TTCTCTGT TCCAGCAG T (nucleotides 1 to 57 of SEQ ID NO: 405) [SEQ ID NO: 409]	GATGTTTGGATGACCCAA ACTCCACTCTCCCTGCCT GTCAGTCTGGAGATCAA GCCTCCATCTCTTGCAGA TCTAGTCAGAGCATTTTA CATAGTAATGGAACACC TATTTAGAATGGTACCTG CAGAAACAGGCCAGTCT CCAAAGCTCCTGATTTGC AAAGTTTCCAAACCGATTT TCTGGGTCCTCAGACAGG TTCAGTGGCAGTGGATCA GGGACAGATTTTCACTC AAGATCAGCAGAGTGGAG GCTGAGGATCTGGGAGTT TATTACTGCTTTCAAGGT TCACATGTTCCATTCACG TTCGGCTCGGGACAAAG TTGGAATAAAA (nucleotides 58 to 393 of SEQ ID NO: 405) [SEQ ID NO: 410]	CGGGCTGATGCTGCACCA ACTGTATCCATCTTCCCA CCTTC (nucleotides 394 to 434 of SEQ ID NO: 405) [SEQ ID NO: 412] KRADAAPTVSIFPPS [SEQ ID NO: 413]
	Without leader [SEQ ID NO: 406]: GATGTTTGGATGACCCAACTCCAC TCTCCCTGCCTGTCAGTCTTGGAGA TCAAGCCTCCATCTCTTGCAGATCT AGTCAGAGCATTTTACATAGTAATG GAAACACCTATTAGAAATGGTACCT GCAGAAACAGGCCAGTCTCCAAAG CTCCTGATTTGCAAAAGTTTCCAACC GATTTTCTGGGTCCTCCAGACAGGTT	DVLMQTPLSLPVSLGDAQ ASISCRSSQSILHSNGNT YLEWYLQKPGQSPKLLIC KVSNNRFSGVDPDRFSGSGS GTDFTLKISRVEAEDLGV YYCFQGSHPVPTFGSGTK LEIK		DVLMQTPLSLPVSLGDAQ ASISCRSSQSILHSNGNT YLEWYLQKPGQSPKLLIC KVSNNRFSGVDPDRFSGSGS GTDFTLKISRVEAEDLGV YYCFQGSHPVPTFGSGTK LEIK	

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CAGTGGCAGTGGATCAGGGACAGAT TTCACACTCAAGATCAGCAGAGTGG AGGCTGAGGATCTGGGAGTTTATTA CTGCTTTCAAGGTTACATGTTCCA TTCACGTTTCGGCTCGGGACAAAGT TGGAAATAAAACGGGCTGATGCTGC ACCAACTGTATCCATCTTCCCACCT TC			[SEQ ID NO: 411]	
7G6-LC α 1	With leader [SEQ ID NO: 414]: ATGGGCTGGTCTGTCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGCTGCTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGACAGCTGCTCCATCTCCTG CAGATCCTCCCAGTCCATCCTGCAC TCCAACGGCAACACCTACCTGGAAT GGTTCAGCAGCGGCTGGCCAGTC TCCAGACGGCTGATCTACAAGTG TCCAACCGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCAACCTGAAGATCTCC CGGTGGAAGCCGAGGACGTGGCG TGTAATACTGTTTCAAGGCTCCCA CGTGCCCTTCACTTCCGGCCAGGC ACCAAGCTGGAATCAAAACGAAGT TGGTGCACCATCTGTCTTCTATCTT CCCGCATCTGATGACAGTGTGAA TCTGGAACCTGCCTCTGTTGTGCTC TGCTGAATAACTTCTATCCACAGAG GGCCAAAGTACAGTGAAGGTGGAT	With leader [SEQ ID NO: 416]: MGWSCIIILFLVATATGVHSDV MTQSPSLPVTILGQPASISCRS SQSILHSNGNTYLEWFQRPQG SPRRLIYKVSNRFSVPDRFSG SGSGDTFLKISRVEAEDVGVI YCFQGSHPVFTFGQGTLEIKR TVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEV THQGLSPVTKSFNRGEC Without leader [SEQ ID NO: 417]: DVVMTQSPSLPVTILGQPASIS CRSSQSIILHSNGNTYLEWFQQR PGQSPRRLIYKVSNRFSVPDR FSGSGGTDFTLKISRVEAEDV GVYFCFQGSHPVFTFGQGTLE IKRTVAAPSVFIFPPSDEQLK GTASVVCCLNNFYPREAKVQWK	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotide 1 to 57 of SEQ ID NO: 414) [SEQ ID NO: 418]	GACGTCGTGATGACACAG TCCCCCTGTCCCTGCCT GTGACCCCTGGACAGCCT GCCTCCATCTCTGCAGA TCTCTCCAGTCCATCCTG TACTCCAAAGGCAACACC TACCTGGAATGGTCCAG CAGCGGCTGGCCAGTCT CCCAGACGGCTGATCTAC AAGGTGTCCAAACCGGTTT TCCGGCTGCCCCGACAGA TTCTCCGGCTCTGGCTCT GGACCGACTTCACCTG AAGATCTCCCGGTGGAA GCCGAGACGTGGGCGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTGGCAATCAAA (nucleotide 58 to 393 of SEQ ID NO: 414) [SEQ ID NO: 419]	CGAACTGTGGTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGGAACCTGCCTCT GTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTG AGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCGAAGTCACC CATCAGGCGCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT (nucleotide 394 to 714 of SEQ ID NO: 414) [SEQ ID NO: 421]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AACGCCCTCCAATCGGGTAACCTCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCAAAAAGAGCTTCA ACAGGGAGAGTGTGA Without leader [SEQ ID NO: 415]: GACGTGCTGATGACACAGTCCCCC TGTCCCTGCCCTGTGACCCCTGGACA GCCTGCCCTCCATCTCTGCAGATCC TCCAGTCCATCCTGCACTCCACAG GCAACACCTACCTGGAATGGTTCCA GCAGCGCCTGGCCAGTCTCCCA CGGCTGATCTACAAGGTGTCCAACC GGTTCTCCGGCGTGCCCGACAGATT CTCGGGCTCTGGCTCTGGCACCGAC TTCACCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGACTA CTGTTTCAAGGCTCCACAGTGCCC TTCACCTTCGGCCAGGGCACCAGC TGGAAATCAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGTGCCTGTGAA TAACCTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACCTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC	VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHVVYA CEVTHQGLSSPVTKSFNRGEC		DVVMTQSPPLSLPTLIGQP ASISCRSSQSIILHSNGNT YLEWFQQRPGQSPRRLLIY KVSNNRFSGVDPDRFSGSGS GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 420]	RTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSTL TLSKADYEKKHVVYACEVT HQGLSSPVTKSFNRGEC [SEQ ID NO: 422]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGCACCTACAGCCTCAGCAGCACC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTCGAA GTCACCCATCAGGGCCTGAGCTCG CCGTCACAAAGAGCTTCAACAGGGG AGAGTGTGA				
7G6-LC2u2	With leader [SEQ ID NO: 423]: ATGGGCTGGTCCCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCAGCTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGACAGCCTGCCTCCATCTCTCTG CAGATCTCCAGTCCATCTCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGCGCCTGGCCAGTC TCCAGACTGCTGATGCAAGGTG TCCAACCGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCTGAAGATCTCC CGGTGGAAGCCGAGGACGTGGCG TGTAATACTGTTTCAAGGCTCCCA CGTGCCCTTACCTTCGGCCAGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAATACTCTGTTGTGTGCC TGCTGAATACTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC	With leader [SEQ ID NO: 425]: MGWSCILFLVATATGVHSDVV MTQSPSLPVTILGQSPASISCRS SQSILHSNGNTYLEWYQQRPGQ SPRLICKVSNRFSGVDPDRFSG SGSGDTFLKISRVEADVGVY YCFQGSHPVFTFGQGTKEIKR TVAAPSVFIPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKKHVYACEV THQGLSPVTKSFNRGEC Without leader [SEQ ID NO: 426]: DVMTQSPSLPVTILGQSPASIS CRSQSILHSNGNTYLEWYQQR PGQSPRLICKVSNRFSGVDPDR FSGSGSDFTLKISRVEADV GVYCFQGSHPVFTFGQGTKE IKRTVAAPSVFIPPSDEQLK GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHYA CEVTHQGLSPVTKSFNRGEC	ATGGGCTG GTCCTGCA TCATCTCTG TTTCTGGT GGCCACCG CCACCCGC GTGCACAG C (Nucleotides 1 to 57 of SEQ ID NO: 427)	GACGTCGTGATGACACAG TCCCCCTGTCCCTGCCT GTGACCCCTGGACAGCCT GCCTCCATCTCTGCAGA TCCTCCAGTCCATCTCTG CACTCCAACGGCAACACC TACCTGGAATGGTATCAG CAGGGCTGGCCAGTCT CCAGACTGCTGATCTGC AAGGTGTCAAACCGGTTT TCCGGCTGCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCGGGTGGA GCCGAGGACGTGGCGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCAAC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 423) [SEQ ID NO: 428]	CGAACTGTGGTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCCCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCGAAAGTCACC CATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT (Nucleotides 394 to 714 of SEQ ID NO: 423) [SEQ ID NO: 430] RTVAAPSVFIPPSDEQL KSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQE

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGACCCCTGACGCTGAGCAAGCAG ACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCAACAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 424]: GACGTCGTGATGACACAGTCCCCC TGTCCTGCTGTGACCCCTGGGACA GCCTGCCCTCCATCTCCTGCAGATCC TCCAGTCCATCCTGCACCTCCAACG GCAACACCTACCTGGAATGGTATCA GCAGGGCCTGGCCAGTCTCCAGA CTGCTGATCTGCAAGGTGTCCACC GGTCTCCGGCGTGCCCGACAGATT CTCGGCTCTGGCTCTGGCACCGAC TTCACCCCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGTGACTA CTGTTTCAAGGCTCCACGTGCC TTCACCTTCGGCCAGGCCACCAAGC TGAAATCAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTCTGTTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCTGCGAA			YLEWYQRPQGSPRLILC KVSNRFSGVDPDRFSGSGS GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 429]	SVTEQDSKDSYSLSTL TLISKADYEKKHYACEVT HQGLSSPVTKSFNRGEC [SEQ ID NO: 431]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	GTACCCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG AGAGTGTGA				
7G6-LC α 3	With leader [SEQ ID NO: 432]: ATGGGTGGTCCCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGACGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTCCAGCAGCGGCTGGCCAGTC TCCCCGTAGACTGATCTGCAAGTG TCCAAACGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGAAGCCGAGGACGTGGCGG TGTAAGTACTGTTTCAAGGCTCCCA CGTGGCTTACCTTCGGCCAGGGC ACCAAGCTGGAATCAAACGAATG TGGTGCACCATCTGCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTCCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAGTCTACGC	With leader [SEQ ID NO: 434]: MGWSCIIILFLVATATGVHSDVV MTQSPSLPVTIGQPASISCRS SQSILHSNGNTYLEWFQQRPGQ SPRRLLICKVSNRFSGVDPDRFSG SGSGLDFTLKISRVEAEDVGVY YCFQGSHPVFTFGQGTKEIKR TVAAPSVFIKPPSDEQLKSGTA SVVCLINNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSPVTKSFNRGEC Without leader [SEQ ID NO: 435]: DVVMTQSPSLPVTIGQPASIS CRSSQSIILHSNGNTYLEWFQQR PGQSPRRLLICKVSNRFSGVDPDR FSGSGSGTDFTLKISRVEAEDV GVYCFQGSHPVFTFGQGTKE IKRTVAAPSVFIKPPSDEQLK GTASVCLINNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSPVTKSFNRGEC	ATGGGCTG GTCTGCA TCATCTCT TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 432) [SEQ ID NO: 436]	GACGTGCTGATGACACAG TCCCCCTGTCCCTGCCT GTGACCCCTGGGACAGCCT GCCTCCATCTCCTGCAGA TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTCCAG CAGCGGCTGGCCAGTCT CCCCGTAGACTGATCTGC AAGGTGTCACACCGGTTT TCCGGGTGCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGGCGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 432) [SEQ ID NO: 437]	CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCC CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGCTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCAGAGTCACC CATCAGGGCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 432) [SEQ ID NO: 439] RTVAAPSVFIKPPSDEQL KSGTASVCLINNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSSTL TLSKADYEKHKVYACEVT

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 433]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCGTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCCAGTCCATCTGCACCTCCAACG GCAACACCTACCTGGAATGGTTCCA GCAGCGCCTGGCCAGTCTCCCCGT AGACTGATCTGCAAGGTGTCCAACC GGTTCCTCCGGCGTGCCCGACAGATT CTCGGCTCTGGCTCTGGCACCCGAC TTCACCCCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTACTA CTGTTTTC AAGGCTCCCAAGTCCCC TTCACCTTCGGCCAGGGCACCAAGC TGGAAATCAAAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCGAA GTCACCCATCAGGGCCTGAGTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 438]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 440]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LC α 4	<p>With leader [SEQ ID NO: 441]:</p> <p>ATGGGCTGGTCCCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGCGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGCGGCTGGCCAGTC CCCCAGCGGCTGATCTGCAAGGTG TCCAAACGGTTCTCTGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGGAAGCCGAGACGTGGCGG TGTAATACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 443]:</p> <p>MGWSCIIILFLVATATGVHSDVV MTQSPSLPVTILGQSPASISCRS SQSILHSNGNTYLEWYQQRPGQ SPRRLLICKVSNRFSGVDPDRFSG SGSGDTFLKISRVEAEDVGVI YCFQGSHPFTFGQGTKLEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 444]:</p> <p>DVMTQSPSLPVTILGQSPASIS CRSSQSIILHSNGNTYLEWYQQR PGQSPRRLLICKVSNRFSGVDPDR FSGSGDTFTLKISRVEAEDV GVYCYCFQGSHPFTFGQGTKLE IKRTVAAPSVFIIPPSDEQLKS GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 441)</p>	<p>GACGTGCTGATGACACAG TCCCCTGTCCCTGCCT GTGACCCCTGGACAGCCT GCCTCCATCTCCTGCAGA TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTATCAG CAGCGGCTGGCCAGTCC CCAGACGGCTGATCTGC AAGGTGCAACCCGGTTC TCTGGCTGCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGCGGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGCGACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 441)</p> <p>[SEQ ID NO: 446]</p> <p>DVMTQSPSLPVTILGQ ASISCRSSQSIILHSNGNT YLEWYQQRPGQSPRRLLIC KVSNRFSGVDPDRFSGSGS</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGCTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCAGAGTCAACC CATCAGGCGCTGAGCTCG CCCGTCAAAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 441)</p> <p>[SEQ ID NO: 448]</p> <p>RTVAAPSVFIIPPSDEQL KSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSTL TLSKADYEKHKVYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCAAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 442]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCGTGTGACCCCTGGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCCAGTCCATCTGCACCTCCAACG GCAACACCTACCTGGAATGGTATCA GCAGCGCCTGGCCAGTCCCCCAGA CGGCTGATCTGCAAGGTGTCCAACC GGTTCCTGTGGCGTCCCCGACAGATT CTCGGCTCTGGCTCTGGCACCCGAC TTCACCCCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTACTA CTGTTTTC AAGGCTCCCAAGTGCCTC TTCACCTTCGGCCAGGGCACCAAGC TGGAAATCAAAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGTGCCTGTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 447]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 449]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LCzu5	<p>With leader [SEQ ID NO: 450]:</p> <p>ATGGGCTGGTCCCTGCATCATCCTGT TCTGTGGTGGCCACCGCCACCGCGT GCACAGCGACGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTCCAGCAGCGGCTGGCCAGTC CCCCAGACTGCTGATCTGCAAGGTG TCCAAACGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGGAAGCCGAGACGTGGCGG TGTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGGC ACCAAGCTGGAATCAAACGAATG TGGTGCACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 452]:</p> <p>MGWSCIIILFLVATATGVHSDVV MTQSPSLPVTILGQSPASISCRS SQSILHSNGNTYLEWFQQRPGQ SPRLLICKVSNRFSGVDPDRFSG SGSGLDFTLKISRVEAEDVGVY YCFQGSHPFTFGQGTKLEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 453]:</p> <p>DVMTQSPSLPVTILGQSPASIS CRSSQSIILHSNGNTYLEWFQQR PGQSPRLLICKVSNRFSGVDPDR FSGSGTDFTLKISRVEAEDV GVYCFQGSHPFTFGQGTKLE IKRTVAAPSVFIIPPSDEQLKS GTASVCLLNFFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCTCG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 450)</p>	<p>GACGTGCTGATGACACAG TCCCCTGTCCCTGCCT GTGACCTGGGACAGCCT GCCTCCATCTCCTGCAGA TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTCCAG CAGCGGCTGGCCAGTCC CCAGACTGCTGATCTGC AAGGTGTCAAACCGGTTT TCCGGCTGCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGCGGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 450)</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGGAACCTGCCTCT GTTGTGCTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCCCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCAGAGTCACC CATCAGGCTGAGCTCG CCCGTACAAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 450)</p>
				<p>[SEQ ID NO: 454]</p> <p>[SEQ ID NO: 455]</p> <p>DVMTQSPSLPVTILGQ ASISCRSSQSIILHSNGNT YLEWFQQRPGQSPRLLIC KVSNRFSGVDPDRFSGSGS</p>	<p>RTVAAPSVFIIPPSDEQL KSGTASVCLLNFFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSSTLSSTL TLSKADYEKHKVYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 451]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCGTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCCAGTCCATCTGCACCTCCAACG GCAACACCTACCTGGAATGGTTCCA GCAGCGGCCTGGCCAGTCCCCCAGA CTGCTGATCTGCAAGGTGTCCAACC GGTTCCTCCGGCGTGCCCGACAGATT CTCGGCTCTGGCTCTGGCACCCGAC TTCACCCCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTACTA CTGTTTTC AAGGCTCCCAAGTGCCTC TTCACCTTCGGCCAGGGCACCAAGC TGGAATCAAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGTGCCTGTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACCTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 456]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 458]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LC α 6	<p>With leader [SEQ ID NO: 459]:</p> <p>ATGGGTGGTCCCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGCGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGCGGCTGGCCAGTC TCCCCGGCTGCTGATTTCCAAAGTG TCCAAACGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGGAAGCCGAGACGTGGCGG TGTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTCCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 461]:</p> <p>MGWSCIIILFLVATATGVHSDVV MTQSPSLPVTILGQPASISCRS SQSILHSNGNTYLEWYQQRPGQ SPRLLISKVSNRFSGVDPDRFSG SGSDFTLTKISRVEAEDVGVI YCFQGSHPFTFGQTKLEIKR TVAAPSVFIPTSPDEQLKSGTA SVVCLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 462]:</p> <p>DVMTQSPSLPVTILGQPASIS CRSSQSIILHSNGNTYLEWYQQR PGQSPRLLISKVSNRFSGVDPDR FSGSGTDFTLKISRVEAEDV GVYCFQGSHPFTFGQTKLE IKRTVAAPSVFIPTSPDEQLKS GTASVCLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCTCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 459)</p>	<p>GACGTCGTGATGACACAG TCCCCTCTGTCCTGCCT GTGACCCCTGGACACGCCT GCCTCCATCTCTGACAG TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTATCAG CAGCGGCTGGCCAGTCT CCCCGGTGTGATTTCC AAGGTGTCCAAACCGGTTT TCCGGCTGCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGGCGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGCGACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 459)</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCC CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCAGAGTCACC CATCAGGCGCTGAGCTCG CCCGTACAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 459)</p> <p>[SEQ ID NO: 466]</p> <p>RTVAAPSVFIPTSPDEQL KSGTASVCLNNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSTL TLSKADYEKHKVYACEVT</p>

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	CTGCGAAGTCACCCATCAGGGCCTG AGTCGCCCCGTACAAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 460]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCCTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCAGTCCATCTGCACTCCCAACG GCAACACCTACCTGGAATGGTATCA GCAGCGCCTGGCCAGTCTCCCCGG CTGCTGATTTCCAAGGTGTCCAACC GGTCTCCGGCGTGCCCGACAGATT CTCGGCTCTGGCTCTGGCACCGAC TTCACCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTA CTGTTTCAAGGCTCCACGTGCC TTCACCTTCGGCCAGGCCACCAAGC TGAAATCAAAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			KVSNRFSGVPDRFSGSGS GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 465]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 467]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LC α 7	<p>With leader [SEQ ID NO: 468]:</p> <p>ATGGGTGGTCCCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGCGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTCCAGCAGCGGCTGCGCCAGTC TCCAGACGGCTGATCTCCAAGGTG TCCAAACGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGGAAGCCGAGACGTGGCGG TGTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTCCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 470]:</p> <p>MGWSCIIILFLVATATGVHSDVV MTQSPSLPVTILGQSPASISCRS SQSILHSNGNTYLEWFQQRPGQ SPRRLISKVSNRFSGVDPDRFSG SGSGDTFLKISRVEAEDVGVI YCFQGSHPFTFGQTKLEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKKHYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 471]:</p> <p>DVMTQSPSLPVTILGQSPASIS CRSSQSIILHSNGNTYLEWFQQR PGQSPRRLISKVSNRFSGVDPDR FSGSGDTFTLKISRVEAEDV GVYCYCFQGSHPFTFGQTKLE IKRTVAAPSVFIIPPSDEQLKS GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCCCTGCA TCATCTCTG TTTCTGGT GGCCACCG CCACCCGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 468)</p>	<p>GACGTGCTGATGACACAG TCCCCCTGTCCCTGCCT GTGACCCCTGGACAGCCT GCCTCCATCTCTGCAGA TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTTCAG CAGCGGCTGGCCAGTCT CCAGACGGCTGATCTCC AAGGTGCAACCCGGTTC TCCGGCTGCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGCGGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGCGACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 468)</p> <p>[SEQ ID NO: 473]</p> <p>DVMTQSPSLPVTILGQ ASISCRSSQSIILHSNGNT YLEWFQQRPGQSPRRLIS KVSNRFSGVDPDRFSGSGS</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGCTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCAGAGTCAACC CATCAGGCGCTGAGCTCG CCCGTCAAAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 468)</p> <p>[SEQ ID NO: 475]</p> <p>RTVAAPSVFIIPPSDEQL KSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSSTL TLSKADYEKKHYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 469]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCGTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCCAGTCCATCTGCACTCCCAACG GCAACACCTACCTGGAATGGTTCCA GCAGCGCCTGGCCAGTCTCCAGA CGGCTGATCTCCAAGGTGTCCAACC GGTTCCTCCGGCGTGCCCGACAGATT CTCGGCTCTGGCTCTGGCACCCGAC TTCACCCCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTACTA CTGTTTTC AAGGCTCCCAAGTGCCT TTCACCTTCGGCCAGGCAACCAAGC TGGAAATCAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGTGCCTGTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 474]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 476]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LCzu8	<p>With leader [SEQ ID No: 477]:</p> <p>ATGGGTGGTCCCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGCGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCCAGTCCATCGTGAC TCCAAAGGCAACACCTACCTGGAAT GGTCCAGCAGCGGCTGGCCAGTC TCCAGACGGCTGATCTCCAAGTG TCCAAACGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGAAGCCGAGACGTGGCGG TGTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTTGTGCGC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID No: 479]:</p> <p>MGWSCIIILFLVATATGVHSDVV MTQSPSLSPVTIGQPASISCRS SQSIVHSNGNTYLEWFQQRPGQ SPRRLLSKVSNRFSGVDPDRFSG SGSGDTFLKISRVEAEDVGVI YCFQGSHPVFTFGQTKLEIKR TVAAPSVFIFFPSDEQLKSGTA SVVCLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKKHKVYACEV THQGLSPVTKSFNRGEC</p> <p>Without leader [SEQ ID No: 480]:</p> <p>DVVMTQSPSLSPVTIGQPASIS CRSSQSIVHSNGNTYLEWFQQR PGQSPRRLLSKVSNRFSGVDPDR FSGSGSGTDFTLKISRVEAEDV GVYCFQGSHPVFTFGQTKLE IKRTVAAPSVFIFFPSDEQLKS GTASVCLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHKVYA CEVTHQGLSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID No: 477)</p>	<p>GACGTGCTGATGACACAG TCCCCCTGTCCCTGCCT GTGACCCCTGGACACGCTT GCCTCCATCTCCTGCAGA TCCTCCAGTCCATCGTG CACTCCAAACGGCAACACC TACCTGGAATGGTTCAG CAGCGGCTGGCCAGTCT CCAGACGGCTGATCTCC AAGGTGCAACACCGGTTT TCCGGCTGCCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGGCGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID No: 477)</p> <p>[SEQ ID No: 482]</p> <p>DVVMTQSPSLSPVTIGQP ASISCRSSQSIVHSNGNT YLEWFOQRPQSPRRLLIS KVSNRFSGVDPDRFSGSGS</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGTGCCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCAGAGTCACC CATCAGGCGCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID No: 477)</p> <p>RTVAAPSVFIFFPSDEQL KSGTASVCLNNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSSTL TLSKADYEKKHKVYACEV HQGLSPVTKSFNRGEC</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCAAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 478]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCGTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCAGTCCATCGTGCACTCCCAACG GCAACACCTACCTGGAATGGTTCCA GCAGCGCCTGGCCAGTCTCCAGA CGGCTGATCTCCAAGGTGTCCAACC GGTTCCTCCGGCGTGCCCGACAGATT CTCGGCTCTGGCTCTGGCACCCGAC TTCACCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTACTA CTGTTTCAAGGCTCCACGTGCC TTCACCTTCGGCCAGGCCACCAAGC TGGAAATCAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTCTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTCGAA GTCACCCATCAGGGCCTGAGTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 483]	[SEQ ID NO: 484]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LCzu9	<p>With leader [SEQ ID NO: 485]:</p> <p>ATGGGTGGTCCCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGCGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCTCCAGTCCATCGTGCAC TCCAAAGGCAACACCTACCTGAAT GGTCCAGCAGCGGCTGGCCAGTC TCCAGACGGCTGATCTCCAAGTG TCCAAACGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGGAAGCCGAGACGTGGCGG TGTAATACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTCCCTCTGTTGTGTC TGCTGAATACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 487]:</p> <p>MGWSCIIILFLVATATGVHSDVV MTQSPSLPVLTLGQSPASISCRS SQSIVHSNGNTYLNWFQQRPGQ SPRRLISKVSNRFSGVDPDRFSG SGSGDTFLKISRVEAEDVGVI YCFQGSHPFTFGQTKLEIKR TVAAPSVFIIPPDSDEQLKSGTA SVVCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKKHVKYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 488]:</p> <p>DVMTQSPSLPVLTLGQSPASIS CRSSQSIIVHSNGNTYLNWFQQR PGQSPRRLISKVSNRFSGVDPDR FSGSGDTDFTLKISRVEAEDV GVYCYCFQGSHPFTFGQTKLE IKRTVAAPSVFIIPPDSDEQLKS GTASVCLLNFFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHVKYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCTCG TTTCTGGT GGCCACCG CCACCCGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 485)</p>	<p>GACGTGATGATGACACAG TCCCCCTGTCCCTGCCT GTGACCCCTGGACACGCTT GCCTCCATCTCCTGCAGA TCCTCCAGTCCATCGTG CACTCCCAACGGCAACACC TACCTGAATCGTTCAG CAGCGGCTGGCCAGTCT CCAGACGGCTGATCTCC AAGGTGCAACCCGGTTC TCCGGCTGCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGCGGTG TACTAGTGTTCAGGCG TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 485)</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGCTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCAGAGTCAACC CATCAGGCGCTGAGCTCG CCCGTACAAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 485)</p>
				<p>[SEQ ID NO: 490]</p> <p>DVMTQSPSLPVLTLGQSP ASISCRSSQSIIVHSNGNT YLNWFQQRPGQSPRRLISK VSNRFSGVDPDRFSGSGS</p>	<p>RTVAAPSVFIIPPDSDEQL KSGTASVCLLNFFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSSTL TLSKADYEKKHVKYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 486]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCGTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCCAGTCCATCGTGCACTCCAACG GCAACACCTACCTGAACCTGGTTCCA GCAGCGGCCTGGCCAGTCTCCAGA CGGCTGATCTCCAAGGTGTCCAACC GGTTCCTCCGGCGTGCCCGACAGATT CTCGGCTCTGGCTCTGGCACCCGAC TTCACCCCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTACTA CTGTTTTC AAGGCTCCCAAGTGCCTC TTCACCTTCGGCCAGGGCACCAAGC TGGAAATCAAAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 491]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 493]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6- LC α 1 0	<p>With leader [SEQ ID NO: 494]:</p> <p>ATGGGTGGTCCCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCAGCGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG CAGATCTCCAGTCCATCGTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTCCAGCAGCGGCTGCCAGTC TCCAGACGGCTGATCTACAAGTG TCCAAACGGTTCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCTGAAGATCTCC CGGGTGAAGCCGAGACGTGGCGG TGTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTCCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 496]:</p> <p>MGWSCIIILFLVATATGVHSDVV MTQSPSLPVTILGQPASISCRS SQSIVHSNGNTYLEWFQQRPGQ SPRRLIYKVSNRFSGVDPDRFSG SGSGLDFTLKISRVEAEDVGVY YCFQGSHPVFTFGQGTKEIKR TVAAPSVFIFFPSDEQLKSGTA SVVCLINNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSDSYS LSSTLTLSKADYEKHKVYACEV THQGLSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 497]:</p> <p>DVVMTQSPSLPVTILGQPASIS CRSSQSIHVSNGNTYLEWFQQR PGQSPRRLIYKVSNRFSGVDPDR FSGSGSGTDFTLKISRVEAEDV GVYCFQGSHPVFTFGQGTKE IKRTVAAPSVFIFFPSDEQLKS GTASVCLINNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCCCTGCA TCATCTCTG TTTCTGGT GGCCACCG CCACCCGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 494)</p>	<p>GACGTGCTGATGACACAG TCCCCCTGTCCCTGCCT GTGACCCCTGGACACGCCT GCCTCCATCTCCTGCAGA TCCTCCAGTCCATCGTG CACTCCAAACGGCAACACC TACCTGGAATGGTTCAG CAGCGGCTGGCCAGTCT CCAGACGGCTGATCTAC AAGGTGCAACCCGGTTC TCCGGCTGCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG AAGATCTCCCGGTGGAA GCCGAGGACGTGGGCGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 494)</p> <p>[SEQ ID NO: 499]</p> <p>DVVMTQSPSLPVTILGQ ASISCRSSQSIHVSNGNT YLEWFOQRPQSPRRLIY KVSNRFSGVDPDRFSGSG</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGCTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCAGAGTCAAC CATCAGGCTGAGCTCG CCCGTCAAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 494)</p> <p>[SEQ ID NO: 501]</p> <p>RTVAAPSVFIFFPSDEQL KSGTASVCLINNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKSDSYSLSSTL TLSKADYEKHKVYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 495]: GACGTCGTGATGACACAGTCCCCC TGTCCCTGCCGTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCAGTCCATCGTGCACTCCAACG GCAACACCTACCTGGAATGTTCCA GCAGCGCCTGGCCAGTCTCCAGA CGGCTGATCTACAAGGTGTCCAAC GGTTCCTCCGGCGTGCCGACAGATT CTCGGCTCTGGCTCTGGCACCGAC TTCACCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTA CTGTTTCAAGGCTCCACGTGCC TTCACCTTCGGCCAGGCCACCAAGC TGAAATCAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCTGCGAA GTCACCCATCAGGGCCTGAGTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 500]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 502]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LC α 1	With leader [SEQ ID NO: 503]: ATGGGCTGGTCTGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGGT GCACAGCATATCCAGATGACCCAG TCCCTTCCAGCCTGTCCGCCTCTG TGGCGACAGAGTGACCATCACCTG TCGGTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGAAGCCCGCAAGGC CCCTAAGCTGCTGATCTACAAGTG TCCAACCGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CACCAGACTTCACCCTGACCATCTCC AGCCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTTCAAGGCTCCCA CGTGCCCTTACCTTCGGCCAGGGC ACCAAGCTGAAATCAAACGAAGT TGGCTGCACCATCTGTCTTCATCTT CCGCCATCTGATGAGCAGTTGAAA TCTGGAATGCCTCTGTTGTGCC TGCTGAATAACTTCTATCCACAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAGTCTACGC	With leader [SEQ ID NO: 505]: MGWSCIILFLVATATGVHSDIQ MTQSPSSLSASVDRVTITCRS SQSILHSNGNTYLEWYQQKPGK APKLLIYKVSNRFSGVPSRFSG SGSGTDFTLTISLQPEDFATY YCFQGSHPVFTFGQGTKLEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC Without leader [SEQ ID NO: 506]: DIQMTQSPSSLSASVDRVTIT CRSSQSILHSNGNTYLEWYQQK PGKAPKLLIYKVSNRFSGVPSR FSGSGGTDFTLTISLQPEDF ATYYCFQGSHPVFTFGQGTKLE IKRTVAAPSVFIIPPSDEQLKS GTASVVCLLNFFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC	ATGGGCTG GTCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 503) [SEQ ID NO: 507]	GATATCCAGATGACCCAG TCCCCTTCCAGCCTGTCC GCCTCTGTGGCGACAGA GTGACCATCACCTGTCCG TCCTCCAGTCCATCCTG CACTCCAACGGCAACACC TACCTGGAATGGTATCAG CAGAAGCCCGCAAGGCC CCTAAGCTGCTGATCTAC AAGGTGTCCAACCGGTTT TCCGGCGTGCCCTCCAGA TTTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCGT ACCATCTCCAGCCTCCAG CCCGAGGACTTCGCCACC TACTACTGTTTTCAAGGC TCCCACGTGCCCTTACC TTCGGCCAGGCGACCAAG CTGGAATCAAACGAAGT (nucleotides 58 to 393 of SEQ ID NO: 503) [SEQ ID NO: 508] DIQMTQSPSSLSASVGD VTITCRSSQSILHSNGNT YLEWYQQKPGKAPKLLIY KVSNRFSGVPSRFSGSGS	GATATCCAGATGACCCAG TCCCCTTCCAGCCTGTCC GCCTCTGTGGCGACAGA GTGACCATCACCTGTCCG TCCTCCAGTCCATCCTG CACTCCAACGGCAACACC TACCTGGAATGGTATCAG CAGAAGCCCGCAAGGCC CCTAAGCTGCTGATCTAC AAGGTGTCCAACCGGTTT TCCGGCGTGCCCTCCAGA TTTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCGT ACCATCTCCAGCCTCCAG CCCGAGGACTTCGCCACC TACTACTGTTTTCAAGGC TCCCACGTGCCCTTACC TTCGGCCAGGCGACCAAG CTGGAATCAAACGAAGT GTGGCTGCACCATCTGTCT TTCATCTTCCCGCCATCT GATGAGCAGTTGAAATCT GGAAGTGCCTCTGTGTG TGCCTGCTGAATAACTTC TATCCAGAGAGGCCAAA GTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGT AACTCCAGGAGAGTGTCT

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 504]: GATATCCAGATGACCCAGTCCCCTT CCAGCTGTCCGCCCTGTGGGCGA CAGAGTACCATCACCTGTCGGTCC TCCCAGTCCATCCTGCACTCCCAACG GCAACACCTACCTGGAATGGTATCA GCAGAAGCCCGGCAAGGCCCTAAG CTGCTGATCTACAAGGTGTCCAACC GGTTCCTCCGGCTGCCCTCCAGATT CTCGGCTCTGGCTCTGGCACCGAC TTCACCTGACCATCTCCAGCCTCC AGCCCGAGGACTTCGCCACCTACTA CTGTTTCAAGGCTCCCACGTGCC TTCACCTTCGGCCAGGCCACCAAGC TGGAAATCAAAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTCTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACCTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLTISLQPEDFAT YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 509]	ACAGAGCAGGACAGCAAG GACAGCACCTACAGCCTC AGCAGCACCTGACGCTG AGCAAAAGCAGACTACGAG AAACACAAAAGTCTACGCC TCGGAAGTCACCCATCAG GGCTGAGCTCGCCCGTC ACAAAGAGCTTCAACAGG GGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 503) [SEQ ID NO: 510] RTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQE SVTEQDSKDSYSTLSSTL TLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC [SEQ ID NO: 511]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LC α 12	<p>With leader [SEQ ID NO: 512]:</p> <p>ATGGGTGGTCTCGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCGACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCTGCCTCG TGGCGACAGAGTGACCATCACCTG TCGGTCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGAAAGCCGGCAAGGC CCCTAAGCTGCTGATCTGCAAGGTG TCCAAACGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGACCATCTCC AGCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGC ACCAAGCTGGAATCAAACGAATG TGGTGCACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 514]</p> <p>MGWSCIIILFLVATATGVHSDVQ MTQSPSSLSASVDRVTITCRS SQSILHSNGNTYLEWYQKPKG APKLLICKVSNRFSGVPSRFSG SGSGDTLTITISLQPEDFATY YCFQGSHPFTFGQGTKLEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 515]:</p> <p>DVQMTQSPSSLSASVDRVTIT CRSSQSIILHSNGNTYLEWYQK PGKAPKLLICKVSNRFSGVPSR FSGSGDTFTLTISLQPEDF ATYYCFQGSHPFTFGQGTKLE IKRTVAAPSVFIIPPSDEQLKS GTASVCLLNFFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCTCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 512)</p>	<p>GACGTGCAGATGACCCAG TCCCCTCCAGCCTGTCT GCCTCGTGGCGACAGA GTGACCATCACCTGTCTG TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTATCAG CAGAAGCCGGCAAGGCC CCTAAGTCTGTATCTGC AAGGTGTCAAACCGGTTT TCCGGGTGCCCTCCAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG ACCATCTCCAGCCTCCAG CCCGAGGACTTCGCCACC TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 512)</p> <p>[SEQ ID NO: 517]</p> <p>DVQMTQSPSSLSASVDR VTITCRSSQSIILHSNGNT YLEWYQKPGKAPKLLIC KVSNRFSGVPSRFSGSGS</p>	<p>CGAACTGTGGTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCAGAGTCACC CATCAGGCTGAGCTCG CCCGTACAAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 512)</p> <p>[SEQ ID NO: 519]</p> <p>RTVAAPSVFIIPPSDEQL KSGTASVCLLNFFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSTL TLSKADYEKHKVYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 513]: GACGTGCAGATGACCCAGTCCCCTT CCAGCCTGTCTGCCCTCCGTGGCGA CAGAGTGACCATCACCTGTCGGTCC TCCCAGTCCATCTGCACTCCAACG GCAACACCTACCTGGAATGGTATCA GCAGAAGCCCGCAAGGCCCTAAG CTGCTGATCTGCAAGGTGCCAACC GGTCTCCGGCGTGCCCTCCAGATT CTCGGCTCTGGCTCTGGCACCGAC TTCACCCGTGACCATCTCCAGCCTCC AGCCCGAGGACTTGCACACCTACTA CTGTTTTC AAGGCTCCACGTGCC TTCACCTTCGGCCAGGGCACCAAGC TGGAATCAAAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTCTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACCTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLTISLQPEDFAT YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 518]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 520]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6- LC α 1 3	<p>With leader [SEQ ID NO: 521]:</p> <p>ATGGGCTGGTCCATGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCTGCCTCG TGGCGACAGAGTGACCATCACCTG TCGGTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGAAAGCCCGCAAGGC CCCTAAGCTGCTGATCTACAAGTG TCCAAACGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGACCATCTCC AGCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTCCCTCTGTGTGTGCC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 523]:</p> <p>MGWSCIIILFLVATATGVHSDVQ MTQSPSSLSASVDRVTITCRS SQSILHSNGNTYLEWYQKPKG APKLLIYKVSNRFSGVPSRFSG SGSGTDLTITISLQPEDFATY YCFQGSHPFTFGQGTKLEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 524]:</p> <p>DVQMTQSPSSLSASVDRVTIT CRSSQSIILHSNGNTYLEWYQK PGKAPKLLIYKVSNRFSGVPSR FSGSGTDFLTITISLQPEDF ATYYCFQGSHPFTFGQGTKLE IKRTVAAPSVFIIPPSDEQLKS GTASVCLLNFFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCTCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 521)</p>	<p>GACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCT GCCTCGTGGCGACAGA GTGACCATCACCTGTCTG TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGAATGGTATCAG CAGAGCCCGCAAGGCC CTAAGTCTGTATCTAC AAGGTGTCACACCGGTTT TCCGGCTGCCCTCCAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG ACCATCTCCAGCCTCCAG CCCGAGGACTTCGCCACC TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGCGACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 521)</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCAGAGTCAACC CATCAGGCTGAGCTCG CCCGTACAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 521)</p> <p>[SEQ ID NO: 528]</p> <p>RTVAAPSVFIIPPSDEQL KSGTASVCLLNFFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSTL TLSKADYEKHKVYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 522]: GACGTGCAGATGACCCAGTCCCCTT CCAGCCTGTCTGCCCTCCGTGGCGA CAGAGTACCATCACCTGTCGGTCC TCCCAGTCCATCTGCACTCCAACG GCAACACCTACCTGGAATGGTATCA GCAGAAGCCCGGCAAGGCCCTAAG CTGCTGATCTACAAGGTGTCCAACC GGTCTCCGGCGTGCCCTCCAGATT CTCGGCTCTGGCTCTGGCACCGAC TTCACCCGTACCATCTCCAGCCTCC AGCCCGAGGACTTGCACACCTACTA CTGTTTTC AAGGCTCCCAAGTGCCC TTCACCTTCGGCCAGGGCACCAAGC TGGAAATCAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTCTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAGCAGACTACGA GAAACACAAAGTCTACGCCCTCGAA GTCACCCATCAGGGCCTGAGTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLTISLQPEDFAT YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 527]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 529]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6- LC α 1 4	<p>With leader [SEQ ID NO: 530]:</p> <p>ATGGGTGGTCTCGCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCATATCCAGATGACCCAG TCCCTTCCAGCCTGTCCGCCTCTG TGGCGACAGAGTGACCATCACCTG TCGGTCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGAAAGCCGGCAAGGC CCCTAAGCTGCTGATCTGCAAGGTG TCCAAACGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGACCATCTCC AGCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTGTGTGCC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAATCCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 532]:</p> <p>MGWSCIIILFLVATATGVHSDIQ MTQSPSSLSASVDRVTITCRS SQSILHSNGNTYLEWYQQKPKG APKLLICKVSNRFSGVPSRFG SGSGDTLTITISLQPEDFATY YCFQGSHPFTFGQGTKLEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 533]:</p> <p>DIQMTQSPSSLSASVDRVTIT CRSSQSIILHSNGNTYLEWYQQK PGKAPKLLICKVSNRFSGVPSR FSGSGDTFTLTISLQPEDF ATYYCFQGSHPFTFGQGTKLE IKRTVAAPSVFIIPPSDEQLKS GTASVCLLNFFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 530) [SEQ ID NO: 534]</p>	<p>GATATCCAGATGACCCAG TCCCTTCCAGCCTGTCC GCCTCTGTGGCGACAGA GTGACCATCACCTGTCCG TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTATCAG CAGAACCCGGCAAGGCC CCTAAGTCTGTATCTGC AAGGTGTCAAACCGGTTT TCCGGGTGCCCTCCAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG ACCATCTCCAGCCTCCAG CCCGAGGACTTCGCCACC TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 530) [SEQ ID NO: 535]</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGTGCCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCCCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCAGAGTCAACC CATCAGGGCCTGAGCTCG CCCGTACAAAAGAGCTTC AACAGGGGAGAGTGTGA (nucleotides 394 to 714 of SEQ ID NO: 530) [SEQ ID NO: 537]</p> <p>RTVAAPSVFIIPPSDEQL KSGTASVCLLNFFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSTL TLISKADYEKHKVYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 531]: GATATCCAGATGACCCAGTCCCCTT CCAGCCTGTCCGCCTCTGTGGCGA CAGAGTACCATCACCTGTCGGTCC TCCAGTCCATCTGCACTCCCAACG GCAACACCTACCTGGAATGGTATCA GCAGAAGCCCGCAAGGCCCTAAG CTGCTGATCTGCAAGGTGTCCAACC GGTCTCCGGCGTGCCCTCCAGATT CTCGGCTCTGGCTCTGGCACCGAC TTCACCCGTACCATCTCCAGCCTCC AGCCCGAGGACTTGCACACCTACTA CTGTTTTCAGGCTCCCACGTGCC TTCACCTTCGGCCAGGGCACCAGC TGGAATCAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACCTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCC TGACGCTGAGCAAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG			GTDFTLTISLQPEDFAT YYCFQGSHPVFTFGQGTK LEIK [SEQ ID NO: 536]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 538]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	AGAGTGTGA				
7G6-LC α 15	<p>With leader [SEQ ID NO: 539]:</p> <p>ATGGGCTGGTCCATGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCTGCCTCG TGGCGACAGAGTGACCATCACCTG TCGGTCTCTCCAGTCCATCCTGCAC TCCAAAGGCAACACCTACCTGGAAT GGTATCAGCAGAAAGCCCGCAAGGC CCCTAAGCTGCTGATCTCCAAGGTG TCCAAACGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGACCATCTCC AGCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACCTTCGGCCAGGC ACCAAGCTGGAATCAAACGAATG TGGTGACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTCCCTCTGTGTGTGCC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAG ACTACGAGAAACACAAAAGTCTACGC</p>	<p>With leader [SEQ ID NO: 541]:</p> <p>MGWSCIIILFLVATATGVHSDVQ MTQSPSSLSASVDRVTITCRS SQSILHSNGNTYLEWYQQKPGK APKLLISKVSNRFSGVPSRFSG SGSGDTLTITSSLPQEDFATY YCFQGSHPFTFGQGTKEIKR TVAAPSVFIIPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC</p> <p>Without leader [SEQ ID NO: 542]:</p> <p>DVQMTQSPSSLSASVDRVTIT CRSSQSIILHSNGNTYLEWYQQK PGKAPKLLISKVSNRFSGVPSR FSGSGDTFTLTITSSLPQEDF ATYYCFQGSHPFTFGQGTKE IKRTVAAPSVFIIPPSDEQLKS GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC</p>	<p>ATGGGCTG GTCTGCA TCATCTCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 539)</p>	<p>GACGTGCAGATGACCCAG TCCCCTTCAGCCTGTCT GCCTCCGTGGCGACAGA GTGACCATCACCTGTCTG TCCTCCAGTCCATCCTG CACTCCAAACGGCAACACC TACCTGGAATGGTATCAG CAGAACCCGGCAAGGCC CCTAAGTGTGATCTCC AAGGTGTCAAACCGGTTT TCCGGGTGCCCTCCAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCCTG ACCATCTCCAGCCTCCAG CCCGAGGACTTCGCCACC TACTACTGTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 539)</p> <p>[SEQ ID NO: 544]</p> <p>DVQMTQSPSSLSASVDR VTITCRSSQSIILHSNGNT YLEWYQQKPGKAPKLLIS KVSNRFSGVPSRFSGSGS</p>	<p>CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGAACTGCCTCT GTTGTGTGCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAAGTC TACGCTGCAGAGTCAACC CATCAGGCTGAGCTCG CCCGTCAAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 539)</p> <p>[SEQ ID NO: 546]</p> <p>RTVAAPSVFIIPPSDEQL KSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDSYSLSTL TLSKADYEKHKVYACEVT</p>

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCAAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID NO: 540]: GACGTGCAGATGACCCAGTCCCCTT CCAGCCTGTCTGCCCTCCGTGGCGA CAGAGTACCATCACCTGTCGGTCC TCCCAGTCCATCTGCACTCCCAACG GCAACACCTACCTGGAATGGTATCA GCAGAAGCCCGGCAAGGCCCTAAG CTGCTGATCTCCAAGGTGCCAACC GGTTCCTCGGCGTGCCCTCCAGATT CTCGGGCTCTGGCTCTGGCACCGAC TTCACCCCTGACCATCTCCAGCCTCC AGCCCGAGGACTTGGCCACCTACTA CTGTTTTCAGGCTCCCACGTGCC TTCACCTTCGGCCAGGGCACCAAGC TGGAAATCAAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACCTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGACCCC TGACGCTGAGCAAGCAG			GTDFTLTISLQPEDFAT YYCFQGSHPFTFGQGTK LEIK [SEQ ID NO: 545]	HQGLSSPVTKSFNRGEC [SEQ ID NO: 547]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
7G6-Lczu16	With leader [SEQ ID NO: 548]: ATGGGTGGTCTGTCATCATCCTGT TTCTGGTGGCCACCGCCACCGCGT GCACAGCGACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCTGCCTCG TGGCGACAGAGTGACCATCACCTG TCGGTCTCCAGTCCATCGTGAC TCCAACGGCAACACCTACCTGGAAT GGTATCAGCAGAAGCCCGCAAGGC CCCTAAGCTGCTGATCTCCAAGTG TCCAACCGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CACCAGCTTCACTTCACTGACCATCTCC AGCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACTTCCGGCCAGGC ACCAAGCTGGAATCAACGAACTG TGGCTGCACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGACAG ACTACGAGAAACACAAAGTCTACGC CTGCGAAGTACCCATCAGGGCCTG AGCTCGCCCGTCAACAAAGCTTCA ACAGGGGAGAGTGTGA	With leader [SEQ ID NO: 550]: MGWSCIIILFLVATATGVHSDVQ MTQSPSSLSASVGDRTITCRS SQSIVHSNGNTYLEWYQKPGK APKLLISKVSNRFSGVPSRFSG SGSGTDTLTISLQPEDFATY YCFQGSHPVFTFGQGTKEIKR TVAAPSVFIFFPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKKHKVYACEV THQGLSPVTKSFNRGEC Without leader [SEQ ID NO: 551]: DVQMTQSPSSLSASVGDRTIT CRSSQSIHVSNGNTYLEWYQK PGKAPKLLISKVSNRFSGVPSR FSGSGTDTLTISLQPEDF ATYFCFQGSHPVFTFGQGTKE IKRTVAAPSVFIFFPSDEQLKS GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHYA CEVTHQGLSPVTKSFNRGEC	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 548) [SEQ ID NO: 552]	GACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCT GCCTCCGTGGCGACAGA GTGACCATCACCTGTGG TCCTCCAGTCCATCGTG CACTCCAACGGCAACACC TACCTGGAATGGTATCAG CAGAAGCCCGCAAGGCC CCTAAGCTGCTGATCTCC AAGGTGTCACACCGGTTT TCCGGCTGCCCCTCCAGA TTCTCCGGCTCTGGCTCT GGCACCACTTCACTCTG ACCATCTCCAGCTCCAG CCGAGGACTTCGCCACC TACTACTGTTTCAAGGC TCCCACGTGCCCTTCAAC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 548) [SEQ ID NO: 553]	CGAACTGTGGCTGCACCA TCTGTCTTCATCTCCCG CCATCTGATGAGCAGTTG AAATCTGGAACCTGCCTCT GTTGTGTGCCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCGAAGTCACC CATCAGGGCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 548) [SEQ ID NO: 555]
				DVQMTQSPSSLSASVGDRTITCRSSQSIHVSNGNTYLEWYQKPGKAPKLLISKVSNRFSGVPSR FSGSGTDTLTISLQPEDFATYFCFQGSHPVFTFGQGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC	RTVAAPSVFIFFPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC [SEQ ID NO: 556]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	Without leader [SEQ ID NO: 549]: GACGTGCAGATGACCCAGTCCCTT CCAGCTGTCTGCCCTCCGTGGCGA CAGAGTGACCATCACCTGTGGTCC TCCAGTCCATCGTGCACTCCAAG GCAACACCTACCTGGAATGGTATCA GCAGAAGCCCCGGCAAGCCCCCTAAG CTGCTGATCTCCAAGGTGTCCAACC GGTTCTCCGGCGTGCCCTCCAGATT CTCCGGCTCTGGCTCTGGCACCGAC TTCACCCCTGACCATCTCCAGCCTCC AGCCCCGAGGACTTCGCCACCTACTA CTGTTTTCAGGCTCCCACTGTGCC TTCACCTTCGGCCAGGCCACCAAGC TGGAAATCAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTGTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGA GAAACACAAAAGTCTACGCCCTGCGAA GTCACCCCATCAGGGCCTGAGCTCGC CCGTACAAAAGAGCTTCAACAGGGG AGAGTGTGA				

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
7G6-LC α 17	With leader [SEQ ID NO: 557]: ATGGGCTGGTCTCGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCTGCCTCG TGGCGACAGAGTGACCATCACCTG TCGGTCTCCAGTCCATCGTGAC TCCAACGGCAACACCTACCTGAAT GGTATCAGCAGAAGCCCGCAAGGC CCCTAAGCTGCTGATCTCCAAGTG TCCAACCGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CACCAGCTTACCCCTGACCATCTCC AGCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTCAAGGCTCCCA CGTGCCCTTACCTTCGGCCAGGCG ACCAAGCTGGAATCAACGAACTG TGGCTGCACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGACAG ACTACGAGAAACACAAAGTCTAGC CTGCGAAGTACCCCATCAGGCGCTG AGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGTGA	With leader [SEQ ID NO: 559]: MGWSCIIILFLVATATGVHSDVQ MTQSPSSLSASVGDRTITCRS SQSIVHSNGNTYLNWYQQKPGK APKLLISKVSNRFSGVPSRFSG SGSGDTFTLTISLQPEDFATY YCFQGSHPVFTFGQGTKEIKR TVAAPSVFIFFPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEV THQGLSPVTKSFNRGEC Without leader [SEQ ID NO: 560]: DVQMTQSPSSLSASVGDRTIT CRSSQSIHVSNGNTYLNWYQQK PGKAPKLLISKVSNRFSGVPSR FSGSGGTFTLTISLQPEDF ATYFCFQGSHPVFTFGQGTKE IKRTVAAPSVFIFFPSDEQLKS GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSPVTKSFNRGEC	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 557) [SEQ ID NO: 561]	GACGTGCAGATGACCCAG TCCCTTCCAGCCTGTCT GCCTCCGTGGCGACAGA GTGACCATCACCTGTGG TCCTCCAGTCCCATCGTG CACTCCAACGGCAACACC TACCTGAATGGTATCAG CAGAAGCCCGCAAGGCC CCTAAGCTGCTGATCTCC AAGGTGTCACACCGGTTT TCCGGCTGCCCCTCCAGA TTCTCCGGCTCTGGCTCT GGCACCACTTACCCTG ACCATCTCCAGCTCCAG CCGAGGACTTCGCCACC TACTACTGTTTCAAGGC TCCCACGTGCCCTTCAAC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 557) [SEQ ID NO: 562]	CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCC CCATCTGATGAGCAGTTG AAATCTGGAACCTGCCTCT GTTGTGTGCCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCGAAGTCACC CATCAGGCGCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGTGA (nucleotides 394 to 714 of SEQ ID NO: 557) [SEQ ID NO: 564]
				DVQMTQSPSSLSASVGDRTITCRSSQSIHVSNGNTYLNWYQQKPGKAPKLLISKVSNRFSGVPSR FSGSGGTFTLTISLQPEDFATYFCFQGSHPVFTFGQGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	RTVAAPSVFIFFPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	Without leader [SEQ ID NO: 558]: GACGTGCAGATGACCCAGTCCCTT CCAGCTGTCTGCCCTCCGTGGCGA CAGAGTGACCATCACCTGTGGTCC TCCAGTCCATCGTGCACTCCAAG GCAACACCTACCTGAACCTGGTATCA GCAGAAGCCCGGCAAGGCCCTAAG CTGCTGATCTCCAAGGTGTCCAACC GGTTCTCCGGGTGCCCTCCAGATT CTCCGGCTCTGGCTCTGGCACCGAC TTCACCTGACCATCTCCAGCTCC AGCCCGAGGACTTCGCCACCTACTA CTGTTTCAAGGCTCCACGTGCC TTCACCTTCGGCCAGGCCACCAAGC TGGAAATCAAACGAACTGTGGTGC ACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTGTGTGTGCTGCTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACCTCCAGGAGAG TGTACAGAGCAGGACAGCAAGGAC AGCACCTACAGCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGA GAAACACAAAAGTCTACGCTGCGAA GTACCCCATCAGGGCTGAGTCGC CCGTACAAAAGACTTCAACAGGGG AGAGTGTGA				

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
7G6-LC2u18	With leader [SEQ ID NO: 566]: ATGGGCTGGTCTCGCATCATCCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCGATATCCAGATGACCCAG TCCCTTCCAGCCTGTCCGCCTCTG TGGCGACACAGAGTGACCATCACCTG TCGGTCTCTCCAGTCCATCCTGCAC TCCAACGGCAACACCTACCTGGAAT GGTATCAGCAGAAGCCCGCAAGGC CCCTAAGCTGCTGATCTCCAAGTG TCCAACCGGTTCTCCGGCGTGCCCT CCAGATTCTCCGGCTCTGGCTCTGG CAGCGACTTCAACCTGACCATCTCC AGCTCCAGCCCGAGGACTTCGCCA CCTACTACTGTTTCAAGGCTCCCA CGTGCCCTTCACTTCCGGCCAGGC ACCAAGCTGGAATCAACGAACTG TGGCTGCACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTTGAAA TCTGGAAGTGCCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGACAG ACTCAGAGAAACACAAAGTCTACGC CTCGGAAGTACCCATCAGGGCCTG AGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGTGA Without leader [SEQ ID	With leader [SEQ ID NO: 568]: MGWSCIIILFLVATATGVHSDIQ MTQSPSSLSASVGDRTVITCRS SQSILHSNGNTYLEWYQKPGK APKLLISKVSNRFSGVPSRFSG SGSGTDTLTISLQPEDFATY YCFQGSHPVFTFGQGTKEIKR TVAAPSVFIFFPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKKHKVYACEV THQGLSSPVTKSFNRGEC Without leader [SEQ ID NO: 569]: DIQMTQSPSSLSASVGDRTVIT CRSSQSIILHSNGNTYLEWYQK PGKAPKLLISKVSNRFSGVPSR FSGSGGTDTLTISLQPEDF ATYCYFQGSHPVFTFGQGTKE IKRTVAAPSVFIFPPSDEQLK GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHKVYA CEVTHQGLSSPVTKSFNRGEC	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 566) [SEQ ID NO: 570]	GATATCCAGATGACCCAG TCCCTTCCAGCCTGTCC GCCTCTGTGGCGACAGA GTGACCATCACCTGTGG TCCTCCAGTCCATCCTG CACTCCAACGGCAACACC TACCTGGAATGGTATCAG CAGAAGCCCGCAAGGCC CCTAAGCTGTGATCTCC AAGGTGTCCAACCGGTTT TCCGGCTGCCCCTCCAGA TTCTCCGGCTCTGGCTCT GGCACGACTTCAACCTG ACCATCTCAGCCTCCAG CCGAGGACTTCGCCACC TACTACTGTTTCAAGGC TCCCACGTGCCCTTCAAC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 566) [SEQ ID NO: 571]	CGAACTGTGGCTGCACCA TCTGTCTTCATCTTCCC CCATCTGATGAGCAGTTG AAATCTGGAACCTGCCTCT GTTGTGTGCCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGGAA GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCCTCAGCAGCACCTCTG ACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTC TACGCTGCGAAGTCACC CATCAGGCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGTGA (nucleotides 394 to 714 of SEQ ID NO: 566) [SEQ ID NO: 573]
	Without leader [SEQ ID	DIQMTQSPSSLSASVGDRTVITCRSSQSIILHSNGNTYLEWYQKPGKAPKLLISKVSNRFSGVPSR FSGSGGTDTLTISLQPEDFATYCYFQGSHPVFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC	[SEQ ID NO: 572]	DIQMTQSPSSLSASVGDRTVITCRSSQSIILHSNGNTYLEWYQKPGKAPKLLISKVSNRFSGVPSRFSGSGS GTDTLTISLQPEDFATYCYFQGSHPVFTFGQGTKEIK [SEQ ID NO: 574]	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC [SEQ ID NO: 574]

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	NO: 567]: GATATCCAGATGACCCAGTCCCCCTT CCAGCCTGTCCGCCTCTGTGGCGA CAGAGTGACCATCACCTGTGGTCC TCCCAGTCCATCCTGCACCTCCAACG GCAACACCTACCTGGAATGGTATCA GCAGAAGCCCGGCAAGGCCCTAAG CTGCTGATCTCCAAGGTGTCAACC GGTTCCTCCGGGTGCCCTCCAGATT CTCGGGCTCTGGCTCTGGCACCGAC TTCACCCCTGACCATCTCCAGCCTCC AGCCCGAGGACTTCGCCACCTACTA CTGTTTTC AAGGCTCCACAGTGCCC TTCACCTTCGGCCAGGGCACCAAGC TGGAAATCAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTCTGTTGTGTGCTGTGAA TAACTTCTATCCCGAGAGAGGCCAAA GTACAGTGGAAAGGTGGATAACGCC TCCAAATCGGGTAACTCCAGGAGAG TGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGA GAAACACAAAGTCTACGCCTGCGAA GTCACCCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG AGAGTGTGA				
7G6-LCzu21	With leader [SEQ ID NO: 575]: ATGGGCTGGTCTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT	With leader [SEQ ID NO: 577]: MGWSCIILFLVATATGVHSDVV MTQSPSLSPVTLGQPASISCRS	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT	GACGTCGTGATGACACAG TCCCCCCTGTCCCTGCCT GTGACCCCTGGACAGCCT GCCTCCATCTCCTGCAGA	CGAACTGTGGCTGCACCA TCTGTCTTTCATCTTCCCG CCATCTGATGAGCAGTTG AAATCTGGAACCTGCCTCT

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	GCACAGCGACGTCGTGATGACACAG TCCCCCTGTCCCTGCCCTGTGACCC TGGGACAGCCTGCCCTCCATCTCCTG CAGATCCTCCAGTCACATCCTGCAC TCCAACGGCAACACCTACCTGGAAT GGTTCAGCAGCGCCTGGCCAGTC CCCCAGACTGCTGATCTCCAAGTG TCCAACGGTTCCTCCGGCGTGCCCG ACAGATTCTCCGGCTCTGGCTCTGG CACCGACTTCACCCCTGAAGATCTCC CGGGTGAAGCCGAGGACGTGGCG TGTACTACTGTTTTCAAGGCTCCCA CGTGCCCTTACCTTCGGCCAGGC ACCAAGCTGGAATCAACGAAGTG TGGCTGACCATCTGCTTTCATCTT CCGCCATCTGATGACGAGTTGAAA TCTGGAACCTGCTCTGTTGTGTC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGGAAGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAG ACTACGAGAAACACAAAGTCTACGC CTGCGAAGTACCCCATCAGGGCCTG AGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGAGAGTGTGA	SQSILHSNGNTYLEWFQQRPGQ SPRLISKVSNRFSVDPDRFSG SGSGTDTLTKISRVEAEDVGVI YCFQGSHPVFTFGQGTLEIKR TVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSTYS LSSTLTLSKADYEKKHVKYACEV THQGLSSPVTKSFNREGC Without leader [SEQ ID NO: 578]: DVVMTQSPSLPVTLGQPASIS CRSSQSIILHSNGNTYLEWFQQR PGQSPRLISKVSNRFSVDPDR FSGSGTDTLTKISRVEAEDV GVYCFQGSHPVFTFGQGTLE IKRTVAAPSVFIFPPSDEQLKS GTASVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKKHVKYA CEVTHQGLSSPVTKSFNREGC	GGCCACCG CCACCGGC GTGCACAG C (nucleotides 1 to 57 of SEQ ID NO: 575) [SEQ ID NO: 579]	TCCTCCAGTCCATCCTG CACTCAACGGCAACACC TACCTGGAATGGTTCAG CAGCGCCTGGCCAGTCC CCCAGACTGCTGATCTCC AAGGTGTCCAAACCGGTTT TCCGGGTGCCGACAGA TTCTCCGGTCTGGCTCT GGCACCAGTTCACCTG AAGATCTCCGGGTGGA GCCGAGGACGTGGCGTG TACTACTGTTTCAAGGC TCCCACGTGCCCTTCAAC TTCGGCCAGGACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 575) [SEQ ID NO: 580]	GTTGTGTGCCTGCTGAAT AACTTCTATCCAGAGAG GCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGAGCAGGAC AGCAAGGACAGCACCTAC AGCTCAGCAGCACCTG ACGCTGAGCAAGCAGAC TACGAGAAACACAAAGTC TACGCCCTGCAAGTCACC CATCAGGCTGAGCTCG CCCCTCACAAAGAGCTTC AACAGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 575) [SEQ ID NO: 582] RTVAAPSVFIFPPSDEQL KSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQ SVTEQDSKDYSTLSSTL TLSKADYEKKHVKYACEV HQGLSSPVTKSFNREGC [SEQ ID NO: 583]
	Without leader [SEQ ID NO: 576]: GACGTCGTGATGACACAGTCCCCC TGTCCTGCTGTGACCCCTGGACA			DVMTQSPSLPVTLGQP ASISCRSSQSIILHSNGNT YLEWFQQRPGQSPRLIS KVSNRFSVDPDRFSGSGS GTDFTLKISRVEAEDVGV YYCFQGSHPVFTFGQGT LEIK [SEQ ID NO: 581]	

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	GCCTGCCTCCATCTCCTGCAGATCC TCCCAGTCCATCCTGCACTCCACG GCAACACCTACCTGGAATGGTTCCA GCAGCGCCTGGCCAGTCCCCCAGA CTGCTGATCTCCAAGGTGTCCAACC GGTTCTCCGGCGTGCCCGACAGATT CTCCGGCTCTGGCTCTGGCACCGAC TTCACCCCTGAAGATCTCCCGGTGG AAGCCGAGGACGTGGCGGTGTACTA CTGTTTCAAGGCTCCACCGTCCCC TTCACCTTCGGCCAGGCCACCAAGC TGGAAATCAAACGAACTGTGGCTGC ACCATCTGTCTTCACTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCTCTGTGTGTGCCTGTGAA TAACTTCTATCCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCC TCCAATCGGGTAACTCCCAGGAGAG TGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACC TGACGCTGAGCAAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCCAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGG AGAGTGTGA				
7G6-LC2u2	With leader [SEQ ID NO: 584]: ATGGGTGGTCTCTGCATCATCTCTGT TTCTGGTGGCCACCGCCACCGGCGT GCACAGCAGCAGTCGTGATGACACAG TCCCCCTGTCCCTGCCTGTGACCC TGGGACAGCCTGCCTCCATCTCCTG	With leader [SEQ ID NO: 586]: MGWSCIIILFLVATATGVHSDVV MTQSPSLPVTILGQPASISCRS SQSILHSNGNTYLEWYQQRPGQ SPRRLISKVSNRFSGVDPDRFSG	ATGGGCTG GTCCTGCA TCATCCTG TTTCTGGT GGCCACCG CCACCGGC GTGCACAG	GACGTCGTGATGACACAG TCCCCCTGTCTCCTGCCT GTGACCCCTGGACAGCCTT GCCTCCATCTCCTGCAGA TCCTCCAGTCCATCTCTG CACTCCAAACGGCAACACC TACCTGGAATGGTATCAG	CGAACTGTGGCTGCACCA TCTGTCTTCACTCTCCCG CCATCTGATGAGCAGTTG AAATCTGGAACCTGCCTCT GTTGTGTGCCTGCTGAAT AACTTCTATCCCAGAGAG GCCAAAGTACAGTGGAG

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	CAGATCCTCCCAGTCCATCCTGCAC TCCAAACGGCAACACCTACCTGGAAT GGTATCAGCAGCGGCTTGGCCAGTC CCCAGACGGCTGATCTCCAGAGTG TCCAAACGGTTCTCTGGCTGCCCG ACAGATTCTCGGCTCTGGCTCTGG CACCAGACTTCACCCCTGAAGATCTCC CGGGTGAAGCCGAGGACGTGGCG TGTACTACTGTTTTCAAGGCTCCCA CGTGCCCTTCACTTCGGCCAGGGC ACCAAGCTGAAATCAACGAACTG TGGCTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTTGAAA TCTGGAACCTGCCTCTGTTGTGCC TGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAACCTCC AGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTCTACGC CTGCGAAGTACCCCATCAGGCCCTG AGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGA	SGSGTDFTLKISRVEAEDVGVY YCFQGSHPVFTFGQGTGLEIKR TVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC Without leader [SEQ ID NO: 587]: DVVMTQSPSLSPVTLGQPASIS CRSSQILHSNGNTYLEWYQQR PGQSPRRRLISKVSNNRFSGVPDR FSGSGTDFTLKISRVEAEDV GVYCFQGSHPVFTFGQGTGLE IKRTVAAPSVFIFPPSDEQLKLS GTASVVCLLNFFYPREAKVQWK VDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC	C (nucleotides 1 to 57 of SEQ ID NO: 584) [SEQ ID NO: 588]	CAGGGCCTGGCCAGTCC CCCAGACGGCTGATCTCC AAGGTGTCACACCGGTTT TCTGGCTGCCCCGACAGA TTCTCCGGCTCTGGCTCT GGCACCGACTTCACCCTG AAGATCTCCGGGTGGAA GCCGAGGACGTGGGCGTG TACTACTGTTTTCAAGGC TCCCACGTGCCCTTCACC TTCGGCCAGGGCACCAAG CTGGAATCAAA (nucleotides 58 to 393 of SEQ ID NO: 584) [SEQ ID NO: 589]	GTGATAAACGCCCTCCAA TCGGGTAACCTCCAGGAG AGTGTACAGACAGGACG AGCAAGCAGGACGACCTAC AGCCTCAGCAGCACCCTG ACGCTGAGCAAAACGACAG TACGAGAAACACAAAGTCC TACGCCTGCGAAGTCAACC CATCAGGGCCTGAGCTCG CCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT (nucleotides 394 to 714 of SEQ ID NO: 584) [SEQ ID NO: 591] RTVAAPSVFIFPPSDEQL KSGTASVVCCLLNNFYPRE AKVQWKVDNALQSGNSQE SVTEQDSKDSYSLSTL TLISKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC [SEQ ID NO: 592]
	Without leader [SEQ ID NO: 585]: GACGTCGTGATGACACAGTCCCCC TGTCCTGCCTGTGACCCCTGGACA GCCTGCCTCCATCTCCTGCAGATCC TCCAGTCCATCCTGCACCTCCAACG GCAACACCTACCTGGAATGGTATCA			LEV [SEQ ID NO: 590]	

Clone Name (Species & Isotype)	Light Chain DNA Sequence	Light Chain Amino Acid Sequence	cDNA Position Leader	Variable Domain (cDNA) (amino acid)	Constant Domain (cDNA) (amino acid)
	GCAGGGCCCTGGCCAGTCCCCCAGA CGGCTGATCTCCAAGGTGTCCACC GGTCTCTGGCGTGCCCGACAGATT CTCGGGCTCTGGCTCTGGCACCGAC TTCACCCCTGAAGATCTCCCGGGTGG AAGCCGAGGACGTGGCGTGTACTA CTGTTTCAAGGTCCTCCACGTGCCC TTCACCTTCGGCCAGGCCACCAAGC TGGAAATCAAACGAACTGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAA CTGCCCTCTGTTGTGTGCTGTGAA TAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAGGTGGATAACGCC TCCAATCGGGTAACTCCCAGGAGAG TGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGA GAAACACAAAAGTCTACGCCTGCGAA GTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAAGACTTCAACAGGGG AGAGTGTGA				

Table 1 (cont.): 7G6 VH numbered according to Kabat

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
mouse 7G6-Vh	ACCTACTGGATC ACC [SEQ ID NO: 593]	TYWIT [SEQ ID NO: 594]	GATATTTATCCTGGTAGTA TTTGTAACATAATGAGAAATT CAAGAGC [SEQ ID NO: 595]	DIYPGSSICNYNEK FKS [SEQ ID NO: 596]	GAGGATGGTTACGACGCCTGGTTT GCTTAC [SEQ ID NO: 597]	EDGYDAWF AY [SEQ ID NO: 598]
7G6-HCzu1	ACCTACTGGATC ACC [SEQ ID NO: 599]	TYWIT [SEQ ID NO: 600]	GACATCTACCCGGCTCCTCCA TCTGCAACTAACGAGAAATT CAAGTCC [SEQ ID NO: 601]	DIYPGSSICNYNEK FKS [SEQ ID NO: 602]	GAGGACGGCTACGACGCCTGGTTT GCCTAC [SEQ ID NO: 603]	EDGYDAWF AY [SEQ ID NO: 604]
7G6-HCzu2	ACCTACTGGATC ACC [SEQ ID NO: 605]	TYWIT [SEQ ID NO: 606]	GACATCTACCCGGCTCCTCCA TCTGCAACTAACGAGAAATT CAAGTCC [SEQ ID NO: 607]	DIYPGSSICNYNEK FKS [SEQ ID NO: 608]	GAGGACGGCTACGACGCCTGGTTT GCCTAC [SEQ ID NO: 609]	EDGYDAWF AY [SEQ ID NO: 610]
7G6-HCzu3	ACCTACTGGATC ACC [SEQ ID NO: 611]	TYWIT [SEQ ID NO: 612]	GACATCTACCCGGCTCCTCCA TCTGCAACTAACGAGAAATT CAAGTCC [SEQ ID NO: 613]	DIYPGSSICNYNEK FKS [SEQ ID NO: 614]	GAGGACGGCTACGACGCCTGGTTT GCCTAC [SEQ ID NO: 615]	EDGYDAWF AY [SEQ ID NO: 616]
7G6-HCzu4	ACCTACTGGATC ACC [SEQ ID NO: 617]	TYWIT [SEQ ID NO: 618]	GACATCTACCCGGCTCCTCCA TCTGCAACTACGCCAGAAATT CCAGGGC [SEQ ID NO: 619]	DIYPGSSICNYAOK FQG [SEQ ID NO: 620]	GAGGACGGCTACGACGCCTGGTTT GCCTAC [SEQ ID NO: 621]	EDGYDAWF AY [SEQ ID NO: 622]
7G6-HCzu5	ACCTACTGGATC ACC [SEQ ID NO: 623]	TYWIT [SEQ ID NO: 624]	GACATCTACCCGGCTCCTCCA TCTGCAACTAACGAGAAATT CAAGTCC [SEQ ID NO: 625]	DIYPGSSISNYNEK FKS [SEQ ID NO: 626]	GAGGACGGCTACGACGCCTGGTTT GCCTAC [SEQ ID NO: 627]	EDGYDAWF AY [SEQ ID NO: 628]
7G6-HCzu6	ACCTACTGGATC ACC [SEQ ID NO: 629]	TYWIT [SEQ ID NO: 630]	GACATCTACCCGGCTCCTCCA TCTGCAACTAACGAGAAATT CAAGTCC [SEQ ID NO: 631]	DIYPGSSISNYNEK FKS [SEQ ID NO: 632]	GAGGACGGCTACGACGCCTGGTTT GCCTAC [SEQ ID NO: 633]	EDGYDAWF AY [SEQ ID NO: 634]
7G6-HCzu7	ACCTACTGGATC ACC	TYWIT [SEQ ID NO: 635]	GACATCTACCCGGCTCCTCCA TCTGCAACTACGCCAGAAATT	DIYPGSSISNYAOK FQG	GAGGACGGCTACGACGCCTGGTTT GCCTAC	EDGYDAWF AY

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
	[SEQ ID NO: 635] ACCTACTGGATC ACC	ID NO: 636 [SEQ ID NO: 637] TYWIT [SEQ ID NO: 642] TYWIT [SEQ ID NO: 647]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CCAGGGC [SEQ ID NO: 643] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CCAGGGC [SEQ ID NO: 649]	[SEQ ID NO: 638] DIYPGSSISNYAQK FQG [SEQ ID NO: 644] DIYPGSSISNYAQK FQG [SEQ ID NO: 650]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu8	[SEQ ID NO: 641] ACCTACTGGATC ACC	ID NO: 642 [SEQ ID NO: 647] TYWIT [SEQ ID NO: 648]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CCAGGGC [SEQ ID NO: 643] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CCAGGGC [SEQ ID NO: 649]	[SEQ ID NO: 638] DIYPGSSISNYAQK FQG [SEQ ID NO: 644] DIYPGSSISNYAQK FQG [SEQ ID NO: 650]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu9	[SEQ ID NO: 647] ACCTACTGGATC ACC	ID NO: 648 [SEQ ID NO: 649] TYWIT [SEQ ID NO: 654]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CCAGGGC [SEQ ID NO: 643] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CCAGGGC [SEQ ID NO: 649]	[SEQ ID NO: 638] DIYPGSSISNYAQK FQG [SEQ ID NO: 644] DIYPGSSISNYAQK FQG [SEQ ID NO: 650]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu10	[SEQ ID NO: 653] ACCTACTGGATC ACC	ID NO: 654 [SEQ ID NO: 659] TYWIT [SEQ ID NO: 660]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGTCC [SEQ ID NO: 655] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGTCC [SEQ ID NO: 661]	[SEQ ID NO: 638] DIYPGSSISNYAQK FQG [SEQ ID NO: 644] DIYPGSSISNYAQK FQS [SEQ ID NO: 662]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu11	[SEQ ID NO: 659] ACCTACTGGATC ACC	ID NO: 660 [SEQ ID NO: 665] TYWIT [SEQ ID NO: 666]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGTCC [SEQ ID NO: 655] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGTCC [SEQ ID NO: 661]	[SEQ ID NO: 638] DIYPGSSISNYAQK FQS [SEQ ID NO: 662]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu12	[SEQ ID NO: 665] ACCTACTGGATC ACC	ID NO: 666 [SEQ ID NO: 671] TYWIT [SEQ ID NO: 672]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 667] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 673]	[SEQ ID NO: 638] DIYPGSSISNYAQK FQS [SEQ ID NO: 668]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu13	[SEQ ID NO: 671] ACCTACTGGATC ACC	ID NO: 672 [SEQ ID NO: 677] TYWIT [SEQ ID NO: 678]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 667] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 673]	[SEQ ID NO: 638] DIYPGSSISNYAQK VKG [SEQ ID NO: 674]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu14	[SEQ ID NO: 677] ACCTACTGGATC ACC	ID NO: 678 [SEQ ID NO: 683] TYWIT [SEQ ID NO: 684]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 667] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 673]	[SEQ ID NO: 638] DIYPGSSISNYAQK FKG [SEQ ID NO: 680]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]
7G6-HCzu15	[SEQ ID NO: 683] ACCTACTGGATC ACC	ID NO: 684 [SEQ ID NO: 689] TYWIT [SEQ ID NO: 690]	CCAGGGC GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 667] GACATCTACCCGGGCTCCTCCA TCTGCAACTACGCCAGAAAGTT CAAGGGC [SEQ ID NO: 673]	[SEQ ID NO: 638] DIYPGSSISNYAQK FKS [SEQ ID NO: 680]	[SEQ ID NO: 639] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 645] GAGGACGGCTACGACGCTTGGTTT GCCTAC [SEQ ID NO: 651]	[SEQ ID NO: 640] EDGYDAWF AY [SEQ ID NO: 646] EDGYDAWF AY [SEQ ID NO: 652]

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
	[SEQ ID NO: 683] ACCTACTGGATC ACC	[SEQ ID NO: 684] TYWIT [SEQ ID NO: 690]	CAAGTCC [SEQ ID NO: 685] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 691]	[SEQ ID NO: 686] DIYPGSSICNYNEK FKS [SEQ ID NO: 692]	[SEQ ID NO: 687] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 693]	[SEQ ID NO: 688] EDGYDAWF AY [SEQ ID NO: 694]
7G6-HCzu16	[SEQ ID NO: 689] ACCTACTGGATC ACC	[SEQ ID NO: 690] TYWIT [SEQ ID NO: 696]	CAAGTCC [SEQ ID NO: 697] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 697]	[SEQ ID NO: 698] DIYPGSSICNYNEK FKS [SEQ ID NO: 698]	[SEQ ID NO: 699] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 699]	[SEQ ID NO: 700] EDGYDAWF AY [SEQ ID NO: 700]
7G6-HCzu17	[SEQ ID NO: 695] ACCTACTGGATC ACC	[SEQ ID NO: 696] TYWIT [SEQ ID NO: 702]	CAAGTCC [SEQ ID NO: 703] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 703]	[SEQ ID NO: 704] DIYPGSSICNYNEK FKS [SEQ ID NO: 704]	[SEQ ID NO: 705] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 705]	[SEQ ID NO: 706] EDGYDAWF AY [SEQ ID NO: 706]
7G6-HCzu18	[SEQ ID NO: 701] ACCTACTGGATC ACC	[SEQ ID NO: 702] TYWIT [SEQ ID NO: 708]	CAAGTCC [SEQ ID NO: 709] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 709]	[SEQ ID NO: 710] DIYPGSSICNYNEK FKG [SEQ ID NO: 710]	[SEQ ID NO: 711] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 711]	[SEQ ID NO: 712] EDGYDAWF AY [SEQ ID NO: 712]
7G6-HCzu19	[SEQ ID NO: 707] ACCTACTGGATC ACC	[SEQ ID NO: 708] TYWIT [SEQ ID NO: 714]	CAAGTCC [SEQ ID NO: 715] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 715]	[SEQ ID NO: 716] DIYPGSSICNYNEK FKG [SEQ ID NO: 716]	[SEQ ID NO: 717] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 717]	[SEQ ID NO: 718] EDGYDAWF AY [SEQ ID NO: 718]
7G6-HCzu20	[SEQ ID NO: 713] ACCTACTGGATC ACC	[SEQ ID NO: 714] TYWIT [SEQ ID NO: 720]	CAAGTCC [SEQ ID NO: 721] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 721]	[SEQ ID NO: 722] DIYPGSSICNYNEK FKG [SEQ ID NO: 722]	[SEQ ID NO: 723] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 723]	[SEQ ID NO: 724] EDGYDAWF AY [SEQ ID NO: 724]
7G6-HCzu21	[SEQ ID NO: 719] ACCTACTGGATC ACC	[SEQ ID NO: 720] TYWIT [SEQ ID NO: 726]	CAAGTCC [SEQ ID NO: 727] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 727]	[SEQ ID NO: 728] DIYPGSSICNYNEK FKS [SEQ ID NO: 728]	[SEQ ID NO: 729] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 729]	[SEQ ID NO: 730] EDGYDAWF AY [SEQ ID NO: 730]
7G6-HCzu22	[SEQ ID NO: 725] ACCTACTGGATC ACC	[SEQ ID NO: 726] TYWIT [SEQ ID NO: 732]	CAAGTCC [SEQ ID NO: 733] GACATCTACCCGGGCTCCTCCA TCTGCAACTACACGAGAAAGTT CAAGTCC [SEQ ID NO: 733]	[SEQ ID NO: 734] DIYPGSSICNYNEK FKS [SEQ ID NO: 734]	[SEQ ID NO: 735] GAGGACGGCTACGACGCTTGGTTT GCTTAC [SEQ ID NO: 735]	[SEQ ID NO: 736] EDGYDAWF AY [SEQ ID NO: 736]

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
	[SEQ ID NO: 731]	ID NO: 732]	CAAGTCC [SEQ ID NO: 733]	[SEQ ID NO: 734]	[SEQ ID NO: 735]	[SEQ ID NO: 736]

Table 1 (cont.): 7G6 VL numbered according to Kabat

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
mouse 7G6-Vk	AGATCTAGTCAGAGCATTTTA CATAGTAATGGAAACACCTAT TTAGAA [SEQ ID NO: 737]	RSSQILHSNGNT YLE [SEQ ID NO: 738]	AAAGTTTCCAACCG ATTTCT [SEQ ID NO: 739]	KVSNRFS [SEQ ID NO: 740]	TTTCAAGGTTCCACATGTTCCAT TCACG [SEQ ID NO: 741]	FQSHVP FT [SEQ ID NO: 742]
7G6-LCzu1	AGATCCTCCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 743]	RSSQILHSNGNT YLE [SEQ ID NO: 744]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 745]	KVSNRFS [SEQ ID NO: 746]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 747]	FQSHVP FT [SEQ ID NO: 748]
7G6-LCzu2	AGATCCTCCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 749]	RSSQILHSNGNT YLE [SEQ ID NO: 750]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 751]	KVSNRFS [SEQ ID NO: 752]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 753]	FQSHVP FT [SEQ ID NO: 754]
7G6-LCzu3	AGATCCTCCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 755]	RSSQILHSNGNT YLE [SEQ ID NO: 756]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 757]	KVSNRFS [SEQ ID NO: 758]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 759]	FQSHVP FT [SEQ ID NO: 760]

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
						760]
7G6-LCzu4	AGATCCTCCCAAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 761]	RSSQILHSNGNT YLE [SEQ ID NO: 762]	AAGTGTCCAACCG GTTCTCT [SEQ ID NO: 763]	KVSNRFS [SEQ ID NO: 764]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 765]	FGSHVP FT [SEQ ID NO: 766]
7G6-LCzu5	AGATCCTCCCAAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 767]	RSSQILHSNGNT YLE [SEQ ID NO: 768]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 769]	KVSNRFS [SEQ ID NO: 770]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 771]	FGSHVP FT [SEQ ID NO: 772]
7G6-LCzu6	AGATCCTCCCAAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 773]	RSSQILHSNGNT YLE [SEQ ID NO: 774]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 775]	KVSNRFS [SEQ ID NO: 776]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 777]	FGSHVP FT [SEQ ID NO: 778]
7G6-LCzu7	AGATCCTCCCAAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 779]	RSSQILHSNGNT YLE [SEQ ID NO: 780]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 781]	KVSNRFS [SEQ ID NO: 782]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 783]	FGSHVP FT [SEQ ID NO: 784]
7G6-LCzu8	AGATCCTCCCAAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 785]	RSSQIVHSNGNT YLE [SEQ ID NO: 786]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 787]	KVSNRFS [SEQ ID NO: 788]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 789]	FGSHVP FT [SEQ ID NO: 790]
7G6-LCzu9	AGATCCTCCCAAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGAAC [SEQ ID NO: 791]	RSSQIVHSNGNT YLE [SEQ ID NO: 792]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 793]	KVSNRFS [SEQ ID NO: 794]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 795]	FGSHVP FT [SEQ ID NO: 796]

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
7G6-LCzu10	AGATCCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 797]	RSSQIVHSNGNT YLE [SEQ ID NO: 798]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 799]	KVSNRFS [SEQ ID NO: 800]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 801]	FQGSHP FT [SEQ ID NO: 802]
7G6-LCzu11	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 803]	RSSQIVHSNGNT YLE [SEQ ID NO: 804]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 805]	KVSNRFS [SEQ ID NO: 806]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 807]	FQGSHP FT [SEQ ID NO: 808]
7G6-LCzu12	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 809]	RSSQIVHSNGNT YLE [SEQ ID NO: 810]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 811]	KVSNRFS [SEQ ID NO: 812]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 813]	FQGSHP FT [SEQ ID NO: 814]
7G6-LCzu13	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 815]	RSSQIVHSNGNT YLE [SEQ ID NO: 816]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 817]	KVSNRFS [SEQ ID NO: 818]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 819]	FQGSHP FT [SEQ ID NO: 820]
7G6-LCzu14	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 821]	RSSQIVHSNGNT YLE [SEQ ID NO: 822]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 823]	KVSNRFS [SEQ ID NO: 824]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 825]	FQGSHP FT [SEQ ID NO: 826]
7G6-LCzu15	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 827]	RSSQIVHSNGNT YLE [SEQ ID NO: 828]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 829]	KVSNRFS [SEQ ID NO: 830]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 831]	FQGSHP FT [SEQ ID NO: 832]
7G6-LCzu16	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA	RSSQIVHSNGNT YLE [SEQ ID NO: 833]	AAGGTGTCCAACCG GTTCTCC [SEQ ID NO: 834]	KVSNRFS [SEQ ID NO: 835]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 836]	FQGSHP FT [SEQ ID NO: 837]

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
	[SEQ ID NO: 833]	834]	835]	836]		NO: 838]
7G6-LCzu17	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGAAC [SEQ ID NO: 839]	RSSQIVHSNGNT YLE [SEQ ID NO: 840]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 841]	KVSNRFS [SEQ ID NO: 842]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 843]	FQSHVP FT [SEQ ID NO: 844]
7G6-LCzu18	CGGTCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 845]	RSSQILHSNGNT YLE [SEQ ID NO: 846]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 847]	KVSNRFS [SEQ ID NO: 848]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 849]	FQSHVP FT [SEQ ID NO: 850]
7G6-LCzu21	AGATCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 851]	RSSQILHSNGNT YLE [SEQ ID NO: 852]	AAGTGTCCAACCG GTTCTCC [SEQ ID NO: 853]	KVSNRFS [SEQ ID NO: 854]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 855]	FQSHVP FT [SEQ ID NO: 856]
7G6-LCzu22	AGATCTCTCCAGTCCATCCTG CACTCCAACGGCAACACCTAC CTGGAA [SEQ ID NO: 857]	RSSQILHSNGNT YLE [SEQ ID NO: 858]	AAGTGTCCAACCG GTTCTCT [SEQ ID NO: 859]	KVSNRFS [SEQ ID NO: 860]	TTTCAAGGCTCCCACGTGCCCT TCACC [SEQ ID NO: 861]	FQSHVP FT [SEQ ID NO: 862]

Table 1 (cont.): 7G6 VH numbered according to IMGT

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
mouse 7G6-Vh	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 863]	GYFTTY W [SEQ ID NO: 864]	ATTTATCCTGGTAGTAGTATTT GT [SEQ ID NO: 865]	IYPGSSI C [SEQ ID NO: 866]	GCAAGGGAGGATGGTTACGACGCCTG GTTTGCCTAC [SEQ ID NO: 867]	AREDGYDAWFA Y [SEQ ID NO: 868]
7G6-HCzu1	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 869]	GYFTTY W [SEQ ID NO: 870]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 871]	IYPGSSI C [SEQ ID NO: 872]	GCTAGAGAGGACGGCTACGACGCCTTG GTTTGCCTAC [SEQ ID NO: 873]	AREDGYDAWFA Y [SEQ ID NO: 874]
7G6-HCzu2	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 875]	GYFTTY W [SEQ ID NO: 876]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 877]	IYPGSSI C [SEQ ID NO: 878]	GCTAGAGAGGACGGCTACGACGCCTTG GTTTGCCTAC [SEQ ID NO: 879]	AREDGYDAWFA Y [SEQ ID NO: 880]
7G6-HCzu3	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 881]	GYFTTY W [SEQ ID NO: 882]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 883]	IYPGSSI C [SEQ ID NO: 884]	GCTAGAGAGGACGGCTACGACGCCTTG GTTTGCCTAC [SEQ ID NO: 885]	AREDGYDAWFA Y [SEQ ID NO: 886]
7G6-HCzu4	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 887]	GYFTTY W [SEQ ID NO: 888]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 889]	IYPGSSI C [SEQ ID NO: 890]	GCTAGAGAGGACGGCTACGACGCCTTG GTTTGCCTAC [SEQ ID NO: 891]	AREDGYDAWFA Y [SEQ ID NO: 892]
7G6-HCzu5	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 893]	GYFTTY W [SEQ ID NO: 894]	ATCTACCCCGGCTCCTCCATCT CC [SEQ ID NO: 895]	IYPGSSI S [SEQ ID NO: 896]	GCTAGAGAGGACGGCTACGACGCCTTG GTTTGCCTAC [SEQ ID NO: 897]	AREDGYDAWFA Y [SEQ ID NO: 898]

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
7G6-HCzu6	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 899]	GYTFITY W [SEQ ID NO: 900]	ATCTACCCCGGCTCCTCCATCT CC [SEQ ID NO: 901]	IYPGSSI S [SEQ ID NO: 902]	GCTAGAGAGGACGGCTACGACGCTTG GTTTGCCTAC [SEQ ID NO: 903]	AREDGYDAWFA Y [SEQ ID NO: 904]
7G6-HCzu7	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 905]	GYTFITY W [SEQ ID NO: 906]	ATCTACCCCGGCTCCTCCATCT CC [SEQ ID NO: 907]	IYPGSSI S [SEQ ID NO: 908]	GCTAGAGAGGACGGCTACGACGCTTG GTTTGCCTAC [SEQ ID NO: 909]	AREDGYDAWFA Y [SEQ ID NO: 910]
7G6-HCzu8	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 911]	GYTFITY W [SEQ ID NO: 912]	ATCTACCCCGGCTCCTCCATCT CC [SEQ ID NO: 913]	IYPGSSI S [SEQ ID NO: 914]	GCTAGAGAGGACGGCTACGACGCTTG GTTTGCCTAC [SEQ ID NO: 915]	AREDGYDAWFA Y [SEQ ID NO: 916]
7G6-HCzu9	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 917]	GYTFITY W [SEQ ID NO: 918]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 919]	IYPGSSI C [SEQ ID NO: 920]	GCTAGAGAGGACGGCTACGACGCTTG GTTTGCCTAC [SEQ ID NO: 921]	AREDGYDAWFA Y [SEQ ID NO: 922]
7G6-HCzu10	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 923]	GYTFITY W [SEQ ID NO: 924]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 925]	IYPGSSI C [SEQ ID NO: 926]	GCTAGAGAGGACGGCTACGACGCTTG GTTTGCCTAC [SEQ ID NO: 927]	AREDGYDAWFA Y [SEQ ID NO: 928]
7G6-HCzu11	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 929]	GYTFITY W [SEQ ID NO: 930]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 931]	IYPGSSI C [SEQ ID NO: 932]	GCCAAAGAGGACGGCTACGACGCTTG GTTTGCCTAC [SEQ ID NO: 933]	AKEDGYDAWFA Y [SEQ ID NO: 934]
7G6-HCzu12	GGCTACACCTTTA CCACCTACTGG [SEQ ID NO: 935]	GYTFITY W [SEQ ID NO: 936]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 937]	IYPGSSI C [SEQ ID NO: 938]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCCTAC [SEQ ID NO: 939]	AREDGYDAWFA Y [SEQ ID NO: 940]

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
	935]	NO:936]		NO:938]		940]
7G6-HCzu13	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 941]	GYFTTY W [SEQ ID NO: 942]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 943]	IYPGSSI C [SEQ ID NO: 944]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 945]	AREDGYDAWFA Y [SEQ ID NO: 946]
7G6-HCzu14	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 947]	GYFTTY W [SEQ ID NO: 948]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 949]	IYPGSSI C [SEQ ID NO: 950]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 951]	AREDGYDAWFA Y [SEQ ID NO: 952]
7G6-HCzu15	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 953]	GYFTTY W [SEQ ID NO: 954]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 955]	IYPGSSI C [SEQ ID NO: 956]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 957]	AREDGYDAWFA Y [SEQ ID NO: 958]
7G6-HCzu16	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 959]	GYFTTY W [SEQ ID NO: 960]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 961]	IYPGSSI C [SEQ ID NO: 962]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 963]	AREDGYDAWFA Y [SEQ ID NO: 964]
7G6-HCzu17	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 965]	GYFTTY W [SEQ ID NO: 966]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 967]	IYPGSSI C [SEQ ID NO: 968]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 969]	AREDGYDAWFA Y [SEQ ID NO: 970]
7G6-HCzu18	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 971]	GYFTTY W [SEQ ID NO: 972]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 973]	IYPGSSI C [SEQ ID NO: 974]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 975]	AREDGYDAWFA Y [SEQ ID NO: 976]

Clone Name (Species & Isotype)	VH CDR1 DNA Sequence	VH CDR1 Amino Acid Sequence	VH CDR2 DNA Sequence	VH CDR2 Amino Acid Sequence	VH CDR3 DNA Sequence	VH CDR3 Amino Acid Sequence
7G6-HCzu19	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 977]	GYFTTY W [SEQ ID NO: 978]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 979]	IYPGSSI C [SEQ ID NO: 980]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 981]	AREDGYDAWFA Y [SEQ ID NO: 982]
7G6-HCzu20	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 983]	GYFTTY W [SEQ ID NO: 984]	ATCTACCCCGGCTCCTCCATCT GC [SEQ ID NO: 985]	IYPGSSI C [SEQ ID NO: 986]	GCCAAAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 987]	AKEDGYDAWFA Y [SEQ ID NO: 988]
7G6-HCzu23	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 989]	GYFTTY W [SEQ ID NO: 990]	ATCTACCCCGGCTCCTCCATCT CC [SEQ ID NO: 991]	IYPGSSI S [SEQ ID NO: 992]	GCTAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 993]	AREDGYDAWFA Y [SEQ ID NO: 994]
7G6-HCzu24	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 995]	GYFTTY W [SEQ ID NO: 996]	ATCTACCCCGGCTCCTCCATCT CC [SEQ ID NO: 997]	IYPGSSI S [SEQ ID NO: 998]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 999]	AREDGYDAWFA Y [SEQ ID NO: 1000]
7G6-HCzu25	GGCTACACCTTCA CCACCTACTGG [SEQ ID NO: 1001]	GYFTTY W [SEQ ID NO: 1002]	ATCTACCCCGGCTCCTCCATCT CC [SEQ ID NO: 1003]	IYPGSSI S [SEQ ID NO: 1004]	GCCAGAGAGGACGGCTACGACGCTTG GTTTGCTTAC [SEQ ID NO: 1005]	AREDGYDAWFA Y [SEQ ID NO: 1006]

Table 1 (cont.): 7G6 VL numbered according to IMGT

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
mouse 7G6-Vk	CAGAGCATTTTACATAGTAATGGAACACACC TAT [SEQ ID NO: 1007]	QSILHSNGNT Y [SEQ ID NO: 1008]	AAAGTTTC C [SEQ ID NO: 1009]	KVS [SEQ ID NO: 1010]	TTTCAAGGTTCCACATGTTCCATTTC ACG [SEQ ID NO: 1011]	FQGSHPVF T [SEQ ID NO: 1012]
7G6-LCzu1	CAGTCCATCCTGCACTCCAACGGCAACACACC TAC [SEQ ID NO: 1013]	QSILHSNGNT Y [SEQ ID NO: 1014]	AAGGTGTC C [SEQ ID NO: 1015]	KVS [SEQ ID NO: 1016]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1017]	FQGSHPVF T [SEQ ID NO: 1018]
7G6-LCzu2	CAGTCCATCCTGCACTCCAACGGCAACACACC TAC [SEQ ID NO: 1019]	QSILHSNGNT Y [SEQ ID NO: 1020]	AAGGTGTC C [SEQ ID NO: 1021]	KVS [SEQ ID NO: 1022]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1023]	FQGSHPVF T [SEQ ID NO: 1024]
7G6-LCzu3	CAGTCCATCCTGCACTCCAACGGCAACACACC TAC [SEQ ID NO: 1025]	QSILHSNGNT Y [SEQ ID NO: 1026]	AAGGTGTC C [SEQ ID NO: 1027]	KVS [SEQ ID NO: 1028]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1029]	FQGSHPVF T [SEQ ID NO: 1030]
7G6-LCzu4	CAGTCCATCCTGCACTCCAACGGCAACACACC TAC [SEQ ID NO: 1031]	QSILHSNGNT Y [SEQ ID NO: 1032]	AAGGTGTC C [SEQ ID NO: 1033]	KVS [SEQ ID NO: 1034]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1035]	FQGSHPVF T [SEQ ID NO: 1036]
7G6-LCzu5	CAGTCCATCCTGCACTCCAACGGCAACACACC TAC [SEQ ID NO: 1037]	QSILHSNGNT Y [SEQ ID NO: 1038]	AAGGTGTC C [SEQ ID NO: 1039]	KVS [SEQ ID NO: 1040]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1041]	FQGSHPVF T [SEQ ID NO: 1042]

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
7G6-LCzu6	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1043]	QSILHSNGNT Y [SEQ ID NO: 1044]	AAGGTGTC C [SEQ ID NO: 1045]	KVS [SEQ ID NO: 1046]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1047]	FQGSHPVF T [SEQ ID NO: 1048]
7G6-LCzu7	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1049]	QSILHSNGNT Y [SEQ ID NO: 1050]	AAGGTGTC C [SEQ ID NO: 1051]	KVS [SEQ ID NO: 1052]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1053]	FQGSHPVF T [SEQ ID NO: 1054]
7G6-LCzu8	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1055]	QSIVHSNGNT Y [SEQ ID NO: 1056]	AAGGTGTC C [SEQ ID NO: 1057]	KVS [SEQ ID NO: 1058]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1059]	FQGSHPVF T [SEQ ID NO: 1060]
7G6-LCzu9	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1061]	QSIVHSNGNT Y [SEQ ID NO: 1062]	AAGGTGTC C [SEQ ID NO: 1063]	KVS [SEQ ID NO: 1064]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1065]	FQGSHPVF T [SEQ ID NO: 1066]
7G6-LCzu10	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1067]	QSIVHSNGNT Y [SEQ ID NO: 1068]	AAGGTGTC C [SEQ ID NO: 1069]	KVS [SEQ ID NO: 1070]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1071]	FQGSHPVF T [SEQ ID NO: 1072]
7G6-LCzu11	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1073]	QSILHSNGNT Y [SEQ ID NO: 1074]	AAGGTGTC C [SEQ ID NO: 1075]	KVS [SEQ ID NO: 1076]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1077]	FQGSHPVF T [SEQ ID NO: 1078]
7G6-LCzu12	CAGTCCATCCTGCACTCCAACGGCAACACC TAC	QSILHSNGNT Y	AAGGTGTC C	KVS [SEQ ID NO: 1079]	TTTCAAGGCTCCCACGTGCCCTTC ACC	FQGSHPVF T

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
	[SEQ ID NO: 1079]	[SEQ ID NO: 1080]	[SEQ ID NO: 1081]	[SEQ ID NO: 1082]	[SEQ ID NO: 1083]	[SEQ ID NO: 1084]
7G6-LCzu13	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1085]	QSILHSNGNT Y [SEQ ID NO: 1086]	AAGGTGTC C [SEQ ID NO: 1087]	KVS [SEQ ID NO: 1088]	TTTCAAGGCTCCACAGTGCCCTTC ACC [SEQ ID NO: 1089]	FQGSHPVF T [SEQ ID NO: 1090]
7G6-LCzu14	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1091]	QSILHSNGNT Y [SEQ ID NO: 1092]	AAGGTGTC C [SEQ ID NO: 1093]	KVS [SEQ ID NO: 1094]	TTTCAAGGCTCCACAGTGCCCTTC ACC [SEQ ID NO: 1095]	FQGSHPVF T [SEQ ID NO: 1096]
7G6-LCzu15	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1097]	QSILHSNGNT Y [SEQ ID NO: 1098]	AAGGTGTC C [SEQ ID NO: 1099]	KVS [SEQ ID NO: 1100]	TTTCAAGGCTCCACAGTGCCCTTC ACC [SEQ ID NO: 1101]	FQGSHPVF T [SEQ ID NO: 1102]
7G6-LCzu16	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1103]	QSIVHSNGNT Y [SEQ ID NO: 1104]	AAGGTGTC C [SEQ ID NO: 1105]	KVS [SEQ ID NO: 1106]	TTTCAAGGCTCCACAGTGCCCTTC ACC [SEQ ID NO: 1107]	FQGSHPVF T [SEQ ID NO: 1108]
7G6-LCzu17	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1109]	QSIVHSNGNT Y [SEQ ID NO: 1110]	AAGGTGTC C [SEQ ID NO: 1111]	KVS [SEQ ID NO: 1112]	TTTCAAGGCTCCACAGTGCCCTTC ACC [SEQ ID NO: 1113]	FQGSHPVF T [SEQ ID NO: 1114]
7G6-LCzu18	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1115]	QSILHSNGNT Y [SEQ ID NO: 1116]	AAGGTGTC C [SEQ ID NO: 1117]	KVS [SEQ ID NO: 1118]	TTTCAAGGCTCCACAGTGCCCTTC ACC [SEQ ID NO: 1119]	FQGSHPVF T [SEQ ID NO: 1120]

Clone Name (Species & Isotype)	VL CDR1 DNA Sequence	VL CDR1 Amino Acid Sequence	VL CDR2 DNA Sequence	VL CDR2 Amino Acid Sequence	VL CDR3 DNA Sequence	VL CDR3 Amino Acid Sequence
			1117]			1120]
7G6-LCzu21	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1121]	QSI LHSNGNT Y [SEQ ID NO: 1122]	AAGGTGTC C [SEQ ID NO: 1123]	KVS [SEQ ID NO: 1124]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1125]	FQGSHPVF T [SEQ ID NO: 1126]
7G6-LCzu22	CAGTCCATCCTGCACTCCAACGGCAACACC TAC [SEQ ID NO: 1127]	QSI LHSNGNT Y [SEQ ID NO: 1128]	AAGGTGTC C [SEQ ID NO: 1129]	KVS [SEQ ID NO: 1130]	TTTCAAGGCTCCCACGTGCCCTTC ACC [SEQ ID NO: 1131]	FQGSHPVF T [SEQ ID NO: 1132]

[0074] In some embodiments, the anti-Tau antibodies, or antigen-binding fragments thereof, include a heavy chain complementarity determining region 1 (HCDR1), a heavy chain complementarity determining region 2 (HCDR2), and a heavy chain complementarity determining region 3 (HCDR3) as set forth in SEQ ID NO: 196 and a light chain complementarity determining region 1 (LCDR1), a light chain complementarity determining region 2 (LCDR2), and a light chain complementarity determining region 3 (LCDR3) as set forth in SEQ ID NO: 411. In some embodiments, the anti-Tau antibodies, or antigen-binding fragments thereof, include a HCDR1, a HCDR2, and a HCDR3 as set forth in SEQ ID NO: 268 and a LCDR1, a LCDR2, and a LCDR3 as set forth in SEQ ID NO: 465. In some embodiments, the anti-Tau antibodies, or antigen-binding fragments thereof, include a HCDR1, a HCDR2, and a HCDR3 as set forth in SEQ ID NO: 402 and a LCDR1, a LCDR2, and a LCDR3 as set forth in SEQ ID NO: 572.

[0075] In some embodiments, the anti-Tau antibodies or antigen-binding fragments may include a light chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 738, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 740, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 742, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 594, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 596, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 598, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 738, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 740, as defined

according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 742, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 594, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 596, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 598, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 738, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 740, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 742, as defined according to the method of Kabat, and also have a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 594, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 596, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 598, as defined according to the method of Kabat.

[0076] In some embodiments, the anti-Tau antibodies or antigen-binding fragments may include a light chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1008, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1010, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1012, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 864, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 866, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 868, as

defined by IMGT. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1008, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1010, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1012, as defined by IMGT. The antibodies or antigen-binding fragments may include a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 864, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 866, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 868, as defined by IMGT. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1008, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1010, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1012, as defined by IMGT, and also have a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 864, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 866, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 868, as defined by IMGT.

[0077] In some embodiments, the anti-Tau antibodies or antigen-binding fragments may include a light chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 774, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 776, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 778, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 642, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 644, as defined according

to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 646, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 774, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 776, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 778, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 642, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 644, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 646, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 774, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 776, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 778, as defined according to the method of Kabat, and also have a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 642, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 644, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 646, as defined according to the method of Kabat.

[0078] In some embodiments, the anti-Tau antibodies or antigen-binding fragments may include a light chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1044, as defined according to the method of IMGT. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1046, as defined according to the method of IMGT. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1048,

as defined according to the method of IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 912, as defined according to the method of IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 914, as defined according to the method of IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 916, as defined according to the method of IMGT. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1044, as defined according to the method of IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1046, as defined according to the method of IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1048, as defined according to the method of IMGT. The antibodies or antigen-binding fragments may include a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 912, as defined according to the method of IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 914, as defined according to the method of IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 916, as defined according to the method of IMGT. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1044, as defined according to the method of IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1046, as defined according to the method of IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1048, as defined according to the method of IMGT, and also have a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 912, as defined according to the method of IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 914, as defined according to the method of IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 916, as defined according to the method of IMGT.

[0079] In some embodiments, the anti-Tau antibodies or antigen-binding fragments may include a light chain CDR1 amino acid sequence substantially the same as, or identical to,

SEQ ID NO: 846, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 848, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 850, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 732, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 734, as defined according to the method of Kabat. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 736, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 846, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 848, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 850, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 732, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 734, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 736, as defined according to the method of Kabat. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 846, as defined according to the method of Kabat; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 848, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 850, as defined according to the method of Kabat, and also have a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 732, as defined according to the method of Kabat; a CDR2

amino acid sequence substantially the same as, or identical to, SEQ ID NO: 734, as defined according to the method of Kabat; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 736, as defined according to the method of Kabat.

[0080] In some embodiments, the anti-Tau antibodies or antigen-binding fragments may include a light chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1116, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1118, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a light chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1120, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1002, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1004, as defined by IMGT. In some embodiments, antibodies or antigen-binding fragments may include a heavy chain CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1006, as defined by IMGT. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1116, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1118, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1120, as defined by IMGT. The antibodies or antigen-binding fragments may include a heavy chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1002, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1004, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1006, as defined by IMGT. The antibodies or antigen-binding fragments may include a light chain having a CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1116, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1118, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1120, as defined by IMGT, and also have a heavy chain having a

CDR1 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1002, as defined by IMGT; a CDR2 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1004, as defined by IMGT; and a CDR3 amino acid sequence substantially the same as, or identical to, SEQ ID NO: 1006, as defined by IMGT.

[0081] Antigen-binding arrangements of CDRs may also be engineered using antibody-like proteins as CDR scaffolding. Such engineered antigen-binding proteins are within the scope of the disclosure.

[0082] In some embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, certain residues are altered to improve the binding and/or folding characteristics of the antibody or antigen-binding fragment. For example, in some embodiments of the disclosed monoclonal antibodies and antigen-binding fragments, the residue at position 49 of the light chain according to the method of Kabat is not cysteine. In some embodiments of the disclosed monoclonal antibodies and antigen-binding fragments, the residue at position 49 of the light chain according to the method of Kabat is serine. In some embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the residue at position 57 of the heavy chain according to the method of Kabat is not cysteine. In some embodiments, the residue at position 57 of the heavy chain according to the method of Kabat is serine. In some embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the residue at position 34 of the light chain according to the method of Kabat is glutamate. In some embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the residue at position 36 of the light chain according to the method of Kabat is not phenylalanine. The residue at position 36 of the light chain according to the method of Kabat may be tyrosine. In some embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the residue at position 46 of the light chain according to the method of Kabat is not arginine. The residue at position 46 of the light chain according to the method of Kabat may be leucine. In some embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the residue at position 94 of the heavy chain according to the method of Kabat is not lysine. In some embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the residue at position 71 of the heavy chain according to the method of Kabat is not

arginine. The residue at position 71 of the heavy chain according to the method of Kabat may be valine.

[0083] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 411. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 411 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 410 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 196. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 196 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 195 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 411, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 196. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 411 and a sequence substantially the same as, or identical to, SEQ ID NO: 196 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 410 and a sequence substantially the same as, or identical to, SEQ ID NO: 195 is provided.

[0084] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 465. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 465 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 464 may encode this light chain variable

domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 268 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 267 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 465, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 465 and a sequence substantially the same as, or identical to, SEQ ID NO: 268 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 464 and a sequence substantially the same as, or identical to, SEQ ID NO: 267 is provided.

[0085] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 581. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 581 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 580 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 268 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 267 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain

variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 581, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 581 and a sequence substantially the same as, or identical to, SEQ ID NO: 268 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 580 and a sequence substantially the same as, or identical to, SEQ ID NO: 267 is provided.

[0086] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 545 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 544 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 384 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 383 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 545 and a sequence substantially the same as, or identical to, SEQ ID NO: 384 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 544 and a sequence substantially the same as, or identical to, SEQ ID NO: 383 is provided.

[0087] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 545 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 544 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 393 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 392 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 545 and a sequence substantially the same as, or identical to, SEQ ID NO: 393 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 544 and a sequence substantially the same as, or identical to, SEQ ID NO: 392 is provided.

[0088] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 545 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 544 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid

sequence substantially the same as, or identical to, SEQ ID NO: 402. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 402 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 401 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 402. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 545 and a sequence substantially the same as, or identical to, SEQ ID NO: 402 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 544 and a sequence substantially the same as, or identical to, SEQ ID NO: 401 is provided.

[0089] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 572 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 571 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 384 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 383 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, and the heavy chain variable domain

includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 572 and a sequence substantially the same as, or identical to, SEQ ID NO: 384 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 571 and a sequence substantially the same as, or identical to, SEQ ID NO: 383 is provided.

[0090] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 572 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 571 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 393 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 392 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 572 and a sequence substantially the same as, or identical to, SEQ ID NO: 393 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 571 and a sequence substantially the same as, or identical to, SEQ ID NO: 392 is provided.

[0091] The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain that includes an amino acid sequence

substantially the same as, or identical to, SEQ ID NO: 572. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 572 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 571 may encode this light chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a heavy chain variable domain that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 402. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 402 is provided. In some embodiments, an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 401 may encode this heavy chain variable domain amino acid sequence. The described antibodies or antigen-binding fragments that specifically bind Tau may include a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, and the heavy chain variable domain includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 402. In some aspects, an isolated polynucleotide that encodes a sequence substantially the same as, or identical to, SEQ ID NO: 572 and a sequence substantially the same as, or identical to, SEQ ID NO: 402 is provided. In some embodiments an isolated polynucleotide that includes a sequence substantially the same as, or identical to, SEQ ID NO: 571 and a sequence substantially the same as, or identical to, SEQ ID NO: 401 is provided.

[0092] In some embodiments, the antibodies that specifically bind Tau are produced by antibody-producing cells deposited with the American Type Culture Collection (10801 University Blvd., Manassas, Virginia 20110-2209) on October 11, 2017 and have been assigned Accession No. PTA-124523 or PTA-124524. In some embodiments, the antibodies, or antigen-binding fragments thereof, have the binding affinity for monomeric wild-type 2N4R Tau of the antibodies produced by the deposited antibody-producing cells as measured by surface plasmon resonance. In some embodiments, the disclosed antibodies, or antigen-binding fragments thereof, comprise the light and heavy chain CDRs of the antibodies produced by the deposited antibody-producing cells. In some embodiments, the antibodies, or antigen-binding fragments

thereof, comprise the light and heavy chain variable regions of the antibodies produced by the deposited antibody-producing cells.

[0093] The antibodies or antigen-binding fragments that specifically bind Tau described herein include variants having single or multiple amino acid substitutions, deletions, or additions that retain the biological properties (e.g., binding affinity or immune effector activity) of the described antibodies or antigen-binding fragments. The skilled person may produce variants having single or multiple amino acid substitutions, deletions, or additions. These variants may include: (a) variants in which one or more amino acid residues are substituted with conservative or nonconservative amino acids, (b) variants in which one or more amino acids are added to or deleted from the polypeptide, (c) variants in which one or more amino acids include a substituent group, and (d) variants in which the polypeptide is fused with another peptide or polypeptide such as a fusion partner, a protein tag or other chemical moiety, that may confer useful properties to the polypeptide, such as, for example, an epitope for an antibody, a polyhistidine sequence, a biotin moiety and the like. Antibodies or antigen-binding fragments described herein may include variants in which amino acid residues from one species are substituted for the corresponding residue in another species, either at the conserved or nonconserved positions. In other embodiments, amino acid residues at nonconserved positions are substituted with conservative or nonconservative residues. The techniques for obtaining these variants, including genetic (suppressions, deletions, mutations, etc.), chemical, and enzymatic techniques, are known to the person having ordinary skill in the art.

[0094] The antibodies or antigen-binding fragments described herein have binding affinities (in nM) for wild-type monomeric 2N4R Tau that include a dissociation constant (K_D) of less than about 1×10^{-8} M as measured by surface plasmon resonance. In certain embodiments, the antibodies or antigen-binding fragments described herein have binding affinities (in nM) for wild-type monomeric 2N4R Tau that include a dissociation constant (K_D) of less than about 0.5 nM as measured by surface plasmon resonance. In certain embodiments, the antibodies or antigen-binding fragments described herein have binding affinities (in nM) for wild-type monomeric 2N4R Tau that include a dissociation constant (K_D) of less than about 0.3 nM as measured by surface plasmon resonance. In certain embodiments, the antibodies or antigen-binding fragments described herein have binding affinities (in nM) for wild-type monomeric

2N4R Tau that include a dissociation constant (K_D) of less than about 0.2 nM as measured by surface plasmon resonance. In certain embodiments, the antibodies or antigen-binding fragments described herein have binding affinities (in nM) for wild-type monomeric 2N4R Tau that include a dissociation constant (K_D) of less than about 0.15 nM as measured by surface plasmon resonance. In certain embodiments, the antibodies or antigen-binding fragments described herein have binding affinities (in nM) for wild-type monomeric 2N4R Tau that include a dissociation constant (K_D) of less than about 0.1 nM as measured by surface plasmon resonance.

[0095] In any of the embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the antibodies or antigen-binding fragments may bind an epitope comprising HVPG (SEQ ID NO: 1133). In some embodiments, the antibodies or antigen-binding fragments that specifically bind Tau described herein are biepitopic. In certain aspects, the antibodies or antigen-binding fragments that specifically bind Tau described herein bind one or more epitopes within Tau comprising HVPG (SEQ ID NO: 1133). This sequence appears twice in human 2N4R Tau. The first site is in 2N4R Tau within the second repeat region at residues 299-302 and the second site within the fourth repeat region at residues 362-365.

[0096] In any of the embodiments of the antibodies or antigen-binding fragments that specifically bind Tau described herein, the antibodies or antigen-binding fragments may bind an epitope comprising HVPGG (SEQ ID NO: 79). In some embodiments, the antibodies or antigen-binding fragments that specifically bind Tau described herein are biepitopic. In certain aspects, the antibodies or antigen-binding fragments that specifically bind Tau described herein bind one or more epitopes within Tau comprising HVPGG (SEQ ID NO: 79). This sequence appears twice in human 2N4R Tau. The first site is in 2N4R Tau within the second repeat region at residues 299-303 and the second site within the fourth repeat region at residues 362-366. In certain aspects, the antibodies or antigen-binding fragments that specifically bind Tau bind the epitope within Tau comprising HVPGG (SEQ ID NO: 79) within repeat region 2 or repeat region 4 with a peptide binding preference that is at least 10-fold, preferably at least 20-fold, and more preferably at least 30-fold greater than binding to an epitope within Tau comprising HKPGG (SEQ ID NO: 182) within repeat region 3 as determined by a peptide binding assay (e.g., the peptide binding assay described in Example 3). In certain aspects, the antibodies or antigen-binding fragments that specifically bind Tau bind the epitope within Tau comprising HVPGG

(SEQ ID NO: 79) within repeat region 2 or repeat region 4 with a peptide binding preference that is at least 10-fold, preferably at least 20-fold, and more preferably at least 30-fold greater than binding to an epitope within Tau comprising HQPGG (SEQ ID NO: 183) within repeat region 1, as determined by a peptide binding assay (e.g., the peptide binding assay described in Example 3). In certain aspects, the antibodies or antigen-binding fragments that specifically bind Tau bind the epitope within Tau comprising HVPGG (SEQ ID NO: 79) within repeat region 2 or repeat region 4 with a peptide binding preference that is at least 10-fold, preferably at least 20-fold, and more preferably at least 30-fold greater than binding to an epitope within Tau comprising HKPGG (SEQ ID NO: 182) within repeat region 3 and that is at least 10-fold, preferably at least 20-fold, and more preferably at least 30-fold greater than binding to an epitope comprising HQPGG (SEQ ID NO: 183) within repeat region 1, as determined by a peptide binding assay (e.g., the peptide binding assay described in Example 3). In certain aspects, the antibodies or antigen-binding fragments that specifically bind Tau do not bind an epitope within naturally occurring mutant P301S Tau comprising HVSGG (SEQ ID NO: 184) within repeat region 2 as determined by a peptide binding assay (e.g., the peptide binding assay described in Example 4). In certain aspects, the antibodies or antigen-binding fragments that specifically bind Tau do not bind an epitope within naturally occurring mutant P301L Tau comprising HVLGG (SEQ ID NO: 185) within repeat region 2 as determined by a peptide binding assay (e.g., the peptide binding assay described in Example 4). The amino acid sequence HVSGG (SEQ ID NO: 184) is present at residues 299-303 in the 2N4R Tau sequence of P301S *in vitro* and *in vivo* Tauopathy models. The amino acid sequence HVLGG (SEQ ID NO: 185) is present at residues 299-303 of the 2N4R Tau sequence of P301L *in vitro* and *in vivo* Tauopathy models. Antibodies or antigen-binding fragments as provided herein that preferably bind one or more epitopes within Tau comprising HVPGG (SEQ ID NO: 79) within repeat region 2 or repeat region 4 relative to an epitope comprising HKPGG (SEQ ID NO: 182) within repeat region 3 or HQPGG (SEQ ID NO: 183) within repeat region 1 and do not bind an epitope comprising HVSGG (SEQ ID NO: 184), or HVLGG (SEQ ID NO: 185) within repeat region 2 bind 2N4R Tau P301S/L at residues 362-366. Surprisingly, as demonstrated herein, the described antibodies or antigen-binding fragments that preferably bind one or more epitopes within Tau comprising HVPGG (SEQ ID NO: 79) within repeat region 2 or repeat region 4 relative to an epitope comprising HKPGG (SEQ ID NO:

182) within repeat region 3 or HQPGG (SEQ ID NO: 183) within repeat region 1 and that do not exhibit binding to an epitope comprising HVSGG (SEQ ID NO: 184) or HVLGG (SEQ ID NO: 185) within repeat region 2 reduce Tau seeding and transmission *in vivo*.

[0097] In certain embodiments, labelled anti-Tau antibodies are provided. Labels include, but are not limited to, labels or moieties that are detected directly (e.g., fluorescent, chromophoric, electron-dense, chemiluminescent, and radioactive labels) and labels and moieties (e.g., enzymes or ligands) that are detected indirectly (e.g., through enzymatic reaction or molecular interaction). Exemplary labels include but are not limited to radiolabels (e.g., ^{32}P , ^{14}C , ^{111}I , ^{125}I , ^3H , ^{131}I), fluorescent labels (such as DyLight™ 649), epitope tags, biotin, chromophore labels, ECL labels, or enzymes. More specifically, the described labels include ruthenium, ^{111}In -DOTA, ^{111}In -diethylenetriaminepentaacetic acid (DTPA), horseradish peroxidase, alkaline phosphatase and beta-galactosidase, poly-histidine (HIS tag), acridine dyes, cyanine dyes, fluorone dyes, oxazin dyes, phenanthridine dyes, rhodamine dyes, Alexafluor™ dyes, and the like.

[0098] Also disclosed are isolated polynucleotides that encode antibodies or antigen-binding fragments that specifically bind to Tau. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR1 sequence defined according to Kabat substantially the same as, or identical to, SEQ ID NO: 738, for example SEQ ID NO: 737. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR2 defined according to Kabat substantially the same as, or identical to, SEQ ID NO: 740, for example SEQ ID NO: 739. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR3 defined according to Kabat substantially the same as, or identical to, SEQ ID NO: 742, for example SEQ ID NO: 741. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 defined according to Kabat substantially the same as, or identical to, SEQ ID NO: 594, for example SEQ ID NO: 593. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR2 defined according to Kabat substantially the same as, or identical to, SEQ ID NO: 596, for example SEQ ID NO: 595. In some embodiments, the isolated polynucleotides encode an antibody or antigen-

binding fragment thereof having a heavy chain CDR3 defined according to Kabat substantially the same as, or identical to, SEQ ID NO: 598, for example SEQ ID NO: 597. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain with a CDR1 substantially the same as, or identical to, SEQ ID NO: 738, for example SEQ ID NO: 737; a CDR2 substantially the same as, or identical to, SEQ ID NO: 740, for example SEQ ID NO: 739; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 742, for example SEQ ID NO: 741, defined according to Kabat. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 594, for example SEQ ID NO: 593; a CDR2 substantially the same as, or identical to, SEQ ID NO: 596, for example SEQ ID NO: 595; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 598, for example SEQ ID NO: 597, defined according to Kabat. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain CDR1 substantially the same as, or identical to, SEQ ID NO: 738, for example SEQ ID NO: 737; a CDR2 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 740, for example SEQ ID NO: 739; and a CDR3 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 742, for example SEQ ID NO: 741; and a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 594, for example SEQ ID NO: 593; a CDR2 substantially the same as, or identical to, SEQ ID NO: 596, for example SEQ ID NO: 595; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 598, for example SEQ ID NO: 597, defined according to Kabat.

[0099] In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR1 sequence defined according to IMGT substantially the same as, or identical to, SEQ ID NO: 1008, for example SEQ ID NO: 1007. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR2 defined according to IMGT substantially the same as, or identical to, SEQ ID NO: 1010, for example SEQ ID NO: 1009. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR3 defined according to IMGT substantially the same as, or identical to, SEQ ID NO: 1012, for example SEQ ID NO: 1011. In some embodiments, the isolated polynucleotides

encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 defined according to IMGT substantially the same as, or identical to, SEQ ID NO: 864, for example SEQ ID NO: 863. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR2 defined according to IMGT substantially the same as, or identical to, SEQ ID NO: 866, for example SEQ ID NO: 865. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR3 defined according to IMGT substantially the same as, or identical to, SEQ ID NO: 868, for example SEQ ID NO: 867. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain with a CDR1 substantially the same as, or identical to, SEQ ID NO: 1008, for example SEQ ID NO: 1007; a CDR2 substantially the same as, or identical to, SEQ ID NO: 1010, for example SEQ ID NO: 1009; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 1012, for example SEQ ID NO: 1011, defined according to IMGT. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 864, for example SEQ ID NO: 863; a CDR2 substantially the same as, or identical to, SEQ ID NO: 866, for example SEQ ID NO: 865; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 868, for example SEQ ID NO: 867, defined according to IMGT. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain CDR1 substantially the same as, or identical to, SEQ ID NO: 1008, for example SEQ ID NO: 1007; a CDR2 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 1010, for example SEQ ID NO: 1009; and a CDR3 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 1012, for example SEQ ID NO: 1011; and a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 864, for example SEQ ID NO: 863; a CDR2 substantially the same as, or identical to, SEQ ID NO: 866, for example SEQ ID NO: 865; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 868, for example SEQ ID NO: 867, defined according to IMGT.

[0100] In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR1 sequence substantially the same as, or identical to, SEQ ID NO: 774, defined according to Kabat, for example SEQ ID NO: 773. In

some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR2 substantially the same as, or identical to, SEQ ID NO: 776, defined according to Kabat, for example SEQ ID NO: 775. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR3 substantially the same as, or identical to, SEQ ID NO: 778, defined according to Kabat, for example SEQ ID NO: 777. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 642, defined according to Kabat, for example SEQ ID NO: 641. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR2 substantially the same as, or identical to, SEQ ID NO: 644, defined according to Kabat, for example SEQ ID NO: 643. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR3 substantially the same as, or identical to, SEQ ID NO: 646, defined according to Kabat, for example SEQ ID NO: 645. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain with a CDR1 substantially the same as, or identical to, SEQ ID NO: 774, for example SEQ ID NO: 773; a CDR2 substantially the same as, or identical to, SEQ ID NO: 776, for example SEQ ID NO: 775; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 778, for example SEQ ID NO: 777, defined according to Kabat. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 642, for example SEQ ID NO: 641; a CDR2 substantially the same as, or identical to, SEQ ID NO: 644, for example SEQ ID NO: 643; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 646, for example SEQ ID NO: 645, defined according to Kabat. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain CDR1 substantially the same as, or identical to, SEQ ID NO: 774, for example SEQ ID NO: 773; a CDR2 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 776, for example SEQ ID NO: 775; and a CDR3 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 778, for example SEQ ID NO: 777; and a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 642, for example SEQ ID NO: 641; a CDR2 substantially the same as, or identical to, SEQ ID NO: 644, for example

SEQ ID NO: 643; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 646, for example SEQ ID NO: 645, defined according to Kabat.

[0101] In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR1 sequence substantially the same as, or identical to, SEQ ID NO: 1044, defined according to IMGT, for example SEQ ID NO: 1043. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR2 substantially the same as, or identical to, SEQ ID NO: 1046, defined according to IMGT, for example SEQ ID NO: 1045. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR3 substantially the same as, or identical to, SEQ ID NO: 1048, defined according to IMGT, for example SEQ ID NO: 1047. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 912, defined according to IMGT, for example SEQ ID NO: 911. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR2 substantially the same as, or identical to, SEQ ID NO: 914, defined according to IMGT, for example SEQ ID NO: 913. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR3 substantially the same as, or identical to, SEQ ID NO: 916, defined according to IMGT, for example SEQ ID NO: 915. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain with a CDR1 substantially the same as, or identical to, SEQ ID NO: 1044, for example SEQ ID NO: 1043; a CDR2 substantially the same as, or identical to, SEQ ID NO: 1046, for example SEQ ID NO: 1045; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 1048, for example SEQ ID NO: 1047, defined according to IMGT. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 912, for example SEQ ID NO: 911; a CDR2 substantially the same as, or identical to, SEQ ID NO: 914, for example SEQ ID NO: 913; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 916, for example SEQ ID NO: 915, defined according to IMGT. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain CDR1 substantially the same as, or

identical to, SEQ ID NO: 1044, for example SEQ ID NO: 1043; a CDR2 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 1046, for example SEQ ID NO: 1045; and a CDR3 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 1048, for example SEQ ID NO: 1047; and a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 912, for example SEQ ID NO: 911; a CDR2 substantially the same as, or identical to, SEQ ID NO: 914, for example SEQ ID NO: 913; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 916, for example SEQ ID NO: 915, defined according to IMGT.

[0102] In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR1 sequence substantially the same as, or identical to, SEQ ID NO: 846, defined according to Kabat, for example SEQ ID NO: 845. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR2 substantially the same as, or identical to, SEQ ID NO: 848, defined according to Kabat, for example SEQ ID NO: 847. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR3 substantially the same as, or identical to, SEQ ID NO: 850, defined according to Kabat, for example SEQ ID NO: 849. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 732, defined according to Kabat, for example SEQ ID NO: 731. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR2 substantially the same as, or identical to, SEQ ID NO: 734, defined according to Kabat, for example SEQ ID NO: 733. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR3 substantially the same as, or identical to, SEQ ID NO: 736, defined according to Kabat, for example SEQ ID NO: 735. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain with a CDR1 substantially the same as, or identical to, SEQ ID NO: 846, for example SEQ ID NO: 845; a CDR2 substantially the same as, or identical to, SEQ ID NO: 848, for example SEQ ID NO: 847; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 850, for example SEQ ID NO: 849, defined according to Kabat. The isolated polynucleotides may encode an antibody or antigen-binding fragment

thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 732, for example SEQ ID NO: 731; a CDR2 substantially the same as, or identical to, SEQ ID NO: 734, for example SEQ ID NO: 733; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 736, for example SEQ ID NO: 735, defined according to Kabat. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain CDR1 substantially the same as, or identical to, SEQ ID NO: 846, for example SEQ ID NO: 845; a CDR2 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 848, for example SEQ ID NO: 847; and a CDR3 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 850, for example SEQ ID NO: 849; and a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 732, for example SEQ ID NO: 731; a CDR2 substantially the same as, or identical to, SEQ ID NO: 734, for example SEQ ID NO: 733; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 736, for example SEQ ID NO: 735, defined according to Kabat.

[0103] In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR1 sequence substantially the same as, or identical to, SEQ ID NO: 1116, defined according to IMGT, for example SEQ ID NO: 1115. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR2 substantially the same as, or identical to, SEQ ID NO: 1118, defined according to IMGT, for example SEQ ID NO: 1117. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a light chain CDR3 substantially the same as, or identical to, SEQ ID NO: 1120, defined according to IMGT, for example SEQ ID NO: 1119. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 1002, defined according to IMGT, for example SEQ ID NO: 1001. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR2 substantially the same as, or identical to, SEQ ID NO: 1004, defined according to IMGT, for example SEQ ID NO: 1003. In some embodiments, the isolated polynucleotides encode an antibody or antigen-binding fragment thereof having a heavy chain CDR3 substantially the same as, or identical to, SEQ ID NO: 1006, defined according to IMGT, for example SEQ ID NO: 1005. The isolated

polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain with a CDR1 substantially the same as, or identical to, SEQ ID NO: 1116, for example SEQ ID NO: 1115; a CDR2 substantially the same as, or identical to, SEQ ID NO: 1118, for example SEQ ID NO: 1117; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 1120, for example SEQ ID NO: 1119, defined according to IMGT. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 1002, for example SEQ ID NO: 1001; a CDR2 substantially the same as, or identical to, SEQ ID NO: 1004, for example SEQ ID NO: 1003; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 1006, for example SEQ ID NO: 1005, defined according to IMGT. The isolated polynucleotides may encode an antibody or antigen-binding fragment thereof having a light chain CDR1 substantially the same as, or identical to, SEQ ID NO: 1116, for example SEQ ID NO: 1115; a CDR2 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 1118, for example SEQ ID NO: 1117; and a CDR3 encoded by a nucleotide sequence substantially the same as, or identical to, SEQ ID NO: 1120, for example SEQ ID NO: 1119; and a heavy chain CDR1 substantially the same as, or identical to, SEQ ID NO: 1002, for example SEQ ID NO: 1001; a CDR2 substantially the same as, or identical to, SEQ ID NO: 1004, for example SEQ ID NO: 1003; and a CDR3 substantially the same as, or identical to, SEQ ID NO: 1006, for example SEQ ID NO: 1005, defined according to IMGT.

[0104] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 411, for example SEQ ID NO: 410. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 196, for example SEQ ID NO: 195. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 411, for example SEQ ID NO: 410; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 196, for example SEQ ID NO:

195. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0105] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 465, for example SEQ ID NO: 464. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268, for example SEQ ID NO: 267. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 465, for example SEQ ID NO: 464; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268, for example SEQ ID NO: 267. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0106] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 581, for example SEQ ID NO: 580. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268, for example SEQ ID NO: 267. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 581, for example SEQ ID NO: 580; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 268, for example SEQ ID NO: 267. The isolated polynucleotides capable of encoding the variable domain segments provided

herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0107] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, for example SEQ ID NO: 544. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384, for example SEQ ID NO: 383. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, for example SEQ ID NO: 544; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384, for example SEQ ID NO: 383. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0108] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, for example SEQ ID NO: 544. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393, for example SEQ ID NO: 392. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, for example SEQ ID NO: 544; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393, for example SEQ ID NO: 392. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0109] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, for example SEQ ID NO: 544. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 402, for example SEQ ID NO: 401. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 545, for example SEQ ID NO: 544; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 402, for example SEQ ID NO: 401. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0110] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, for example SEQ ID NO: 571. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384, for example SEQ ID NO: 383. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, for example SEQ ID NO: 571; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 384, for example SEQ ID NO: 383. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0111] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence

substantially the same as, or identical to, SEQ ID NO: 572, for example SEQ ID NO: 571. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393, for example SEQ ID NO: 392. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, for example SEQ ID NO: 571; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 393, for example SEQ ID NO: 392. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0112] Polynucleotides described herein may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, for example SEQ ID NO: 571. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 402, for example SEQ ID NO: 401. In some embodiments the described isolated polynucleotides may encode antibodies or antigen-binding fragments that have a light chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 572, for example SEQ ID NO: 571; and a heavy chain variable domain segment that includes an amino acid sequence substantially the same as, or identical to, SEQ ID NO: 402, for example SEQ ID NO: 401. The isolated polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments.

[0113] The polynucleotides capable of encoding the variable domain segments provided herein may be included on the same, or different, vectors to produce antibodies or antigen-binding fragments. Polynucleotides encoding engineered antigen-binding proteins also are within the scope of the disclosure. In some embodiments, the polynucleotides described (and

the peptides they encode) include a leader sequence. Any leader sequence known in the art may be employed. The leader sequence may include, but is not limited to, a restriction site or a translation start site.

[0114] Also provided are vectors comprising the polynucleotides described herein. The vectors can be expression vectors. Recombinant expression vectors containing a sequence encoding a polypeptide of interest are thus contemplated as within the scope of this disclosure. The expression vector may contain one or more additional sequences such as but not limited to regulatory sequences (e.g., promoter, enhancer), a selection marker, and a polyadenylation signal. Vectors for transforming a wide variety of host cells are well known and include, but are not limited to, plasmids, phagemids, cosmids, baculoviruses, bacmids, bacterial artificial chromosomes (BACs), yeast artificial chromosomes (YACs), as well as other bacterial, yeast and viral vectors.

[0115] Recombinant expression vectors within the scope of the description include synthetic, genomic, or cDNA-derived nucleic acid fragments that encode at least one recombinant protein which may be operably linked to suitable regulatory elements. Such regulatory elements may include a transcriptional promoter, sequences encoding suitable mRNA ribosomal binding sites, and sequences that control the termination of transcription and translation. Expression vectors, especially mammalian expression vectors, may also include one or more nontranscribed elements such as an origin of replication, a suitable promoter and enhancer linked to the gene to be expressed, other 5' or 3' flanking nontranscribed sequences, 5' or 3' nontranslated sequences (such as necessary ribosome binding sites), a polyadenylation site, splice donor and acceptor sites, or transcriptional termination sequences. An origin of replication that confers the ability to replicate in a host may also be incorporated.

[0116] The transcriptional and translational control sequences in expression vectors to be used in transforming vertebrate cells may be provided by viral sources. Exemplary vectors may be constructed as described by Okayama and Berg, 3 Mol. Cell. Biol. 280 (1983).

[0117] In some embodiments, the antibody- or antigen-binding fragment-coding sequence is placed under control of a powerful constitutive promoter, such as the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase, beta-actin, human myosin, human hemoglobin, human muscle creatine, and

others. In addition, many viral promoters function constitutively in eukaryotic cells and are suitable for use with the described embodiments. Such viral promoters include without limitation, Cytomegalovirus (CMV) immediate early promoter, the early and late promoters of SV40, the Mouse Mammary Tumor Virus (MMTV) promoter, the long terminal repeats (LTRs) of Moloney leukemia virus, Human Immunodeficiency Virus (HIV), Epstein Barr Virus (EBV), Rous Sarcoma Virus (RSV), and other retroviruses, and the thymidine kinase promoter of Herpes Simplex Virus. In one embodiment, the antibody or antigen-binding fragment thereof coding sequence is placed under control of an inducible promoter such as the metallothionein promoter, tetracycline-inducible promoter, doxycycline-inducible promoter, promoters that contain one or more interferon-stimulated response elements (ISRE) such as protein kinase R 2',5'-oligoadenylate synthetases, Mx genes, ADAR1, and the like.

[0118] Vectors described herein may contain one or more Internal Ribosome Entry Site(s) (IRES). Inclusion of an IRES sequence into fusion vectors may be beneficial for enhancing expression of some proteins. In some embodiments the vector system will include one or more polyadenylation sites (e.g., SV40), which may be upstream or downstream of any of the aforementioned nucleic acid sequences. Vector components may be contiguously linked, or arranged in a manner that provides optimal spacing for expressing the gene products (i.e., by the introduction of “spacer” nucleotides between the ORFs), or positioned in another way. Regulatory elements, such as the IRES motif, may also be arranged to provide optimal spacing for expression.

[0119] The vectors may comprise selection markers, which are well known in the art. Selection markers include positive and negative selection markers, for example, antibiotic resistance genes (e.g., neomycin resistance gene, a hygromycin resistance gene, a kanamycin resistance gene, a tetracycline resistance gene, a penicillin resistance gene), glutamate synthase genes, HSV-TK, HSV-TK derivatives for ganciclovir selection, or bacterial purine nucleoside phosphorylase gene for 6-methylpurine selection (Gadi et al., 7 Gene Ther. 1738-1743 (2000)). A nucleic acid sequence encoding a selection marker or the cloning site may be upstream or downstream of a nucleic acid sequence encoding a polypeptide of interest or cloning site.

[0120] The vectors described herein may be used to transform various cells with the genes encoding the described antibodies or antigen-binding fragments. For example, the vectors

may be used to generate antibody or antigen-binding fragment-producing cells. Thus, another aspect features host cells transformed with vectors comprising a nucleic acid sequence encoding an antibody or antigen-binding fragment thereof that specifically binds Tau, such as the antibodies or antigen-binding fragments described and exemplified herein.

[0121] Numerous techniques are known in the art for the introduction of foreign genes into cells and may be used to construct the recombinant cells for purposes of carrying out the described methods, in accordance with the various embodiments described and exemplified herein. The technique used should provide for the stable transfer of the heterologous gene sequence to the host cell, such that the heterologous gene sequence is heritable and expressible by the cell progeny, and so that the necessary development and physiological functions of the recipient cells are not disrupted. Techniques which may be used include but are not limited to chromosome transfer (e.g., cell fusion, chromosome mediated gene transfer, micro cell mediated gene transfer), physical methods (e.g., transfection, spheroplast fusion, microinjection, electroporation, liposome carrier), viral vector transfer (e.g., recombinant DNA viruses, recombinant RNA viruses) and the like (described in Cline, 29 Pharmac. Ther. 69-92 (1985)). Calcium phosphate precipitation and polyethylene glycol (PEG)-induced fusion of bacterial protoplasts with mammalian cells may also be used to transform cells.

[0122] Cells suitable for use in the expression of the antibodies or antigen-binding fragments described herein are preferably eukaryotic cells, more preferably cells of plant, rodent, or human origin, for example but not limited to NS0, CHO, CHOK1, perC.6, Tk-ts13, BHK, HEK293 cells, COS-7, T98G, CV-1/EBNA, L cells, C127, 3T3, HeLa, NS1, and Sp2/0 myeloma cells cell lines, among others. In addition, expression of antibodies may be accomplished using hybridoma cells. Methods for producing hybridomas are well established in the art.

[0123] Cells transformed with expression vectors described herein may be selected or screened for recombinant expression of the antibodies or antigen-binding fragments described herein. Recombinant-positive cells are expanded and screened for subclones exhibiting a desired phenotype, such as high level expression, enhanced growth properties, or the ability to yield proteins with desired biochemical characteristics, for example, due to protein modification or altered post-translational modifications. These phenotypes may be due to inherent properties of a given subclone or to mutation. Mutations may be effected through the use of chemicals, UV-

wavelength light, radiation, viruses, insertional mutagens, inhibition of DNA mismatch repair, or a combination of such methods.

[0124] In certain embodiments, an isolated cell line expressing any of the anti-Tau antibodies described herein are provided. In one embodiment, the isolated cell line is a hybridoma. In one embodiment, the isolated cell line is the hybridoma from which monoclonal antibody 7G6 is produced. In one embodiment, the isolated cell line is Freestyle® 293-F cells from which 7G6-HCzu8-LCzu6-HEK is produced and which cell line has been deposited with the American Type Culture Collection, Manassas, Va., USA, on October 11, 2017, with the ATCC Patent Deposit Designation PTA-124523. In one embodiment, the isolated cell line is Freestyle® 293-F cells from which 7G6-HCzu25-LCzu18-HEK is produced and which cell line has been deposited with the American Type Culture Collection, Manassas, Va., USA, on October 11, 2017, with the ATCC Patent Deposit Designation PTA-124524.

[0125] Cells that express the provided anti-Tau antibodies or antigen-binding fragments provided herein may be employed in methods of producing the anti-Tau antibodies or antigen-binding fragments by culturing the cells under conditions suitable for expression of the respective antibody or antigen-binding fragment. In some embodiments, the anti-Tau antibody or antigen-binding fragment is recovered from the culture medium.

[0126] In certain embodiments, any of the antibodies or antigen-binding fragments that specifically bind Tau as provided herein is useful for detecting the presence of Tau in a biological sample. The term “detecting” as used herein encompasses quantitative or qualitative detection. In certain embodiments, the biological sample may be derived from a cell or tissue, such as cerebrospinal fluid, a cell or tissue of the brain (e.g., cortex or hippocampus), or blood, a histological preparation, and the like. In some embodiments the described methods include detecting Tau in a sample by contacting the biological sample with:

(a) any one of antibody ms7G6, antibody 7G6-HCzu8-LCzu6, antibody 7G6-HCzu8-LCzu21, antibody 7G6-HCzu23-LCzu15, antibody 7G6-HCzu24-LCzu15, antibody 7G6-HCzu25-LCzu15, antibody 7G6-HCzu23-LCzu18, antibody 7G6-HCzu24-LCzu18, antibody 7G6-HCzu25-LCzu18, or an antigen-binding fragment thereof;

(b) an antibody, or antigen-binding fragment thereof, that comprises heavy chain CDR1, CDR2, and CDR3 amino acid sequences and light chain CDR1, CDR2, and CDR3 amino acid sequences of antibody ms7G6, antibody 7G6-HCzu8-LCzu6, or antibody 7G6-HCzu25-LCzu18, as described in Table 1;

(c) an antibody, or antigen-binding fragment thereof, that comprises the heavy chain variable domain segment and light chain variable domain segment of any one of antibody ms7G6, antibody 7G6-HCzu8/LCzu6, antibody 7G6-HCzu8/LCzu21, antibody 7G6-HCzu23/LCzu15, antibody 7G6-HCzu24/LCzu15, antibody 7G6-HCzu25/LCzu15, antibody 7G6-HCzu23/LCzu18, antibody 7G6-HCzu24/LCzu18, or antibody 7G6-HCzu25/LCzu18, as described in Table 1; or

(d) an antibody having the amino acid sequence of antibody produced by any one of the cell lines deposited with the ATCC having accession number PTA-124523 or PTA-124524, or an antigen binding fragment thereof.

[0127] In certain embodiments, the method comprises contacting the biological sample with an anti-Tau antibody as provided herein under conditions permissive for binding of the anti-Tau antibody to Tau, and detecting whether a complex is formed between the anti-Tau antibody and Tau. In some embodiments of these methods, the anti-Tau antibody is detectably labelled. The method may be an *in vitro* or *in vivo* method. The complex formed between the anti-Tau antibody and Tau in a test biological sample can be compared to the complex formed in a control biological sample (e.g., a biological sample from a healthy subject). The amount of the complex formed between the anti-Tau antibody and Tau in a test biological sample can also be quantified and compared to the amount of the complex formed in a control biological sample or to the average amount of the complex known to be formed in healthy subjects.

[0128] In a further aspect, the invention provides pharmaceutical formulations comprising any of the antibodies or antigen-binding fragments that specifically bind Tau as described herein, e.g., for use in any of the therapeutic methods provided herein. In some embodiments, a pharmaceutical formulation comprises any of the antibodies or antigen-binding fragments that specifically bind Tau provided herein and a pharmaceutically acceptable carrier.

[0129] Pharmaceutical formulations of an anti-Tau antibody or antigen-binding fragment as described herein are prepared by mixing such antibody or antigen-binding fragment

having the desired degree of purity with one or more optional pharmaceutically acceptable carriers, diluents, and/or excipients (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Pharmaceutically acceptable carriers, diluents, and excipients are generally nontoxic to recipients at the dosages and concentrations employed, and include, but are not limited to: sterile water, buffers such as phosphate, citrate, and other organic acids; antioxidants including 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 (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; 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 polyethylene glycol (PEG). Exemplary pharmaceutically acceptable carriers herein further include interstitial drug dispersion agents such as soluble neutral-active hyaluronidase glycoproteins (sHASEGP), for example, human soluble PH-20 hyaluronidase glycoproteins, such as rHuPH20 (HYLENEX™, Baxter International, Inc.). Certain exemplary sHASEGPs and methods of use, including rHuPH20, are described in US Patent No. 7,871,607 and U.S. Publication No. 2006/0104968. In one aspect, a sHASEGP is combined with one or more additional glycosaminoglycanases such as chondroitinases.

[0130] Exemplary lyophilized antibody formulations are described in US Patent No. 6,267,958. Aqueous antibody formulations include those described in US Patent No. 6,171,586 and WO2006/044908, the latter formulations including a histidine-acetate buffer.

[0131] The anti-Tau antibody or antigen-binding fragment as an active ingredient in a pharmaceutical formulation may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-

particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

[0132] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g. films, or microcapsules.

[0133] The formulations to be used for *in vivo* administration are generally sterile. Sterility may be readily accomplished, e.g., by filtration through sterile filtration membranes.

[0134] Any of the antibodies or antigen-binding fragments that specifically bind Tau (or formulations thereof) provided herein may be used in therapeutic methods.

[0135] In one aspect, an anti-Tau antibody or antigen-binding fragment for use as a medicament is provided. In some embodiments, an anti-Tau antibody or antigen-binding fragment for use in the reduction of insoluble Tau is provided. In some embodiments, an anti-Tau antibody or antigen-binding fragment for use in inhibiting Tau aggregation is provided. In further aspects, an anti-Tau antibody or antigen-binding fragment for use in treating a Tauopathy is provided. Exemplary Tauopathies that can be treated with the disclosed anti-Tau antibodies or antigen-binding fragments include Alzheimer's disease (AD), progressive supranuclear palsy (PSP), and frontotemporal dementia (FTD). An exemplary FTD that can be treated is Pick's disease (PiD).

[0136] In certain embodiments, an anti-Tau antibody or antigen-binding fragment for use in a method of treatment is provided. In some embodiments, an anti-Tau antibody or antigen-binding fragment for use in a method of reducing insoluble Tau in a subject is provided. In some embodiments, an anti-Tau antibody or antigen-binding fragment for use in a method of inhibiting Tau aggregation in a subject is provided. In certain embodiments, an anti-Tau antibody or antigen-binding fragment for use in a method of treating a subject having a Tauopathy is provided. The method of treatment of a Tauopathy comprises administering to the subject the anti-Tau antibody or antigen-binding fragment in an amount effective to treat the Tauopathy. In certain embodiments, the Tauopathy is any one of the Tauopathies described above. In preferred embodiments, the subject is a mammal, preferably a human.

[0137] In a further aspect, also provided herein is the use of an anti-Tau antibody or antigen-binding fragment as described herein in the manufacture or preparation of a medicament.

In some embodiments, the medicament is for reduction of insoluble Tau. In some embodiments, the medicament is for inhibition of Tau aggregation. In some embodiments, the medicament is for treatment of a Tauopathy. In certain embodiments, the Tauopathy is any one of the Tauopathies described above.

[0138] An anti-Tau antibody or antigen-binding fragment as described herein can be administered by any suitable means, including parenteral, intrapulmonary, and intranasal, and, if desired for local treatment, intralesional administration. Parenteral infusions include intramuscular, intravenous, intraarterial, intraperitoneal, or subcutaneous administration. Dosing can be by any suitable route, e.g. by injections, such as intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic. Various dosing schedules including but not limited to single or multiple administrations over various time-points, bolus administration, and pulse infusion are contemplated herein.

[0139] The anti-Tau antibodies or antigen-binding fragments provided herein are to be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the agent, the method of administration, the scheduling of administration, and other factors known to medical practitioners.

[0140] For the prevention or treatment of disease, the appropriate dosage of the anti-Tau antibody or antigen-binding fragment will depend on the type of disease to be treated, the type of antibody, the severity and course of the disease, whether the antibody or antigen-binding fragment is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, and the discretion of the attending physician. The antibody or antigen-binding fragment is suitably administered to the patient at one time or over a series of treatments. Depending on the type and severity of the disease, about 1 $\mu\text{g/kg}$ to 15 mg/kg of antibody or antigen-binding fragment can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 $\mu\text{g/kg}$ to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a

desired suppression of disease symptoms occurs. One exemplary dosage of the antibody or antigen-binding fragment would be in the range from about 0.05 mg/kg to about 100 mg/kg. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 10 mg/kg, 30 mg/kg, or 100 mg/kg (or any combination thereof) may be administered to the patient. Such doses may be administered intermittently, for example, every week or every three weeks (e.g. such that the patient receives from about two to about twenty, or e.g. about six doses of the antibody). An initial higher loading dose, followed by one or more lower doses may be administered. However, other dosage regimens may be useful. The progress of this therapy may be monitored by conventional techniques and assays.

[0141] Also provided herein is an article of manufacture containing material(s) useful for the treatment, prevention and/or diagnosis of the disorders described above. The article of manufacture comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is an anti-Tau antibody or antigen-binding fragment as described herein. The label or package insert indicates that the composition is used for treating the condition of choice. Alternatively, or additionally, the article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

[0142] Illustrative Embodiments

[0143] Provided here are illustrative embodiments of the disclosed technology. These embodiments are illustrative only and do not limit the scope of the present disclosure or of the claims attached hereto.

[0144] Embodiment 1. A monoclonal antibody, or an antigen-binding fragment thereof, that specifically binds a human Tau, the antibody comprising:

a heavy chain complementarity determining region 1 (HCDR1), a heavy chain complementarity determining region 2 (HCDR2), and a heavy chain complementarity determining region 3 (HCDR3) as set forth in SEQ ID NO: 196 and a light chain complementarity determining region 1 (LCDR1), a light chain complementarity determining region 2 (LCDR2), and a light chain complementarity determining region 3 (LCDR3) as set forth in SEQ ID NO: 411;

a HCDR1, a HCDR2, and a HCDR3 as set forth in SEQ ID NO: 268 and a LCDR1, a LCDR2, and a LCDR3 as set forth in SEQ ID NO: 465; or

a HCDR1, a HCDR2, and a HCDR3 as set forth in SEQ ID NO: 402 and a LCDR1, a LCDR2, and a LCDR3 as set forth in SEQ ID NO: 572.

[0145] Embodiment 2. The monoclonal antibody or antigen-binding fragment according to Embodiment 1, wherein:

the HCDR1 comprises SEQ ID NO: 594, the HCDR2 comprises SEQ ID NO: 596, the HCDR3 comprises SEQ ID NO: 598, the LCDR1 comprises SEQ ID NO: 738, the LCDR2 comprises SEQ ID NO: 740, and the LCDR3 comprises SEQ ID NO: 742 as defined according to the method of Kabat;

the HCDR1 comprises SEQ ID NO: 864, the HCDR2 comprises SEQ ID NO: 866, the HCDR3 comprises SEQ ID NO: 868, the LCDR1 comprises SEQ ID NO: 1008, the LCDR2 comprises SEQ ID NO: 1010, and the LCDR3 comprises SEQ ID NO: 1012 as defined by IMGT;

the HCDR1 comprises SEQ ID NO: 642, the HCDR2 comprises SEQ ID NO: 644, the HCDR3 comprises SEQ ID NO: 646, the LCDR1 comprises SEQ ID NO: 774, the LCDR2 comprises SEQ ID NO: 776, and the LCDR3 comprises SEQ ID NO: 778 as defined according to the method of Kabat;

the HCDR1 comprises SEQ ID NO: 912, the HCDR2 comprises SEQ ID NO: 914, the HCDR3 comprises SEQ ID NO: 916, the LCDR1 comprises SEQ ID NO: 1044, the LCDR2 comprises SEQ ID NO: 1046, and the LCDR3 comprises SEQ ID NO: 1048 as defined by IMGT;

the HCDR1 comprises SEQ ID NO: 732, the HCDR2 comprises SEQ ID NO: 734, the HCDR3 comprises SEQ ID NO: 736, the LCDR1 comprises SEQ ID NO: 846, the LCDR2 comprises SEQ ID NO: 848, and the LCDR3 comprises SEQ ID NO: 850 as defined according to the method of Kabat; or

the HCDR1 comprises SEQ ID NO: 1002, the HCDR2 comprises SEQ ID NO: 1004, the HCDR3 comprises SEQ ID NO: 1006, the LCDR1 comprises SEQ ID NO: 1116, the LCDR2 comprises SEQ ID NO: 1118, and the LCDR3 comprises SEQ ID NO: 1120 as defined by IMGT.

[0146] Embodiment 3. The monoclonal antibody or antigen-binding fragment according to Embodiment 1 or 2, wherein the residue at position 49 of the light chain according to the method of Kabat is not cysteine.

[0147] Embodiment 4. The monoclonal antibody or antigen-binding fragment according to Embodiment 3, wherein the residue at position 49 of the light chain according to the method of Kabat is serine.

[0148] Embodiment 5. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the residue at position 57 of the heavy chain according to the method of Kabat is not cysteine.

[0149] Embodiment 6. The monoclonal antibody or antigen-binding fragment according to Embodiment 5, wherein the residue at position 57 of the heavy chain according to the method of Kabat is serine.

[0150] Embodiment 7. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the residue at position 34 of the light chain according to the method of Kabat is glutamate.

[0151] Embodiment 8. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the residue at position 36 of the light chain according to the method of Kabat is not phenylalanine.

[0152] Embodiment 9. The monoclonal antibody or antigen-binding fragment according to Embodiment 8 wherein the residue at position 36 of the light chain according to the method of Kabat is tyrosine.

[0153] Embodiment 10. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the residue at position 46 of the light chain according to the method of Kabat is not arginine.

[0154] Embodiment 11. The monoclonal antibody or antigen-binding fragment according to Embodiment 10 wherein the residue at position 46 of the light chain according to the method of Kabat is leucine.

[0155] Embodiment 12. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the residue at position 94 of the heavy chain according to the method of Kabat is not lysine.

[0156] Embodiment 13. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the residue at position 71 of the heavy chain according to the method of Kabat is not arginine.

[0157] Embodiment 14. The monoclonal antibody or antigen-binding fragment according to the method of Embodiment 13 wherein position 71 of the heavy chain according to the Kabat method is valine.

[0158] Embodiment 15. The monoclonal antibody or antigen-binding fragment according to Embodiment 1 or Embodiment 2, the antibody comprising:

- a heavy chain variable domain (HCVD) comprising SEQ ID NO: 268 and a light chain variable domain (LCVD) comprising SEQ ID NO: 465;
- a HCVD comprising SEQ ID NO: 268 and a LCVD comprising SEQ ID NO: 581;
- a HCVD comprising SEQ ID NO: 384 and a LCVD comprising SEQ ID NO: 545;
- a HCVD comprising SEQ ID NO: 393 and a LCVD comprising SEQ ID NO: 545;
- a HCVD comprising SEQ ID NO: 402 and a LCVD comprising SEQ ID NO: 545;
- a HCVD comprising SEQ ID NO: 384 and a LCVD comprising SEQ ID NO: 572;
- a HCVD comprising SEQ ID NO: 393 and a LCVD comprising SEQ ID NO: 572; or
- a HCVD comprising SEQ ID NO: 402 and a LCVD comprising SEQ ID NO: 572.

[0159] Embodiment 16. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment, wherein the antibody is produced by the cell line having ATCC deposit number PTA-124523.

[0160] Embodiment 17. The monoclonal antibody or antigen-binding fragment according to any one of Embodiments 1 to 15, wherein the antibody is produced by the cell line having ATCC deposit number PTA-124524.

[0161] Embodiment 18. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment, wherein the antibody is a murine antibody, a chimeric antibody, or a humanized antibody.

[0162] Embodiment 19. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the antibody is IgG1.

[0163] Embodiment 20. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the antibody binds monomeric wild-type human 2N4R Tau with a K_D of less than about 0.5 nM as measured by surface plasmon resonance.

[0164] Embodiment 21. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment, wherein the antibody or antigen-binding fragment binds to human Tau at an epitope comprising the amino acid sequence HVPG (SEQ ID NO: 1133).

[0165] Embodiment 22. The monoclonal antibody or antigen-binding fragment according to Embodiment 21, wherein the antibody or antigen-binding fragment is biepitopic and binds to human Tau at an epitope comprising the amino acid sequence HVPG (SEQ ID NO: 1133) within repeat region 2 or repeat region 4.

[0166] Embodiment 23. The monoclonal antibody or antigen-binding fragment according to any one of Embodiments 1 to 20, wherein the antibody or antigen-binding fragment binds to human Tau at an epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79).

[0167] Embodiment 24. The monoclonal antibody or antigen-binding fragment according to Embodiment 23, wherein the antibody or antigen-binding fragment is biepitopic and binds to human Tau at an epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 2 or repeat region 4.

[0168] Embodiment 25. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment,

wherein the antibody or antigen-binding fragment binds human Tau at the epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 2 with a binding preference that is at least about 10-fold greater than binding at an epitope comprising the amino acid sequence HKPGG (SEQ ID NO: 182) within repeat region 3 or than binding at an epitope comprising the amino acid sequence HQPGG (SEQ ID NO: 183) within repeat region 1, or

wherein the antibody or antigen-binding fragment binds human Tau at the epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 4 with a binding preference that is at least about 10-fold greater than binding at an epitope comprising the amino acid sequence HKPGG (SEQ ID NO: 182) within repeat region 3 or than binding at an epitope comprising the amino acid sequence HQPGG (SEQ ID NO: 183) within repeat region 1,

as determined by a peptide binding assay.

[0169] Embodiment 26. The monoclonal antibody or antigen-binding fragment according to any preceding Embodiment wherein the antibody or antigen-binding fragment does not bind Tau at an epitope comprising the amino acid sequence HVSGG (SEQ ID NO: 184) within repeat region 2 or at an epitope comprising the amino acid sequence HVLGG (SEQ ID NO: 185) within repeat region 2.

[0170] Embodiment 27. A labeled antibody or antigen-binding fragment comprising the antibody or antigen-binding fragment according to any preceding Embodiment.

[0171] Embodiment 28. A nucleic acid molecule encoding the monoclonal antibody or antigen-binding fragment of any one of Embodiments 1 to 26.

[0172] Embodiment 29. A vector comprising the nucleic acid molecule of Embodiment 28.

[0173] Embodiment 30. A cell that expresses the nucleic acid molecule of Embodiment 28.

[0174] Embodiment 31. A method of producing an anti-Tau antibody or antigen-binding fragment comprising culturing a cell according to Embodiment 30 under conditions suitable for producing the antibody or antigen-binding fragment.

[0175] Embodiment 32. The method according to Embodiment 31 further comprising recovering the antibody or antigen-binding fragment.

[0176] Embodiment 33. A pharmaceutical composition comprising the antibody or antigen-binding fragment of any one of Embodiments 1 to 26 and a pharmaceutically acceptable carrier.

[0177] Embodiment 34. The antibody or antigen-binding fragment according to any one of Embodiments 1 to 26 for use as a medicament.

[0178] Embodiment 35. The antibody or antigen-binding fragment according to any one of Embodiments 1 to 26 for use in the treatment of a Tauopathy.

[0179] Embodiment 36. The antibody or antigen-binding fragment according to any one of Embodiments 1 to 26 for use in the preparation of a medicament for the treatment of a Tauopathy.

[0180] Embodiment 37. The antibody for use in accordance with Embodiment 35 or 36 wherein the Tauopathy is Alzheimer's disease, frontotemporal dementia, or progressive supranuclear palsy.

[0181] Embodiment 38. The antibody for use in accordance with Embodiment 37 wherein the frontotemporal dementia is Pick's Disease.

[0182] Embodiment 39. A method for decreasing sarkosyl-insoluble Tau levels, the method comprising administering to the subject the monoclonal antibody or antigen-binding fragment of any one of Embodiments 1 to 26.

[0183] Embodiment 40. A method for inhibiting Tau aggregation, the method comprising administering to the subject the monoclonal antibody or antigen-binding fragment of any one of Embodiments 1 to 26.

[0184] Embodiment 41. The method according to Embodiment 39 or 40 wherein the method is performed *in vitro* or *in vivo*.

[0185] Embodiment 42. A method of treating a Tauopathy in a subject, the method comprising: administering to the subject the monoclonal antibody or antigen-binding fragment of any one of Embodiments 1 to 26 under conditions effective to treat the Tauopathy in the subject.

[0186] Embodiment 43. The method according to Embodiment 42, wherein the Tauopathy is Alzheimer's disease, frontotemporal dementia, or progressive supranuclear palsy.

[0187] Embodiment 44. The method according to Embodiment 43, wherein the frontotemporal dementia is Pick's disease.

[0188] The following examples are provided to supplement the prior disclosure and to provide a better understanding of the subject matter described herein. These examples should not be considered to limit the described subject matter. It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be apparent to persons skilled in the art and are to be included within the scope of the invention and can be made without departing from the true scope of the invention.

Example 1: Generation of monoclonal antibodies

[0189] To generate anti-Tau antibodies recognizing the microtubule binding region (MTBR) of Tau, the peptide sequence CNIKHVPGGGSVQIVYKPVD (SEQ ID NO: 186) (Peptide antigen) was synthesized. Residues 2-20 of SEQ ID NO: 186 correspond to the amino acid sequence that spans the juncture between the second (i.e. not present in the 3R isoform) and third repeat regions of Tau (**Figure 2**). The sequence also includes the hexapeptide motif known as PHF6 (VQIVYK) (SEQ ID NO: 187) (von Bergen *et al.*, *PNAS*, 2000, 97(10): 5129-5134), which is one of the sites that initiates the aggregation of Tau. Peptide antigen was coupled to the Keyhole Limpet Hemocyanin (KLH) carrier protein via the N-terminal cysteine residue that does not naturally occur in the full length Tau-441 human protein sequence. The final immunogen was prepared by mixing the Peptide antigen-conjugated KLH with Freund's complete adjuvant (1:2 (v/v)). Tau knockout mice (Jackson #007251) were immunized with 0.08 mL per mouse of a 2.5 mg/mL immunogen solution. Approximately 3 weeks following the initial injection, the mice received a boost immunization with Peptide antigen-conjugated KLH without adjuvant at 0.05 mL per mouse at the same protein concentration as before.

[0190] One month after the boost immunization, antisera were collected from the mice and antibody titers assessed by ELISA to measure immunoreactivity against the original immunizing Tau peptide and both 2N4R and 1N3R recombinant Tau proteins. Briefly, either 150 ng of Peptide antigen conjugated to BSA or 50 ng of 2N4R or 1N3R recombinant Tau

protein (Enzo Life Sciences, cat. no's BML-SE321 and BML-SE323 respectively) were used to coat each well of a 96-well plate (Costar cat. no. 2797) in 10 mM phosphate buffer, pH 7.0 at 37°C for 1 hour. Plates were blocked in a final concentration of 1% BSA diluted in PBS at room temperature for 30 minutes. Blocking solution was removed and various dilutions of anti-sera in the same blocking buffer were added to the plate for 1 hour at room temperature. The plate was washed several times with PBS prior to the addition of an HRP-labelled anti-mouse IgG antibody for 30 minutes at room temperature. Following additional wash steps, antibody binding was detected by addition of 3,3',5,5'-Tetramethylbenzidine (TMB) substrate. The enzymatic reaction was stopped with an equal volume of 2M H₂SO₄ and the well optical density was determined using a platereader at wavelength 450 nm.

[0191] Once mice with a high antibody titer had been determined, cells were isolated from the medial iliac lymph nodes and fused using polyethylene glycol with mouse myeloma SP2 cells to generate hybridomas. Fused cells were seeded into 96-well plates and cultured in hypoxanthine-aminopterin-thymidine (HAT) selection medium. Culture supernatants were initially screened for Tau binding using the standard peptide and recombinant Tau ELISA assays as detailed in the previous paragraph. To give an approximation of relative binding, culture supernatant that was positive in the peptide ELISA and either recombinant protein, 2N4R or 1N3R, or both, were then evaluated in a competitive ELISA system. A 96-well plate was coated with 2N4R recombinant Tau, blocked and washed as before. At the primary antibody step, culture supernatant was diluted 1 in 10 and incubated with different dilutions of free antigen (2N4R Tau) for 1 hour at room temperature before addition to the plate. Once antibody/antigen complexes were added to the plate, the protocol for the remainder of the assay was identical to the standard ELISA procedure. Single cell clones were confirmed by serial dilution and microscopy. The resulting final hybridomas were cryopreserved in serum free medium.

Antibody purification from hybridomas

[0192] Hybridomas were grown in Hybridoma-SFM (Life Technologies) media containing 1% FBS, 1 ng/mL human IL-6 (R&D Systems) and Penicillin/Streptomycin. Cultures were scaled up to 100 mL and supernatant was harvested when cells reached a high density and were approximately 30% viable. Antibody was purified using Protein G columns, eluted with

glycine/HCl, pH2.5 and immediately neutralized. Purified antibody was then dialyzed into 25 mM sodium phosphate (pH6.5) and 150 mM NaCl, aliquoted, and stored at -80 °C.

[0193] Hybridoma clones generating antibodies that recognized the original immunization peptide and full length recombinant 2N4R Tau protein were produced (Table 2).

Example 2: Affinity of murine antibodies to recombinant monomeric Tau protein expressed in *E.coli*

[0194] Kinetic analysis of the interaction of the anti-Tau mouse monoclonal antibodies generated in Example 1 with human wild type Tau (2N4R) and the equivalent P301S mutant Tau protein was conducted using a BIAcore™ T100 instrument. Recombinant human full length Tau proteins were expressed in *E.coli* and then purified by Cellufine™ phosphate affinity chromatography followed by ammonium sulfate precipitation and reverse phase HPLC chromatography.

[0195] Purified antibodies from hybridomas were captured by protein A/G immobilized on a CM5 sensor chip (GE Healthcare). The wild type and P301S Tau proteins were then injected onto the sensor chip at five different concentrations and the affinity (equilibrium dissociation constant, K_D) was calculated according to the manufacturer's instruction. The results are shown in Table 2.

Table 2. Calculated affinity of seven anti-Tau mouse antibodies to 2N4R wild-type and P301S mutant recombinant Tau proteins.

Antibody	Isotype	Wild type 2N4R Tau K_D (nM)	P301S-2N4R Tau K_D (nM)	Fold difference
6B2	IgG1, k	1.3	108	83.1
8E5	IgG2b, k	0.39	3.35	8.6
4E6	IgG1, k	1.0	33.5	33.5
5D1	IgG1, k	0.9	10.1	11.2
1F1	IgG2a, k	0.41	1.42	3.5
5H7	IgG2a, k	0.61	3.8	6.2

7G6	IgG2b, k	0.052	0.57	11.0
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Example 3: Fine epitope mapping of the ms7G6 antibody

[0196] The recognition sequence of the murine 7G6 (“ms7G6” or “7G6”) antibody against the full length wild type 2N4R human Tau protein sequence (Tau441) was fine epitope-mapped using peptide chip microarrays.

[0197] All procedures were performed by PEPperPrint GmbH, Germany. The full length 2N4R wild type human Tau sequence was elongated with a neutral GSGSGSG linker sequence (SEQ ID NO: 188) at the C-terminus and translated into overlapping 15-mer peptides. The resulting peptide microarray containing 441 different peptides was printed in duplicate onto a glass chip along with 82 spots of an additional HA-tag control peptide (YPYDVPDYAG) (SEQ ID NO: 189).

[0198] The ms7G6 anti-Tau antibody was diluted to a concentration of 1 µg/mL in PBS (pH 7.4) containing 0.05% Tween 20 and 10% Rockland blocking buffer (MB-070). The diluted antibody was incubated on the chip for 16 hours at 4°C with shaking at 140 rpm. Primary antibody was removed and the chip was washed in PBS (pH 7.4)/0.05% Tween 20. Wash buffer was removed and goat anti-mouse IgG (H+L) DyLight™680 (1:5000) and an anti-HA tag DyLight™ 800 (1:2000) in the same buffer as the primary antibody was then incubated for 45 minutes at room temperature on the chip. Detection antibody was removed and the chip was washed once again as previously. Fluorescence images were acquired on the LI-COR Odyssey™ Imaging System and the microarray data was finally analyzed using the PepSlide™ Analyser software.

[0199] The fluorescent image of the chip (**Figure 3A**) and resulting intensity plot (**Figure 3B**) show that ms7G6 binds to two major sites on the full length Tau protein. It was also found that the minimum required sequence for ms7G6 binding at both sites is HVPGG (SEQ ID NO: 79) which is found at amino acid positions 299 to 303 (in the second repeat) and 362 to 366 (in the fourth repeat). Minor binding was observed at two additional sites: HQPGG (SEQ ID NO: 183) at amino acid positions 268 to 272, and HKPGG (SEQ ID NO: 182) at positions 330 to 334. Calculation of average signal intensities demonstrated that the mouse 7G6 antibody showed a 41-fold or 38-fold preference in binding to the HVPGG (SEQ ID NO: 79) site normally

contained within the second repeat region of full length 4R Tau compared to the HQPGG (SEQ ID NO: 183) (repeat region 1) or HKPGG (SEQ ID NO: 182) (repeat region 3) sequences, respectively. Similarly, a 35-fold or 33-fold preference in binding to the HVPGG (SEQ ID NO: 79) site normally contained within the fourth repeat region of full length 4R Tau compared to the HQPGG (SEQ ID NO: 183) (repeat region 1) or HKPGG (SEQ ID NO: 182) (repeat region 3) sequences, respectively, was observed.

Example 4: 7G6 epitope substitution scanning

[0200] To determine the amino acid stringency of the epitope recognized by the ms7G6 antibody, substitution scanning of the naturally occurring Tau peptide sequence ¹KDNIKHVPGGGSVQI¹⁵ (SEQ ID NO: 26) was performed. All procedures were undertaken by PEPperPrint GmbH, Germany and were based upon an exchange of all positions in the starting peptide with each of the 20 naturally-occurring amino acids.

[0201] Every possible 15-mer peptide was synthesized and printed in triplicate onto a glass chip to give a microarray containing 900 peptide spots. Additional copies of the wild type peptide as well as the HA-tag control peptide were also spotted onto the chip as controls. The peptide chip was then probed with ms7G6 under the same conditions as described in Example 3 (Fine epitope mapping of the ms7G6 antibody) and the resulting data analyzed using the PepSlide™ Analyser software (**Figure 4** illustrating results with SEQ ID NOs: 38 to 78). The substitution scanning showed that, within the peptide epitope of ¹HVPGG⁵ (SEQ ID NO: 79), antibody ms7G6 shows some flexibility in the second position with a number of possible residues. There is also some binding when the 5th amino acid (glycine) is substituted to either an alanine or serine. The middle proline residue is needed for antibody binding and may not be substituted with any other naturally-occurring amino acid. This amino acid can correspond to the P301 residue (within amino acids 299 to 303 of Tau441, Uniprot accession number P10636-8) which is commonly mutated to a serine or leucine residue to mimic human Tauopathy in a number of preclinical *in vitro* and *in vivo* models. The substitution scanning data indicates that the ms7G6 antibody preferentially recognizes the amino acid sequence HVPGG (SEQ ID NO: 79) binding site at amino acids 362 – 366 in the mutant P301S protein.

Example 5: *In vitro* Tau aggregation

[0202] To determine whether the ms7G6 antibody could functionally inhibit Tau aggregation *in vitro*, aggregation assays were performed with recombinant Tau protein.

[0203] Wild type or P301S mutant Tau protein was diluted to a concentration of 60 μ M in buffer containing 25 mM HEPES (pH 7.4), 100 mM NaCl and 0.5 mM TCEP in a final volume of 20 μ l. The mixture was heated in a thermal cycler at 98°C for 30 minutes and then allowed to cool to room temperature. Mouse IgG2b control or ms7G6 antibodies were diluted to a final concentration of 8.3 μ M in 25 mM HEPES (pH7.4), 100 mM NaCl and HALT Protease and Phosphatase inhibitors. Diluted antibodies or buffer controls were mixed with the Tau proteins and incubated at 37°C for 30 minutes. To induce Tau aggregation, heparin was added to each reaction to a 12 μ M final concentration in a final volume of 100 μ l. The final reaction conditions were 12 μ M Tau, 8.3 μ M antibody, 0.1 mM TCEP and 12 μ M Heparin in 25 mM HEPES pH7.4/100 mM NaCl buffer. The final reaction mixtures were incubated at 37°C for at least 6 days with sampling throughout to measure Tau aggregation.

[0204] The aggregation of Tau was measured on days 0, 1, 2, 5 and 6 by removing 10 μ L of the reaction mixture and placing into a 384-well, black-bottomed plate (Greiner). Thioflavin S dye was added to each well to a final concentration of 15 μ M, and the plate was incubated at room temperature in the dark for 30 minutes. Fluorescence was measured on a Pherastar™ platereader with excitation and emission wavelengths at 485 nm and 520 nm, respectively.

[0205] As shown in **Figures 5A and 5B**, the degree and rate of heparin-induced aggregation was higher for the P301S Tau protein compared to the wild type. The ms7G6 antibody substantially reduced the aggregation of both P301S Tau and wild-type Tau *in vitro* compared to IgG, as indicated by the lower amount of fluorescence generated. This suggests that, even for the P301S protein, ms7G6 binding to residues 362-366 alone could inhibit aggregation under these conditions.

Example 6: *In vitro* cell seeding model

[0206] To determine whether ms7G6 or a humanized version known as 7G6-zuHC25-zuLC18 (see Example 10) had an effect on cells, each antibody was tested in an *in vitro* cell-based model of Tau seeding and aggregation.

[0207] The 2N4R isoform of human wild type Tau was expressed in *E.coli* and then purified as previously described (Soeda *et al.*, *Nat Commun.* 2015, 6: 10216). Recombinant Tau (40 μ M) was mixed with heparin (240 μ g/mL) and incubated at 37°C for 48 to 96 hours in 100 mM sodium acetate, pH 7.0, containing 2 mM DTT. Aggregated Tau protein was collected by ultracentrifugation and resuspended in 100 mM sodium acetate pH 7.0 or PBS. The solution was then sonicated to produce the recombinant Tau seeds.

[0208] Neuro-2a (ATCC) cells were transfected in suspension with cDNA expression plasmids encoding 0N4R P301S Tau using Lipofectamine LTX (Thermo Fisher Scientific) and plated at a density of 1.5×10^4 cells per well into a 96-well plate in DMEM medium containing 10% fetal bovine serum. Cells were left to attach overnight at 37°C prior to adding Tau seeds. In parallel, various concentrations of anti-Tau antibodies were mixed with 1 μ g/mL of Tau seed and were also incubated overnight at 37°C. The following day, culture medium was removed and medium containing the mixture of anti-Tau antibodies and seed were added. Plates were cultured again overnight at 37°C.

[0209] Cells were fixed with a final concentration of 4% paraformaldehyde and immunostained by H-150 (Santa Cruz Technology, sc-5587), thioflavin S (Sigma-Aldrich, T-1892) and DAPI (Wako, 340-07971). Images were captured and analysed using the InCell Analyzer 2200 and Toolbox.

[0210] As shown in **Figures 6A, 6B, 6C, and 6D**, a significant decrease in Thioflavin S staining (aggregated Tau) was observed in response to both ms7G6 and 7G6-HCzu25-LCzu18 treatment. This indicates that both antibodies were able to block the Tau seeding effect in this cell-based model under these assay conditions.

Example 7: Efficacy in a preclinical *in vivo* model of Tauopathy by pre-incubating recombinant P301S Tau seeds with antibodies

[0211] The effects of three new antibodies, including ms7G6, were tested in a short term *in vivo* model of Tau deposition by pre-incubating the relevant antibodies with recombinant P301S Tau seeds. The seeds with or without antibody were then injected into the brains of P301S transgenic mice.

Intracerebroventricular (ICV) injection of Tau seeds

[0212] Pre-formed fibrillar (PFF) Tau was generated by mixing recombinant 2N4R P301S Tau (40 μ M) and heparin (240 μ g/mL), followed by an incubation step at 37°C for 48 to 96 hours in 100 mM sodium acetate, pH7.0, containing 2 mM DTT. Aggregated Tau was collected by ultracentrifugation and resuspended in 100 mM sodium acetate, pH7.0. The resulting fibrils were sonicated and used as seeds for injection. Tau seeds at a concentration of 0.83 mg/mL were incubated with 1 mg/mL IgG₁ or 2 mg/mL anti-Tau antibody for 1 hour at 37°C. The Tau seeds/antibody mixtures, controls (i.e., Tau alone) or vehicle was injected into the intracerebroventricular (ICV) zone of 2-3.5 months old P301S transgenic mice (MRC Technology, United Kingdom). These mice overexpress human 0N4R P301S Tau under the control of the murine neuron-specific Thy-1 promoter on a CBAxC57/bl6 background.

[0213] It has been reported previously that these animals, if untreated, develop widespread Tau pathology in the brain and spinal cord with significant motor deficits at 5 to 6 months of age (Allen *et al.*, *J Neurosci.* 2002, 22(21):9340-51). In the current experiment using younger P301S mice, animals were sacrificed two weeks after the ICV injection, brains were removed, and the tissue region of interest collected. Tissue samples were then fractionated into sarkosyl-soluble and insoluble Tau (Sahara *et al.*, *J Neurochem.* 2002 Dec;83(6):1498-508) as described below.

Extraction of sarkosyl-insoluble Tau from seed-injected P301S mouse brain

[0214] Tissue was homogenized in 19 volumes (tissue weight/volume) of extraction buffer containing 50 mM Tris-HCl (pH7.5) (Invitrogen), 5 mM EDTA (Nippon Gene), 1 mM EGTA (Nacalai Tesque), 1% NP-40 (Fluka), 0.25% deoxycholic acid sodium salt (Sigma Aldrich), 0.1 M NaCl, 0.5 mM PMSF (Sigma Aldrich), 1 $\times$ PhosSTOP™ (Roche, Basel, Schweiz), and 1 $\times$ Complete EDTA(-) (Roche). Homogenates were centrifuged at 163,000 g at

4°C for 20 minutes and the resulting supernatants were collected and retained as the Tris buffer-soluble fraction. The pellet was resuspended in about 10 volumes (tissue weight/volume) of buffer containing 10 mM Tris-HCl (pH7.5), 0.5 M NaCl, 1 mM EGTA, 10% sucrose (Wako Pure Chemical), and 1% sarkosyl prior to sonication. Sarkosyl-treated samples were incubated at 37°C for 60 minutes, and then centrifuged at 163,000 g at 4 °C for a further 20 minutes. The supernatants were collected as the sarkosyl-soluble fraction. Finally, about 10 volumes of PBS (Gibco) was added to the pellet which was then sonicated. This formed the sarkosyl-insoluble fraction.

Detection of Sarkosyl-insoluble Tau by Western blotting

[0215] Sarkosyl-insoluble fractions were solubilized in NuPAGE™ LDS sample buffer and NuPAGE™ sample reducing agent (Invitrogen), heated at 70°C for 10 minutes, and separated using 12.5% polyacrylamide gels (DRC). Proteins were transferred to 0.2 µm PVDF membranes (Bio-Rad, Hercules, CA, USA) and blots were blocked in 2.5% skimmed milk (Yukikirushi) in TBS (Takara) containing 0.05% Tween (Nacalai tesque) for 1 hour at room temperature. After blocking, blots were probed with the human-specific monoclonal anti-Tau antibody HT7 (1:1000 or 1:2000, Thermo Fisher Scientific, Waltham, MA, USA) in blocking buffer for 1 hour at room temperature. The blots were washed in TBS-T for 30 minutes and then incubated with HRP-conjugated anti-mouse IgG (1:2000, GE healthcare) for a further 1 hour at room temperature. Secondary antibody was removed and blots were washed as described above. Tau proteins were detected by chemiluminescent horseradish peroxidase (HRP) substrate (Merck Millipore) and quantified using the Fusion FX (Vilber-Lourmat, France) analyzer. To determine the amount of Tau, serial dilutions of standards Tau derived from the originating sarkosyl-insoluble fraction of P301S spinal cord were loaded onto each gel.

[0216] As shown in **Figure 7**, pre-incubation of P301S seeds with ms7G6 but not control IgG, 8E5 or 1F1 showed a significant decrease in sarkosyl-insoluble Tau levels compared with vehicle. This suggested that ms7G6 was a superior antibody in this paradigm compared to the other anti-Tau antibodies generated.

Example 8: Validation of the P301S seeding and transmission *in vivo* model

[0217] To determine whether any transmission from one brain region to another of pathological Tau could occur in a rodent preclinical model, the same seeding experiment was performed in P301S transgenic mice as described in Example 7 but with some modifications. In this case, 20 μ L of recombinant P301S Tau seeds at a concentration of 0.9 mg/mL was injected ICV into the brains of 2.5 to 3 month old mice. Mice were sacrificed at either 2, 4 or 6 weeks following the initial seed injection, brains were removed and both hippocampus and cortex were retained. The sarkosyl-insoluble Tau was prepared and detected as described above.

[0218] As shown in **Figure 8**, a sharp increase in insoluble Tau levels was observed in the hippocampus between 2 and 4 weeks post seed-injection but only low levels of insoluble Tau was observed in the cortex at the same time point. However, between 4 and 6 weeks following seed injection a greater increase of insoluble Tau was observed in the cortex compared with the no-seed control group. This shows that, in this model, insoluble Tau can form in the hippocampus, prior to the cortex, suggestive of a secondary transmission event.

Example 9: Effect of peripheral once weekly dosing of 7G6 in the P301S seed injection *in vivo* model.**a) Experiment 1**

[0219] The P301S Tau seed injection into P301S transgenic mice was performed as described in Example 8 with minor modifications. About seven to about four hours prior to Tau seed injection, mice received a dose of either 40 mg/kg IgG2b control antibody (BioXCell) or ms7G6 antibody intraperitoneally. Each antibody was formulated in 25 mM phosphate buffer (pH6.5) with 150 mM NaCl. A vehicle treatment control group was also included which received buffer alone. Following Tau seed injection into the brain, mice received further doses of antibody or buffer once weekly for a period of 6 weeks. Animals were then sacrificed, brain tissues isolated, and insoluble Tau was prepared and measured as described in Example 7.

b) Experiment 2

An exact repeat of Experiment 1 (Example 9a) was performed.

c) Experiment 3

[0220] A repeat of Experiment 1 (Example 9a) was performed again except two dosing levels of ms7G6, 20 and 40 mg/kg, were administered and the animals were sacrificed 8 weeks after seed injection rather than 6 weeks as in the previous two experiments.

[0221] As shown in Figures 9 and 10, these three experiments demonstrate that ms7G6 can cause a reduction in insoluble Tau levels in this seed injection model with P301S recombinant Tau seeds in a P301S transgenic mouse. The reduction observed in the cortex suggests that the antibody may slow pathological Tau transmission. It was ascertained in example 4 that the ms7G6 antibody is unable to bind to the HVSGG sequence (SEQ ID NO: 184) (aa299-303) that is present in the P301S site of the mutant protein. Taken together, this means that the *in vivo* effects of ms7G6 in this *in vivo* model are driven by the binding to Tau at the remaining HVPGG (SEQ ID NO: 79) epitope within the fourth repeat region (aa362-366).

Example 10: Antibody Humanization**10A. Materials & Methods****10A.a. *In silico* modeling**

[0222] Discovery Studio 4.5 was used to generate a molecular model of the ms7G6 Fv region. The top 1 to 3 crystal structures with the most homologous protein sequences to the ms7G6 variable heavy (VH) and variable kappa (VK) domains were used as a template for generating twenty-five homology models using the “Create Homology Models” function. The model with the lowest energy score was selected and the energy was first minimized for just the hydrogens and then for all atoms. Framework residues differing between the mouse sequences (HCzu1 and LCzu1) were highlighted and those closest to the CDRs or at the VH/VK interface were identified as residues that may be important for maintaining Tau binding by the CDRs or for antibody stability, respectively. CDR residues differing between the mouse sequences

(HCzu1 and LCzu1) were highlighted and residues were identified that may be not important for maintaining Tau binding by the CDRs.

10A.b. Gene synthesis and cloning

10A.b.1. InFusion™ cloning

[0223] Humanized heavy and light variable domains were codon-optimized for expression in CHO cells and were synthesized by GeneArt. The variable domains were synthesized with a Kozak translation initiation sequence and an Ig secretion leader sequence and included 15 base-pairs at the 5' and 3' ends homologous to the cloning site within the subcloning vector. PCR fragments synthesized by GeneArt were subcloned into an expression plasmid containing a human gamma or kappa constant region using an InFusion™ HD cloning kit (Clontech). All clones were sequenced to confirm the presence and fidelity of the inserts.

10A.b.2. QuikChange™

[0224] Point mutations were made using Stratagene's QuikChange™ XL according to the manufacturer's protocol. All clones were sequenced to confirm the presence of the mutation.

10A.c. Cell Culture

10A.c.1. HEK transient mAb production

[0225] For each milliliter of 3×10^6 cells to be transfected with ExpiFectamine™ (Thermo), 333.3 ng HC plasmid and 333.3 ng LC plasmid were incubated for 5 -10 min in 50 μ L Opti-MEM (Thermo). Likewise, 2.67 μ L ExpiFectamine™ was incubated in 50 μ L Opti-MEM. The ExpiFectamine™ solution was added to the DNA mixture and incubated for 20-30 min at room temperature. The DNA:ExpiFectamine™ mixture was added to the cells while swirling and incubated at 37°C, 8% CO₂, shaking at 125 rpm. The following day, 5 μ L of enhancer 1 and 50 μ L of enhancer 2 per mL of cells were added to the transfection with continued incubation for another 7-10 days. After 48-72 h, cells were fed at a final concentration of 10 g/L Yeastolate (BD Biosciences), 5 mM valeric acid (Sigma-Aldrich), and 1:100 CD Lipid Concentrate (Thermo).

10A.c.2. CHO transient mAb production

[0226] For each milliliter of 6×10^6 cells to be transfected with ExpiFectamine™ CHO (Thermo), 500 ng HC plasmid and 500 ng LC plasmid was mixed in Opti-PRO™ (Thermo) in 40 μ L total volume. Likewise, 3.2 μ L ExpiFectamine™ CHO was mixed in 36.8 μ L Opti-PRO. The ExpiFectamine™ CHO solution was added to the DNA mixture and incubated for 1 - 5 min at room temperature. The DNA:ExpiFectamine™ CHO mixture was added to the cells while swirling and incubated at 37°C, 8% CO₂, shaking at 125 rpm. The following day, 6 μ L of enhancer and 160 μ L of feed per mL of cells were added to the transfection, and cells were transferred to 32°C, 5% CO₂. At day 5, an additional 160 μ L of feed per mL of cells was added. At day 12 to 14, the supernatants were harvested.

10A.d. MAb purification

10A.d.1. Batch purification

[0227] Prosep™-vA High Capacity Protein A resin (Millipore) or CaptureSelect™ KappaSelect LC-kappa resin (Thermo) was equilibrated with DPBS, and 50 μ L were added to 2 mL of sample. Following incubation at room temperature for 1 hour, the medium and resin were added to a filter plate and washed twice with 1 mL DPBS. The sample was eluted from the resin by addition of 400 μ L 0.1 M Glycine, pH 2.9 followed by centrifugation at 15,000 x g for 30 s. The sample was neutralized with 20 μ L of 1 M Tris, pH 8.0. The samples were concentrated to ~ 100 μ L by centrifugation at 15,000 x g for 5 minutes using 0.5 mL Amicon™ Ultra, 10k cutoff filters (Millipore) and were buffer-exchanged into DPBS using 0.5 mL Zeba™ desalting columns, 7K MWCO, according to the manufacturer's protocol.

10A.d.2. Column purification

[0228] Purification was performed using an AKTA Xpress purification platform (GE Healthcare). Up to 1 L conditioned medium was loaded onto a 5 mL MabSelect™ SURE column (GE Healthcare) equilibrated in 20 mM sodium phosphate, 150 mM NaCl, pH 7.0. The column was washed extensively with equilibration buffer following loading until a stable baseline was observed. Bound material was eluted using 100 mM glycine, pH 2.9. Eluted material was immediately injected on to a 26/10 HiPrep desalting column (GE Healthcare)

equilibrated in 1x phosphate-buffered saline (PBS) and eluted in the same buffer. Peak fractions were pooled. The material was analyzed for protein content by BCA assay (Thermo) and purity by reducing and non-reducing SDS-PAGE.

10A.e. 2N4R Tau-binding ELISA

[0229] A black Nunc MaxiSorp 96-well plate was coated with 2 µg/mL (unless otherwise indicated) of recombinant wild-type 2N4R Tau in DPBS overnight at 4°C. The following day the plate was aspirated and washed three times with Wash Buffer (PBS + 0.05% Tween-20). The wells were incubated with Assay Buffer (1% w/v BSA [heat shock fraction, Sigma], 0.05% Tween-20 [BioRad], DPBS) for 1 h at room temperature. The Assay Buffer was aspirated and the wells were washed three times as above. Various concentrations of mAbs in DPBS were added to each well for 1 hour at room temperature while shaking on a microtiter plate shaker. Samples were aspirated and the wells were washed three times as above. HRP-conjugated goat anti-mouse IgG (H+L) (JIRL 115-035-146), gt anti-hu IgG (H+L) (JIRL 109-035-127), or Streptavidin-HRP (JIRL 016-030-084) was diluted 1:5000 in Assay Buffer and added to the wells. Following incubation and shaking at room temperature for 1 hour, samples were aspirated and the wells were washed three times as above. QuantaBlu (Thermo) was added to each well and incubated for 15 min at room temperature. The relative fluorescence units (RFU) were measured with the excitation and emission wavelengths set at 320 and 460 nm, respectively, using a Spectramax™ M5 plate reader (Molecular Devices).

10A.f. Surface plasmon resonance (SPR) binding analyses

10A.f.1. Anti-human/anti-mouse capture monomeric Tau-binding assay

10A.f.1.i. Chip preparation

[0230] All experiments were performed using a BIAcore™ T-100 instrument (GE Healthcare). 10 µL anti-human IgG (monoclonal mouse anti-human Fc) from human antibody capture kit (GE Healthcare) was diluted to 25 µL/mL in 200 µL final immobilization buffer (10 mM sodium acetate, pH 5.0). The flow rate was set to 5 µL/min, flowpath 1. Fifty µL N-hydroxysuccinamide (NHS) and 50 µL 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (EDC)

were mixed and injected for 420 sec to activate the CM5 chip surface. The diluted antibody was injected for 360 seconds followed by 1 M ethanolamine for 420 seconds. The flowpath was then switched to flowpath 2. A new EDC/NHS mixture was prepared and the procedure was repeated for flow cell 2. The surface was conditioned by 2 injections of 30 sec using flowpath 1,2 at 30 $\mu\text{L}/\text{min}$ of 3M MgCl_2 . For the anti-mouse surface, 10 μL anti-mouse IgG (polyclonal rabbit anti-mouse IgG) from mouse antibody capture kit (GE Healthcare) was diluted to 30 $\mu\text{L}/\text{mL}$ in 324 μL final immobilization buffer (10 mM sodium acetate, pH 5.0). The flow rate was set to 5 $\mu\text{L}/\text{min}$, flowpath 3. Fifty μL NHS and 50 μL EDC were mixed and injected for 420 sec to activate the chip surface. The diluted antibody was injected for 420 sec. 1 M ethanolamine was injected for 420 sec. Flow path was switched to flowpath 4. A new EDC/NHS mixture was prepared and the procedure was repeated for flow cell 4. The surface was conditioned by 2 injections of 30 sec using flowpath 3,4 at 30 $\mu\text{L}/\text{min}$ of 10 mM glycine, pH 1.7.

Final immobilization levels were:

Flow cell 1 – 10,000 RU (anti-human)

Flow cell 2 – 10,092 RU (anti-human)

Flow cell 3 – 11,824 RU (anti-mouse)

Flow cell 4 – 11,216 RU (anti-mouse)

10A.f.1.ii. Binding assay

[0231] The running buffer used for the binding assay was PBS-P+/0.2% BSA. All antibodies were diluted to 1 $\mu\text{g}/\text{mL}$ in PBS-P+/0.2% BSA (same preparation as used for running buffer), centrifuged at 14,000g for 5 min at room temperature, and the supernatant was transferred to a new tube. Analyte (Tau monomer 2N4R wt, 2.15 mg/mL, 47 μM) was diluted to 100 nM in PBS-P+/0.2% BSA, centrifuged at 14,000g for 5 min at room temperature, and the supernatant transferred to a new tube. 100 nM solution was serially-diluted 5-fold into PBS-P+/0.2% BSA. Final concentrations were 100 nM, 20 nM, 4 nM, 0.8 nM, 0.16 nM, 0.032 nM, and 0 nM. Humanized antibodies were captured on flow cell 2 at a flow rate of 10 $\mu\text{L}/\text{min}$ for a contact time of 60 sec. Murine antibodies were captured on flow cell 4 at a flow rate of 10 $\mu\text{L}/\text{min}$ for a contact time of 60 sec. Dilutions of Tau protein were injected over all 4 flow cells at a flow rate of 30 $\mu\text{L}/\text{min}$ for a contact time of 240 sec. Dissociation was followed for 900 sec.

Following each cycle, surface was regenerated by a 30 sec injection (flowpath 1,2) at 30 $\mu\text{L}/\text{min}$ of 3M MgCl_2 , a 30 sec injection (flowpath 3,4) at 30 $\mu\text{L}/\text{min}$ of 10 mM glycine, pH 1.7, a 30 sec injection (flowpath 1,2) at 30 $\mu\text{L}/\text{min}$ of 3 M MgCl_2 , followed by two 30-sec injections (flowpath 3,4) at 30 $\mu\text{L}/\text{min}$ of 10 mM glycine, pH 1.7. After the run, data collected was fitted to a steady-state binding model using all concentrations using BIAEvaluations. Kinetic data fitting was performed using a 1:1 Langmuir model, excluding the 100 nM trace (inclusion of 100 nM trace resulted in unacceptably high X^2 values). A subset of antibody binding data was also analyzed using a 2-state model.

10A.f.2. Anti-human capture monomeric Tau-binding assay

10A.f.2.i. Chip preparation

[0232] Chip preparation was performed using a BIAcore™ T-100 instrument. Chip preparation was performed using the method wizard for immobilization. Running buffer was HBS-P+. Fifteen μL anti-human IgG (monoclonal mouse anti-human Fc) from human antibody capture kit (GE Healthcare) was diluted to 25 $\mu\text{L}/\text{mL}$ in 300 μL final immobilization buffer (10 mM sodium acetate, pH 5.0). The flow rate was set to 5 $\mu\text{L}/\text{min}$. Immobilization was performed on all four flow cells with a ligand contact time of 360 sec. The surface was conditioned by two injections of 30 sec using flowpath 1,2, 3, 4 at 30 $\mu\text{L}/\text{min}$ of 3 M MgCl_2 .

Final immobilization levels were:

Flow cell 1 – 7341 RU

Flow cell 2 – 7683 RU

Flow cell 3 – 7530 RU

Flow cell 4 – 6303 RU

10A.f.2.ii. Binding assay

[0233] Binding experiments were performed using a BIOcore™ T-100 instrument or a T-200 instrument. Running buffer used for the binding assay was PBS-P+/0.2% BSA. All antibodies were diluted to 2 $\mu\text{g}/\text{mL}$ in PBS-P+/0.2% BSA (the same preparation as used for the running buffer), centrifuged at 14,000g for 5 min at room temperature, and the supernatant transferred to new tube. Analyte (Tau monomer 2N4R wt, 2.15 mg/mL, 47 μM) was diluted to

100 nM in PBS-P+/0.2% BSA, centrifuged at 14,000g for 5 min at room temperature, and the supernatant transferred to a new tube. 100 nM solution was serially-diluted 5-fold into PBS-P+/0.2% BSA. Final concentrations were 100 nM, 20 nM, 4 nM, 0.8 nM, 0.16 nM, 0.032 nM, and 0 nM. Humanized antibodies were captured on flow cells 2, 3, and 4 sequentially at a flow rate of 10 μ L/min for a contact time of 60 sec. Dilutions of Tau protein were injected over all 4 flow cells at a flow rate of 30 μ L/min for a contact time of 240 sec. Dissociation was followed for 900 sec. Following each cycle, the surface was regenerated by two sequential injections of 30 sec at 30 μ L/min of 3 M MgCl₂ over all four flow cells. After the run, kinetic data fitting was performed using a 1:1 Langmuir model, excluding the 100 nM trace (inclusion of 100 nM trace resulted in unacceptably high X2 values).

10A.f.3. Streptavidin capture monomeric Tau-binding assay

10A.f.3.i. Antibody preparation

[0234] 400 μ g of each antibody was diluted to 2 mg/mL and buffer-exchanged into 0.1 M sodium bicarbonate, pH 8.3 using 0.5 mL Zeba™ 40 kDa MWCO desalting columns (Thermo). NHS-PEG4-biotin, prepared immediately before use by dissolving in water to a 20 mM final stock concentration, was added to antibodies at a 5:1 molar ratio (biotin:MAb) and conjugated for 1 hr at room temperature. Excess biotin was removed by two sequential buffer exchanges into 1x DPBS using 0.5 mL Zeba™ 40 kDa MWCO desalting columns. For the BIAcore™ assay, antibodies were diluted to 2 μ g/mL in PBS-P+/0.2% BSA (the same preparation used for the running buffer), centrifuged at 14,000g for 5 min at room temperature, and the supernatant transferred to a new tube. Injection time was subsequently determined for each antibody to achieve a capture level of ~ 225 RU.

[0235] Wild-type 2N4R Tau protein (2.15 mg/mL, 47 μ M) was diluted to 100 nM in PBS-P+/0.2% BSA, centrifuged at 14,000g for 5 min at room temperature, and supernatant transferred to a new tube. 20 nM solution was serially-diluted 5-fold into PBS-P+/0.2% BSA. Final concentrations were 20 nM, 4 nM, 0.8 nM, 0.16 nM, and 0 nM.

10A.f.3.ii. Binding assay

[0236] The biosensor chip used was a CAP chip from the biotin CAPture™ kit (GE Healthcare, cat 28-9202-34). All experiments were performed using a T-100 instrument. CAP reagent was immobilized on all four flow cells (flowpath 1,2,3,4) at a flow rate of 2 μ L/min for 5 min (final streptavidin level was $\sim$ 3500 RU). Biotinylated humanized antibodies, biotinylated chimeric 7G6, or biotinylated murine ms7G6 were captured on flow cells 2, 3, and 4 sequentially at a flow rate of 10 μ L/min for a contact time of 80 sec to 146 sec (biotinylated chimeric antibody contact time was 240 sec). Dilutions of Tau protein were injected over all four flow cells at a flow rate of 30 μ L/min for a contact time of 180 sec in sequence from 0 nM to 20 nM. Following the last injection (20 nM Tau), dissociation was followed for 900 sec. After each cycle, the surface was regenerated by one injection of 120 sec 10 μ L/min of 6 M Guanidine HCl, 0.25 M NaOH over all four flow cells. Samples were assayed in duplicate, except for murine 7G6 and 7G6-zuHC25-zuLC18, which were analyzed in duplicate on two separate flow cells (total of 4 analyses for each). After the run, kinetic data fitting was performed using a 1:1 Langmuir model using single cycle kinetics.

10A.g. Size exclusion chromatography-high performance liquid chromatography (SEC-HPLC)

[0237] SEC-HPLC was performed on an Agilent 1260 quaternary pump HPLC system equipped with an AdvanceBio™ SEC 300A, 2.7 μ m, 4.6 mm ID x 50 mm guard column, and AdvanceBio™ SEC 300A, 2.7 μ m, 4.6 mm ID x 300 mm column (Agilent). The isocratic flow of a mobile phase consisting of 0.1 M sodium phosphate (pH 6.5) was at 0.35 mL/min. The separation was conducted at ambient temperature. The column effluent was monitored at 280 nm. Fifty μ g of sample (10 μ L of 5 mg/mL sample) was injected for each run; each sample was analyzed twice. Peak integration was performed using Agilent OpenLAB software. Retention time, peak height, peak area, peak width, and peak symmetry were reported. The percentage of aggregates and monomers were calculated based on the peak area.

10A.h. Differential Scanning Calorimetry (DSC) analysis

[0238] VP Capillary Differential Scanning Calorimeter (VP-CapDSC; MicroCal, VP-CapDSC, s/n 12-07-149 with Origin-7 graphing and MicroCal VP-Capillary DSC Software v.2.0) was used to decipher and compare the higher order structure and thermal stability of various F(ab')₂ fragments and controls. Samples were allowed to acclimate to ambient temperature for 30 minutes, followed by vortexing. The entire sample (0.4 – 0.5 mL) was added to appropriate wells of an assay plate (Microliter Analytical Supply, 96 well, 500 µL, round well and bottom, cat # 07-2100; Sun Suri plate cover cat # 300-005). 0.5 mL of 20% Contrad solution and 0.5 mL water were added to the appropriate wells of the assay plate. Sealed plates were placed into an auto-sampler at 10°C.

[0239] The run was programmed and initiated using the following assay parameters:

DSC Controls:

Start Temperature = 25°C

Final Temperature = 100°C

Scan Rate = 100°C/Hr

Number of Rescans = 0

Rescan Cooling Rate = EXP

Pre-scan Thermostat = 10 Minutes

Post-scan Thermostat = 5 Minutes

Post-Cycle Thermostat = 25°C

Filtering Period = 10 Seconds

Autofill Cells at = 30°C

Feedback Mode/Gain = None

Unique Scans

Sample Parameters:

Concentration = mM

File Parameters = Auto #

Rinse Station = select Wash 2 (So will Wash 2 (1xPBS) then Wash 1 (Water))

Thermostat Control Set Point = 25°C

Pulse Control:

Pulse Size = -3

Duration = 600

Pulse Off

Y-Axis Scale Units = mCal/Minute

Clean in-line with Contrad/Contrad at 25-70°C, 100°C/Hour followed by two Buffer/Buffer injections.

10B. Results

10B.a. IGHV1/IGKV2 humanization

10B.a.1 7G6 in silico modelling

[0240] The human germline variable domain protein sequences most homologous to mouse ms7G6 mAb were retrieved using BLAST at <http://www.ncbi.nlm.nih.gov/igblast/> and <http://www.imgt.org/3Dstructure-DB/cgi/DomainGapAlign.cgi>. IGHV1-46*03 and IGKV2-30*02 variable domain families were the most homologous sequences to ms7G6 (Figure 11). Mouse framework sequences were replaced with the closest homologous human germline sequences to generate CDR-grafted humanized variants.

[0241] The mouse and CDR-grafted sequences were used to generate *in silico* models of the variable domains. The theoretical structure of the mouse and humanized models were superimposed, and residues in close proximity to the CDRs were analyzed for potential structural influence on the overall structure of the CDR loops. While most of the differing residues were not located at the dimer interface or were distal to the CDRs, several residues were found to be in close proximity (within 5 Å) of the CDRs.

[0242] In the V κ domain, the hydroxyl group in mouse Tyr36 formed a potential hydrogen bond with Trp100 in CDRH3. The human Phe36 loses this hydrogen bond, which may affect the structural integrity of CDRH3. Human Arg46 is much bulkier than the mouse Leu46, and Arg46 may sterically hinder proper folding of the CDRs. Similarly, in the V $\hbar$ domain, position 71 was positioned against the CDRs. The human Arg71 may sterically hinder proper folding of the CDRs compared to the mouse Val71. The human Val78 was positioned similarly

and is bulkier than the mouse Ala78. Therefore Val78 may, but was unlikely to, affect the integrity of the CDRs.

[0243] The mouse ms7G6 antibody contained two unpaired cysteines that may be problematic in the development of the mAb due to the presence of free thiols which could contribute to product aggregation, oxidation, cysteinylolation, or glutathionylation. One Cys was located at position 57 in CDRH2 and the second was at position 49 in FWRL2.

[0244] The Kabat definition of CDRH2 extends 8 C-terminal amino acids longer than the IMGT definition. The latter 8 amino acids were analyzed for their proximity and potential contribution to antigen binding. Asn58 was within the potential antigen binding site at the potential CDR-antigen interface at the top of the variable domains. Residues 60, 61, 64, and 65 differing between mouse and the human germline sequence were outside of the potential antigen binding site and were not likely to directly contact the antigen or provide structural support for proper CDR folding.

10B.a.2. Humanized Vh1 and Vκ2 variants and analysis for Tau binding by ELISA

[0245] A series of humanized mutants were generated using the germline variable domain Vh1 and Vκ2 families to evaluate the importance of mouse residues at the positions predicted by *in silico* modeling to be important for CDR-antigen interactions (Figure 12). Humanized and mouse 7G6 residues were analyzed at Vh positions 60, 61, 64, 65, 71, and 78 in various combinations (7G6-HCzu1-4), as well as the C57S mutation (7G6-HCzu5). Combinations of human and mouse residues at positions 36, 46, and 49 in ms7G6 Vκ were also analyzed (7G6-LCzu1-5) as well as the C49S mutation (7G6-LCzu6). MAbs were expressed in a matrix format whereby every combination of humanized HCs and LCs were cotransfected, except 7G6-HCzu5 was only coexpressed with 7G6-LCzu2 and 7G6-LCzu6 was only coexpressed with 7G6-HCzu3.

[0246] To test direct binding to Tau, 2N4R Tau was coated on 96-well plates and various concentrations of humanized mAbs were added to the wells. MAbs bound to Tau were detected with either an HRP-conjugated anti-mouse antibody (mouse [ms]7G6) or anti-human antibody (remaining samples). Samples were incubated for 1 h at room temperature in 96-well plates coated with 2N4R Tau. Following washing, HRP-conjugated anti-mouse or anti-human

detection antibodies were added to the wells. The anti-mouse antibody was used to detect ms7G6. The amount of HRP activity in each well was measured by QuantaBlu fluorescent substrate and the RFUs were detected by a SpectraMax M5 plate reader.

[0247] Data from the samples, grouped according to the LC variant, except the cysteine mutants which are grouped on the bottom-most graph, is shown in **Figures 13A-13F**. Amongst all of the 7G6 HC and LC variants, there was little difference in Tau binding (Figures 13A-F; Table 3). Although ms7G6 showed better binding than the humanized variants, it should be noted that this result may be misleading due to the differing detection antibodies between the mouse and human samples. mAb2 corresponds to non-Tau-binding control IgG antibody.

Table 3. EC50s* of humanized 7G6 Vh1/Vk2 variants binding Tau

Ab	EC50
7G6-HCzu1-LCzu1	119.2
7G6-HCzu2-LCzu1	104.7
7G6-HCzu3-LCzu1	131.4
7G6-HCzu4-LCzu1	184.7
7G6-HCzu1-LCzu2	133.1
7G6-HCzu2-LCzu2	208.9
7G6-HCzu3-LCzu2	171.6
7G6-HCzu4-LCzu2	168.2
7G6-HCzu1-LCzu3	164.9
7G6-HCzu2-LCzu3	152.3
7G6-HCzu3-LCzu3	188.9
7G6-HCzu4-LCzu3	176.5
7G6-HCzu1-LCzu4	191.7
7G6-HCzu2-LCzu4	226.9
7G6-HCzu3-LCzu4	253
7G6-HCzu4-LCzu4	282.6
7G6-HCzu1-LCzu5	167.1
7G6-HCzu2-LCzu5	186.9
7G6-HCzu3-LCzu5	183.6
7G6-HCzu4-LCzu5	199.4
7G6-HCzu5-LCzu2	147
7G6-HCzu5-LCzu2	154.2
7G6-HCzu3-LCzu6	135
ms7G6	34.36

*The EC50s were determined by fitting a non-linear regression curve in GraphPad Prism 6.05.

[0248] To reduce any potential immunogenicity, another series of mutants was generated with increasing numbers of human residues (7G6-HCzu6, 7G6-HCzu 7, and 7G6-HCzu 8; Figure 12). Since Vh Ser57 showed little difference in binding to Cys57, most of the mutants contained Ser57. To further confirm that serine was a viable substitution for cysteine at position 57, two mutant pairs differing at only position 57 were generated (7G6-HCzu7 and 7G6-HCzu9 and 7G6-HCzu8 and 7G6-HCzu10; Figure 12).

[0249] All V κ variants were engineered with Ser49, except 7G6-LCzu10 which was made to determine whether the human residue Tyr49 was a viable substitute for Cys49. 7G6-LCzu7 was analogous to 7G6-LCzu1 and 7G6-LCzu3 except with Ser49. 7G6-LCzu21 was analogous to 7G6-LCzu5 and 7G6-LCzu22 was analogous to 7G6-LCzu4, again with Ser49. 7G6-LCzu8 had a valine at position 30 to determine whether the human residue at this position retained Tau binding. Position 34 was somewhat buried in the structure and it was possible it did not contribute to antigen binding, therefore the human residue Asn34 at the end of CDRL1 was engineered into 7G6-LCzu9. All HC variants were coexpressed with 7G6-LCzu6 and all LC variants were coexpressed with 7G6-HCzu5.

[0250] Tau binding was analyzed by a direct ELISA as above. Samples were incubated for 1 hour at room temperature in 96-well plates coated with wild-type 2N4R Tau. After a wash step, HRP-conjugated anti-mouse or anti-human detection antibodies were added to the wells. The anti-mouse antibody was used to detect ms7G6. The amount of HRP activity in each well was measured by QuantaBlu fluorescent substrate and the RFUs were detected by a SpectraMax M5 plate reader. A majority of the mAbs showed little difference in Tau binding in a direct ELISA assay (**Figure 14**; Table 4). The notable exception was LCzu9 which exhibited no binding, even at the highest concentrations. Therefore, V κ Glu34 was critical for antigen binding. In addition, LCzu22 showed reduced binding; V κ Tyr36 in combination with Arg46 resulted in disruption of the antigen binding site.

Table 4. EC50s* of humanized 7G6 Vh1/V κ 2 variants binding Tau

	EC50
7G6-HCzu5-LCzu6	299.8
7G6-HCzu6-LCzu6	320.9
7G6-HCzu7-LCzu6	270.3
7G6-HCzu8-LCzu6	256.5

7G6-HCzu9-LCzu6	250.4
7G6-HCzu10-LCzu6	277.7
7G6-HCzu5-LCzu7	212.1
7G6-HCzu5-LCzu8	221
7G6-HCzu5-LCzu9	NB
7G6-HCzu5-LCzu10	209.6
7G6-HCzu5-LCzu21	301.5
7G6-HCzu5-LCzu22	813.9
ms7G6	86.33

*The EC50s were determined by fitting a non-linear regression curve in GraphPad Prism 6.05. NB (no binding) indicates little to no binding to Tau.

[0251] Binding of humanized and mouse antibodies were analyzed by surface plasmon resonance (BIAcore™) to determine their relative association rates (k_a), dissociation rates (k_d), and equilibrium binding constants (K_D). Anti-mouse or anti-human antibodies were immobilized on a CM5 chip and sample mAbs were captured on the chip. 2N4R Tau was flowed over the chip and binding observed. The binding constants k_a , k_d , and K_D were determined using a 1:1 Langmuir fitting model. Antibody ms7G6 derived from hybridoma or IgG2a or IgG2b recombinant material showed no difference in the association or dissociation rates (Table 5). Among the 7G6 HC variants, there were only slight differences, and the cysteine to serine mutations did not affect Tau binding. 7G6-LCzu2, LCzu6, LCzu7, LCzu8, and LCzu21 bound Tau similarly, demonstrating that the amino acids differing between these mAbs had little impact on binding. The humanized samples demonstrated better binding to Tau than the mouse mAbs, but this was most likely due to the necessity of using different capture antibodies in this assay format.

Table 5. BIAcore™ analysis of mouse and humanized Vh1/Vκ2

MAB	Species/Isotype	k_a ($\times 10^5 \text{ M}^{-1}\text{sec}^{-1}$)	k_d ($\times 10^{-3} \text{ sec}^{-1}$)	K_D (nM)
7G6-HCzu1-LCzu1	human/IgG1	25.70	0.519	0.202
7G6-HCzu2-LCzu1	human/IgG1	28.30	0.640	0.226
7G6-HCzu3-LCzu1	human/IgG1	27.70	0.856	0.309
7G6-HCzu4-LCzu1	human/IgG1	35.70	0.847	0.237
7G6-HCzu1-LCzu2	human/IgG1	22.00	0.241	0.110
7G6-HCzu2-LCzu2	human/IgG1	21.20	0.214	0.101

7G6-HCzu3-LCzu2	human/IgG1	20.00	0.242	0.121
7G6-HCzu4-LCzu2	human/IgG1	20.00	0.242	0.121
7G6-HCzu5-LCzu2	human/IgG1	18.60	0.237	0.127
7G6-HCzu3-LCzu6	human/IgG1	19.00	0.227	0.120
7G6-HCzu5-LCzu6	human/IgG1	21.4	0.206	0.0961
7G6-HCzu6-LCzu6	human/IgG1	22.1	0.213	0.0961
7G6-HCzu7-LCzu6	human/IgG1	20.8	0.226	0.109
7G6-HCzu8-LCzu6	human/IgG1	21.7	0.21	0.0968
7G6-HCzu9-LCzu6	human/IgG1	20.6	0.193	0.0938
7G6-HCzu10-LCzu6	human/IgG1	19.8	0.213	0.108
7G6-HCzu5-LCzu7	human/IgG1	31.4	0.304	0.0968
7G6-HCzu5-LCzu8	human/IgG1	36	0.298	0.0828
7G6-HCzu5-LCzu9	human/IgG1	no binding	no binding	no binding
7G6-HCzu5-LCzu10	human/IgG1	32.7	0.53	0.162
7G6-HCzu5-LCzu21	human/IgG1	29.3	0.278	0.095
7G6-HCzu5-LCzu22	human/IgG1	18.8	2.77	1.48
Hybridoma ms7G6	mouse/IgG2b	4.64	1.533	3.305
recombinant ms7G6	mouse/IgG2b	3.73	1.556	4.170
recombinant ms7G6	mouse/IgG2a	5.49	1.497	2.725

[0252] These data, along with the data from ELISA assay, demonstrated the requirement for 7G6 V κ Glu34 and the detrimental combination of 7G6 V κ Tyr36 and Arg46. 7G6 V κ residues Tyr36 and Leu46 in LCzu6 were slightly favored over the human Phe36 and Arg46 residues in 7G6-LCzu7 and 7G6-LCzu8, but retaining the human residues at these positions outweighed the minor reduction in the k_d . The human V κ Tyr57 in 7G6-LCzu10 had a significant impact on the k_d .

10B.a.3. SDS-PAGE analysis of HC/LC stability for Vh1 and V κ 2 variants

[0253] Two micrograms of each mAb were mixed with 4x NuPAGE™ LDS Sample Buffer and separated non-reduced on a 4-12% Bis-Tris SDS-PAGE gel in MOPS buffer. Gels were stained with InstantBlue™ and destained in water. All mAbs with Cys49 in the LC (7G6-LCzu2, 7G6-LCzu3, 7G6-LCzu4, and 7G6-LCzu5) were not stable, and under non-reducing conditions, HC-HC-LC trimers, HC-HC dimers, and free LC were separated by SDS-PAGE (**Figure 15**). 7G6-LCzu2 had fewer lower molecular weight species, likely due to this V κ having two additional mouse residues, Tyr36 and Leu46, stabilizing the Vh-V κ interaction.

7G6-LCzu3, 7G6-LCzu4, and 7G6-LCzu5 had one or both of these residues changed to the human Phe36 and/or Arg46. The least stable mAbs were the LCzu3 variants with both human residues. 7G6-LCzu7, 7G6-LCzu8, 7G6-LCzu9, and 7G6-LCzu22 had a small amount of free light chain, suggesting the HC and LC interaction in these samples may not be optimal, resulting in a small amount of antibodies not forming the HC-LC interchain disulfide bond. As with 7G6-LCzu3, these LC variants have human residues at one or both positions 36 and 46. 7G6-LCzu10 and 7G6-LCzu21 also have human residues at these positions, but no free LC was seen, possibly a result of incomplete staining by the InstantBlue™ stain.

10B.b IGHV3/IGKV1 humanization

10B.b.1 Humanized Vh3 and Vk1 variants and analysis for Tau binding by ELISA

[0254] The humanized 7G6 variants discussed above utilized the human germline variable domain families IGHV1 and IGKV2 chosen based on their similarity to ms7G6. However, these families are underrepresented in the human population, thereby increasing the chance the humanized variants would be immunogenic in patients (Brezinschek HP, Foster SJ, Dörner T, Brezinschek RI, Lipsky PE. Pairing of variable heavy and variable kappa chains in individual naive and memory B cells. *J Immunol.* 1998 May 15;160(10):4762-7; Jayaram N, Bhowmick P, Martin AC. Germline Vh/VK pairing in antibodies. *Protein Eng Des Sel.* 2012 Oct;25(10):523-9; Tiller T, Schuster I, Deppe D, Siegers K, Strohner R, Herrmann T, Berenguer M, Poujol D, Stehle J, Stark Y, Heßling M, Daubert D, Felderer K, Kaden S, Kölln J, Enzelberger M, Urlinger S. A fully synthetic human Fab antibody library based on fixed Vh/VK framework pairings with favorable biophysical properties. *MAbs.* 2013 May-Jun;5(3):445-70). Therefore the ms7G6 CDRs were grafted onto the more common IGHV3 and IGKV1 families (**Figure 16**).

[0255] The aforementioned in silico model of ms7G6 was analyzed as above for human residues in close proximity (5 Å) of the CDRs. Human residues in Vh at positions 49, 71, 76, 78, and 94 and in Vk at positions 2 and 57 were identified as potential critical framework residues. Two humanized variants of the Vh and Vk were generated, one with all human framework

residues (7G6-HCzu11; 7G6-LCzu11) and one with potentially critical residues back-mutated (7G6-HCzu12; 7G6-LCzu12) (**Figure 17**). Both HCs were coexpressed with both LCs.

[0256] 2N4R Tau was coated on 96-well plates and various concentrations of humanized mAbs were added to the wells as above. MAbs bound to Tau were detected with either an HRP-conjugated anti-mouse antibody (ms7G6) or anti-human antibody (remaining samples). All humanized mAbs bound similarly to Tau, but the 7G6-HCzu12-LCzu12 mAb had the lowest EC₅₀ (**Figure 18 & Table 6**). Both mouse mAbs showed better binding than the humanized variants, possibly due to the different detection antibodies used between the mouse and human samples. These data suggest that at least some of the human residues in proximity to the CDRs negatively affect antigen binding.

Table 6. EC₅₀s of humanized 7G6Vh1/Vκ2 variants binding Tau

Ab	EC ₅₀
ms7G6	89.88
7G6-HCzu11-LCzu11	245.9
7G6-HCzu11-LCzu12	284.2
7G6-HCzu12-LCzu11	218.4
7G6-HCzu12-LCzu12	153.4

The EC₅₀s were determined by fitting a non-linear regression curve in GraphPad Prism 6.05.

[0257] To reduce potential immunogenicity, another series of mutants was generated with increasing numbers human residues. Residues in the C-terminal half of CDRH2 had little impact on Tau binding in Vh1-based variant 7G6-HCzu4. Therefore, these residues were changed to the Vh3 germline residues in 7G6-HCzu13, 7G6-HCzu14, 7G6-HCzu19 and 7G6-HCzu20 (**Figure 17**). Variants of 7G6-HCzu12 were made such that mouse residues were replaced with human in order of probable increasing importance on antigen binding, based on the in silico ms7G6 model. For instance, the sidechain of Ser76 was on a loop facing away from the CDRs and was the least likely residue to impact the CDR-antigen interaction. Therefore it was the first residue to be changed to human residue Asn76 in 7G6-HCzu15. Residue 49 was mutated next (7G6-HCzu16), then 78 (7G6-HCzu17), 71 (7G6-HCzu18), and finally 94 (7G6-HCzu20).

[0258] With little difference between 7G6-LCzu11 and 7G6-LCzu12, it was expected that human residues at positions 2 and 57 would have little impact on antigen binding. Therefore, each of these was mutated one at a time. For position 57, tyrosine and serine substitutions were analyzed. A valine at position 30 was introduced in 7G6-LCzu16 and 7G6-LCzu17. The human residue Asn34 at the end of CDRL1 was engineered into 7G6-LCzu17. All HC variants were coexpressed with 7G6-LCzu12 and all LC variants were coexpressed with 7G6-HCzu12.

[0259] A majority of the mAbs showed little difference in Tau binding in a direct ELISA assay (**Figure 19 & Table 7**). The notable exception was LCzu17 which exhibited no binding, even at the highest concentrations. Therefore, V κ Glu34 was critical for antigen binding.

Table 7. EC50s of humanized 7G6Vh1/V κ 2 variants binding Tau

Ab	EC50
7G6-HCzu12-LCzu12	283.4
7G6-HCzu13-LCzu12	320.1
7G6-HCzu14-LCzu12	335.1
7G6-HCzu15-LCzu12	358
7G6-HCzu16-LCzu12	313.1
7G6-HCzu17-LCzu12	341.6
7G6-HCzu18-LCzu12	278.4
7G6-HCzu19-LCzu12	216.4
7G6-HCzu20-LCzu12	317.2
7G6-HCzu12-LCzu13	263.3
7G6-HCzu12-LCzu14	248.6
7G6-HCzu12-LCzu15	287.6
7G6-HCzu12-LCzu16	328.8
7G6-HCzu12-LCzu17	NB
ms7G6	86.33

The EC50s were determined by fitting a non-linear regression curve in GraphPad Prism 6.05. NB (no binding) indicates little to no binding to Tau.

10B.b.2 BIAcore™ analysis of Tau affinity for Vh3 and Vk1 variants

[0260] Binding of humanized and mouse antibodies were analyzed by BIAcore™ to determine their relative association rates (k_a), dissociation rates (k_d), and equilibrium binding constants (K_D). Anti-mouse or anti-human antibodies were immobilized on a CM5 chip and sample mAbs were captured on the chip. 2N4R Tau was flowed over the chip and binding observed. The binding constants k_a , k_d , and K_D were determined using a 1:1 Langmuir fitting model. Both 7G6-HCzu12-based mAbs had similar k_a and k_d values (**Table 8**). However, the k_a of 7G6-HCzu11 was decreased, though the k_d was unaffected. Therefore, human residues in the Vh3 framework impact binding to Tau. As with the ELISA assay, 7G6-LCzu17 did not bind Tau. The difference in k_d between 7G6-HCzu12, 7G6-HCzu13, and 7G6-HCzu14 suggests the CDRH2 C-terminal human residues have a negative impact on antigen binding. The decrease in k_d was not observed for 7G6-HCzu19 and 7G6-HCzu20 which also have human residues in the region; however, these mAbs had a decrease in k_a . 7G6-HCzu15 did not bind to the chip very well, and the data from this mAb were questionable. While no specific data on the single S76N mutation was available, the k_a and k_d values for 7G6-HCzu16, 7G6-HCzu17, 7G6-HCzu18 were similar to 7G6-HCzu12 suggesting the S76N mutation should not affect Tau binding. The k_a for 7G6-HCzu20 was less than 7G6-HCzu19 and may be a result of the K94R mutation. Therefore human residues at position 49, 71, 76, and 78 did not appear to affect Tau binding. The humanized samples demonstrated better binding to Tau than the mouse mAbs, but this was most likely due to the necessity of using different capture antibodies in this assay format.

Table 8. BIAcore™ analysis of mouse and humanized 7G6 Vh3/Vκ1 mAbs

MAB	Species/Isotype	k_a ($\times 10^5 \text{ M}^{-1}\text{sec}^{-1}$)	k_d ($\times 10^{-3} \text{ sec}^{-1}$)	K_D (nM)
7G6-HCzu11-LCzu11	human/IgG1	8.53	0.175	0.205
7G6-HCzu12-LCzu11	human/IgG1	13.80	0.181	0.132
7G6-HCzu12-LCzu12	human/IgG1	14.90	0.193	0.129
7G6-HCzu12-LCzu12	human/IgG1	17.2	0.151	0.0875
7G6-HCzu13-LCzu12	human/IgG1	14.2	0.239	0.168
7G6-HCzu14-LCzu12	human/IgG1	14.6	0.194	0.133
7G6-HCzu15-LCzu12	human/IgG1	20.2	0.278	0.138
7G6-HCzu16-LCzu12	human/IgG1	15.3	0.174	0.114
7G6-HCzu17-LCzu12	human/IgG1	17	0.124	0.073
7G6-HCzu18-LCzu12	human/IgG1	15.7	0.128	0.0815
7G6-HCzu19-LCzu12	human/IgG1	12.5	0.152	0.121
7G6-HCzu20-LCzu12	human/IgG1	11.4	0.136	0.119
7G6-HCzu12-LCzu13	human/IgG1	14	0.124	0.0888
7G6-HCzu12-LCzu14	human/IgG1	17.3	0.119	0.0689
7G6-HCzu12-LCzu15	human/IgG1	14.7	0.141	0.0959
7G6-HCzu12-LCzu16	human/IgG1	14.9	0.148	0.099
7G6-HCzu12-LCzu17	human/IgG1	no binding	no binding	no binding
Hybridoma ms7G6	mouse/IgG2b	4.64	1.533	3.305
recombinant ms7G6	mouse/IgG2b	3.73	1.556	4.170
recombinant ms7G6	mouse/IgG2a	5.49	1.497	2.725

[0261] There was little difference between the k_a or k_d values for any 7G6 LC variant, except 7G6-LCzu17, which did not bind Tau due to Asn34. Therefore, the human Ile2 had no effect on antigen binding. Cysteine, serine, and tyrosine all appeared to be tolerated at position 57. A valine at position 30 had no impact on Tau binding.

10B.b.3 SDS-PAGE analysis of HC/LC stability for Vh3 and Vκ1 variants

[0262] Two micrograms of each mAb were mixed with 4x NuPAGE™ LDS Sample Buffer and separated non-reduced on a 4-12% Bis-Tris SDS-PAGE gel in MOPS buffer. Gels were stained with InstantBlue and destained in water. The more human 7G6-HCzu11, especially when paired with the less human 7G6-LCzu12, resulted in HC-LC dimers and free HC (**Figure 20A**). Further, 7G6-HCzu18 and 7G6-HCzu19 showed significant fragments (**Figures 20B and 20C**). These two antibodies differ from the others at position 71. Therefore, the human residue

Arg41, while not impacting Tau binding, contributed to destabilization of the HC-LC interaction. All LC variants showed no antibody fragments. Contrary to Vh1-Vκ2 mAbs analyzed above, Cys49 did not produce HC-HC-LC trimers, HC-HC dimers, or free LC.

10B.c. Screening of Humanized Antibodies

[0263] Based on human-ness of the sequences, BIAcore™ affinity data and SDS-PAGE stability data from the IGHV1/IGKV2 humanization, 7G6-HCzu8 was chosen as the most human sequence with the highest affinity for Tau. 7G6-LCzu6 and 7G6-LCzu21 had comparable stability in SDS-PAGE and affinity for Tau but differed by one amino acid at position 36. Both light chains were chosen to be coexpressed with 7G6-HCzu8 to determine the best IGHV1/IGKV2-based mAb.

[0264] Another round of mutagenesis was performed on the most human, highest affinity, and most stable IGHV3 and IGKV1 variants to remove the unpaired cysteines at position 57 and 49, respectively. 7G6-HCzu17 and 7G6-HCzu18 were chosen as the most human framework residues with the highest affinity. 7G6-HCzu18 was super-humanized by introducing human residues into the C-terminal portion of CDRH2 to generate 7G6-HCzu21, but the affinity was never analyzed. 7G6-HCzu18, 7G6-HCzu21, and 7G6-HCzu17 all contained a cysteine at position 57, and a serine was introduced at position 57 in all three variants to generate 7G6-HCzu23, 7G6-HCzu24, and 7G6-HCzu25, respectively (**Figure 17**). 7G6-LCzu14 and 7G6-LCzu15 were the most human Vκ sequences with the highest affinity. 7G6-LCzu14 retained Cys49 and was therefore mutated to remove the unpaired cysteine and was named 7G6-LCzu18. Each IGHV3 HC was paired with each IGKV1 LC.

10B.c.1 Intact mass analysis

[0265] The mass of each mAb was analyzed by ESI-MS to confirm the theoretical mass matched the observed mass. MAbS were digested with IdeS to generate F(ab')₂ fragments, followed by reduction with 2 mM DTT and heating at 60°C for 3 min. The mass of the Fd (Vh-CH1) and LC fragments were analyzed by ESI-MS. 7G6-HCzu8 contained an N-terminal pyroglutamic acid, a typical post-translational modification of N-terminal glutamines. All observed masses were within 3 Daltons of the predicted masses (**Table 9**).

Table 9. ESI-MS analysis of humanized variants

	Fd	PyrQ	Cys	Calculated	Observed	dMass
7G6-HCzu8-LCzu6	25447	17	4	25426	25425	-1
7G6-HCzu8-LCzu21	25447	17	4	25426	25425	-1
7G6-HCzu23-LCzu15	25349		4	25345	25345	0
7G6-HCzu24-LCzu15	25526		4	25522	25522	0
7G6-HCzu25-LCzu15	25469		4	25465	25463	-2
7G6-HCzu23-LCzu18	25349		4	25345	25345	0
7G6-HCzu24-LCzu18	25526		4	25522	25521	-1
7G6-HCzu25-LCzu18	25469		4	25465	25462	-3
	LC	Cys	Calculated	Observed	dMass	
7G6-HCzu8-LCzu6	24007	4	24003	24003	0	
7G6-HCzu8-LCzu21	23991	4	23987	23988	1	
7G6-HCzu23-LCzu15	23953	4	23949	23949	0	
7G6-HCzu24-LCzu15	23953	4	23949	23949	0	
7G6-	23953	4	23949	23948	-1	

HCzu25- LCzu15					
7G6- HCzu23- LCzu18	23967	4	23963	23963	0
7G6- HCzu24- LCzu18	23967	4	23963	23963	0

10B.c.2 Tau binding BIAcore™ assay

[0266] Tau binding for humanized mAbs was analyzed by BIAcore™ in two different formats. The first format was performed as above, i.e. mAbs were captured with an immobilized species-specific anti-Fc antibody. The limitation of this format is seen in Tables 5 and 8 where the affinities of the parental mouse and humanized mAbs cannot be directly compared due to the differences in the capture antibodies. In the second format, biotinylated mAbs were captured on a streptavidin-coated chip. This latter format allowed direct comparison of Tau binding affinity between humanized and the parental mouse antibody since the capture method was identical.

10B.c.2.i Fc-specific capture

[0267] The final humanized mAbs were analyzed by BIAcore™ to determine the k_a , k_d , and K_D for binding to Tau as above (**Table 10**). There was a significant change in the off rate (k_d) from 7G6-HCzu23 to 7G6-HCzu24, while 7G6-HCzu24 was similar to 7G6-HCzu25, which was also seen in the overall affinity K_D as well. This confirmed the importance of retaining mouse residues in CDRH2, as seen above in Table 7.

Table 10. BIAcore™ analysis of humanized 7G6 mAbs binding monomeric Tau (anti-human capture)

MAb	k_a ($\times 10^5 \text{ M}^{-1}\text{sec}^{-1}$)	k_d ($\times 10^{-3} \text{ sec}^{-1}$)	K_D (nM)
7G6-HCzu8-LCzu6	14.9	0.22	0.15
7G6-HCzu23-LCzu15	16.1	0.39	0.25
7G6-HCzu24-LCzu15	8.09	0.11	0.13
7G6-HCzu25-LCzu15	9.85	0.13	0.13
7G6-HCzu23-LCzu18	17.1	0.37	0.22
7G6-HCzu24-LCzu18	9.48	0.09	0.09
7G6-HCzu25-LCzu18	11.1	0.14	0.13

10B.c.2.ii Streptavidin capture

[0268] Biotinylated humanized and mouse mAbs were captured on a streptavidin-coated chip and k_a , k_d , and K_D were determined for binding to Tau (**Table 11**). 7G6-HCzu8-LCzu21 showed a slight drop in affinity (< 2-fold) compared with 7G6-HCzu8-LCzu6. Similarly, 7G6-HCzu23 variants had an ~2-fold drop in affinity compared to 7G6-HCzu24 and 7G6-HCzu25 mAbs, as seen in Table 11. The affinity of 7G6-HCzu8-LCzu6, 7G6-HCzu24-LCzu15, 7G6-HCzu24-LCzu18, 7G6-HCzu25-LCzu15, and 7G6-HCzu25-LCzu18 were all similar. Overall, these antibodies showed an ~1.4-fold drop in affinity compared with the ms7G6, reflected mainly in a slightly faster off-rate for the humanized forms.

Table 11. BIAcore™ analysis of humanized 7G6 mAbs and mouse 7G6 binding monomeric Tau (streptavidin capture)

MAb	k_a ($\times 10^5 \text{ M}^{-1} \text{ sec}^{-1}$)	k_d ($\times 10^{-3} \text{ sec}^{-1}$)	K_D (nM)
7G6-HCzu8-LCzu6	28.20	0.258	0.0915
7G6-HCzu8-LCzu21	22.80	0.313	0.1380
7G6-HCzu23-LCzu15	21.80	0.332	0.1520
7G6-HCzu23-LCzu18	21.40	0.390	0.1820
7G6-HCzu24-LCzu15	54.20	0.487	0.0898
7G6-HCzu24-LCzu18	38.10	0.304	0.0797
7G6-HCzu25-LCzu15	27.10	0.270	0.0998
7G6-HCzu25-LCzu18	35.00	0.307	0.0881
ms7G6	31.10	0.195	0.0636

10B.c.3 Analysis of homogeneity and aggregation by SEC-HPLC

[0269] Each mAb was analyzed by SEC-HPLC to determine the homogeneity of the mAb in solution. The profiles of 7G6-HCzu8-LCzu6 and 7G6-HCzu8-LCzu21 mAbs were identical, with a main peak at 14.5 min and wide shoulder suggesting possible product heterogeneity beyond 16 minutes (**Figure 21A**). The profiles of 7G6-HCzu23, 7G6-HCzu24, and 7G6-HCzu25 mAbs were identical, with a tight peak around 14.7 min (**Figure 21B**).

10B.c.4 DSC analysis

[0270] The thermal melting curves of F(ab')₂ fragments were analyzed by differential scanning calorimetry (DSC). The profiles of the chimeric, 7G6-HCzu8 and 7G6-HCzu25 F(ab')₂ were similar to control non-Tau binding human IgG1 antibodies, mAb1 and mAb2. 7G6-HCzu23 and 7G6-HCzu24, however, contained a second peak, indicating instability of the F(ab')₂ fragment, possibly the dissociation of the HC-LC interaction (**Figures 22A-L**). The transition midpoints of 7G6-HCzu8-LCzu21, 7G6-HCzu25-LCzu15, and 7G6-HCzu25-LCzu18 were similar, ranging from 77.4 to 77.6°C. The midpoint of 7G6-HCzu8-LCzu6 was one degree higher at 78.6°C (**Table 12**).

Table 12. Melting transition midpoints of humanized 7G6 F(ab')₂ fragments

Analysis 1	Transition Midpoint -1	Transition Midpoint -2
7G6-HCzu8-LCzu6	N/A	78.61
7G6-HCzu23-LCzu15	67.81	73.41
7G6-HCzu24-LCzu15	68.04	73.38
7G6-HCzu25-LCzu15	N/A	77.42
7G6-HCzu23-LCzu18	67.81	73.41
7G6-HCzu24-LCzu18	68.78	73.26
7G6-HCzu25-LCzu18	N/A	77.6
Analysis 2	Transition Midpoint -1	Transition Midpoint -2
7G6-HCzu8-LCzu6	N/A	78.58
7G6-HCzu8-LCzu21	N/A	77.51

10B.d T cell epitope analysis

[0271] Humanized sequences were analyzed *in silico* by Stealth Biologics for potential immunoreactive T cell epitopes. Two sequences for each variable region germline family were analyzed, each contained differing amounts of human and mouse residues. mAb1-2a and mAb1-2b represented IGHV1-46a/IGKV2-30a and mAb3-1a and mAb3-1b represented IGHV3-23b/IGKV1-39b. Though only four sequences were analyzed for each variable domain, all potential T cell epitopes present in the tested humanized mAbs were represented. Peptide epitopes having identity to greater than 5% of human germline sequences were considered lower risk, as were peptides binding only one or two HLA alleles.

[0272] **Figures 23 and 24** summarize the analysis of epitopes present in the mAbs. The peptides in the tables were identified as having 5% or less identity to human germline

sequences. The percent homology of the peptides to variable domain germline sequences was also taken into consideration. Peptides with ~5% or less homology to variable region germline sequences and/or were predicted to bind three or more HLA alleles were identified as higher risk (highlighted in gray).

[0273] 7G6-HCzu8 and 7G6-HCzu25 both contained a common low-risk peptide at position 32 with no homology to germline sequences that bound 3 alleles (**Figures 23A and 23B**). Peptide 2 was predicted to be a low risk in 7G6-HCzu25, but the 7G6-HCzu8 peptide 2 was not. Peptide 64 was present as a risk in both HCs, predictively binding 3 alleles. The peptide sequence in 7G6-HCzu8 may present less of a risk as it has some homology to germline variable domains. Peptide 70 in 7G6-HCzu8, but not 7G6-HCzu25, posed a slight risk.

[0274] There was one difference between 7G6-LCzu6 and 7G6-LCzu21 where peptide 38 in 7G6-LCzu21 was predicted to bind 1 HLA allele but presented a very low risk (**Figures 24A-24D**). Between 7G6-LCzu15 and 7G6-LCzu18 there was only one difference with peptide 2 that posed a higher risk in 7G6-LCzu15 than 7G6-LCzu18 as there was little to no homology to variable domain germline sequences. Comparing 7G6-LCzu6/7G6-LCzu21 with 7G6-LCzu15/7G6-LCzu18, 7G6-LCzu6/7G6-LCzu21 sequences contained 9 potentially immunogenic peptides while 7G6-LCzu15/7G6-LCzu18 contained 6. Peptides 51 and 52 were the same between all LCs and peptides 88-94 were the same or similar, with the exception being peptide 90 present in 7G6-LCzu6/7G6-LCzu21 that was not present in 7G6-LCzu15/7G6-LCzu18. Peptides 2 and 3 were riskier in 7G6-LCzu6/7G6-LCzu21 than in 7G6-LCzu15/7G6-LCzu18.

10C. Summary

[0275] In summary, ms7G6 was humanized on two different human germline variable domain families with similar affinity to ms7G6.

[0276] The human germlines closest to the mouse sequence were IGHV1-46 and IGKV2-30. Even though several mouse framework residues were suspected to be required to maintain antigen binding, Tau binding was not affected by human framework residue (7G6-HCzu1/7G6-HCzu8). Further, Tau binding was not affected by mutation of the unpaired Cys57

to a serine (7G6-HCzu5/7G6-HCzu8) or super-humanization of CDRH2 at residues 60, 61, 64, and 65 (7G6-HCzu4/7G6-HCzu8). Grafting the V κ CDRs on the IGKV2 did not result in a dramatic decrease in Tau binding, but the addition of one or two mouse framework residues stabilized the HC-LC interaction. Leu46 with or without Tyr36 increased the stability of Vh-V κ interaction, as analyzed by SDS-PAGE, and the Tyr36-Leu46 (7G6-LCzu2/7G6-LCzu6) combination resulted in an antibody with slightly higher affinity to Tau than with Leu46 or Tyr36 alone (7G6-LCzu /7G6-LCzu21 and 7G6-LCzu4/7G6-LCzu22, respectively). Though there was a slight risk in immunogenicity with a leucine at position 46, the risk was low. The unpaired Cys49 could be substituted with a serine, but a tyrosine substitution resulted in an increase in the dissociation rate.

[0277] The human germline variable domain families IGHV3-23 and IGKV1-39 were chosen to potentially reduce the immunogenicity of the humanized mAb by utilizing the more commonly expressed IGHV3 and IGKV1 families. Grafting CDRs onto the IGHV3 germline required one or more mouse residues. Arg94 could not be the human lysine residue. Mouse residues at positions 60, 61, 62, 63, and 65 were required for optimal antigen binding. An arginine at 71 did not affect antigen binding but was required for stability of the Vh-V κ interaction (7G6-HCzu12, 7G6-HCzu13, 7G6-HCzu14, 7G6-HCzu15, 7G6-HCzu16, 7G6-HCzu17, 7G6-HCzu25). Although Val71 resulted in a potentially immunogenic peptide when paired with Phe63 and Ser65, the risk was low. Tau binding was not affected by mutation of the unpaired Cys57 to a serine (7G6-HCzu23, 7G6-HCzu24, 7G6-HCzu25). Human residues throughout the IGKV1 framework did not affect antigen binding or stability (7G6-LCzu18).

[0278] For all antibodies tested, there were little differences in the pI and thermal stability.

Example 11: Immunohistochemistry with 7G6-HCzu25/LCzu18 on human disease brain

[0279] Paraffin-embedded, fixed human brain sections (8 μ m) were dewaxed with multiple changes of xylene and then washed thoroughly in 100% Industrial Methylated Spirit (IMS). Sections were placed into hydrogen peroxide (H₂O₂) and methanol (2 mL hydrogen peroxide per 100 mL methanol) for 10 minutes at room temperature to block endogenous peroxidase and then washed under running tap water for a further 10 minutes. Each section was

then treated with 98% formic acid for 10 minutes at room temperature followed by washing in running tap water for another 10 minutes. Sections were then cooked in citrate buffer (pH 6.0) for 10 minutes at pressure and then washed again in running tap water followed by TBS. After a rinse in de-ionized water, each slide was carefully removed and dried around the tissue edge. Once dry, a wax pen was used to mark around the section before applying a Proteinase K solution for 10 minutes at room temperature.

[0280] Once tissue sections were prepared, staining with the 7G6-HCzu25-LCzu18 antibody at different concentrations was carried out with the Klear Human HRP-Polymer DAB Detection Kit (GBI Labs, Bothwell, WA; Cat No. D103-18) as per the manufacturer's instructions. As shown in **Figure 25**, antibody 7G6-HCzu25-LCzu18 strongly and specifically recognizes pathological Tau in brains from Alzheimer's disease (neurofibrillary tangles and neuropil threads), PSP (tangles, tufted astrocytes and coiled bodies) and Pick's disease (Pick bodies) by immunohistochemistry. The antibody also showed only a very low level of background staining in all tissues tested.

Example 12: Affinity of 7G6-HCzu25-LCzu18 to 2N4R Wild Type Tau

12A. Materials & Methods

12A.c.2. CHO transient mAb production

[0281] 7G6-HCzu25-LCzu18 antibody was produced using the Lonza version 7 platform according to the manufacturer's procedures. DNA fragments encoding 7G6-HCzu25 and 7G6-LCzu18 were cloned into an expression plasmid encoding glutamine synthase from Lonza. According to Lonza's protocol for selecting MSX-resistant cell lines, CHO-K1sv cells were electroporated with the 7G6-HCzu25-LCzu18 expression plasmid, followed by seeding 2500 cells per well in 96-well plates in glutamine-free medium in the presence of 25 or 50 μ M MSX. Wells containing MSX-resistant cell were subjected to several rounds of screening for antibody expression at various cell culture volumes. The cell line 96E7 producing the highest 7G6-HCzu25-LCzu18 antibody titers was chosen for further development and frozen at -80 °C and stored in vapor phase in liquid nitrogen.

[0282] A vial of cell line 96E7 was thawed and cultivated in disposable shake flasks at 36.5°C and 5% CO₂ followed by further expansion every 3-4 days in larger-sized disposable rocking bags at 36.5°C and 5% CO₂. A 200 L stainless steel seed bioreactor was employed to final expansion at 36.5°C with controlled pH and dissolved oxygen prior to the inoculation of a 1000 L stainless steel fed-batch production bioreactor. After 15 days at fed-batch mode and 36.5°C with controlled pH and dissolved oxygen, the supernatant was harvested through depth filtration.

12A.d. MAb purification

[0283] Purification was performed using an AKTApurification platform (GE Healthcare). The purification process consisted of the following steps: Protein A capture chromatography, viral inactivation, depth filtration, anion-exchange flow through chromatography, viral reduction filtration, concentration and final buffer exchange.

[0284] The primary capture step was performed using Amsphere A3 Protein A resin (JSR). The 14.1 L column was equilibrated using 50 mM sodium phosphate, 1 M NaCl, pH 7.0 then loaded up to 45 g protein per liter of resin per cycle. After loading, the column was washed with equilibration buffer followed by 25 mM Bis-Tris, pH 7.0 until UV returned to baseline. Bound material was eluted from the column using 100 mM Glycine, pH 3.4. The pH of the eluate was adjusted to pH 3.6 using 2 M Acetic Acid for low pH viral inactivation. Following a minimum 30 minute static hold, the eluate was neutralized to pH 6.8 using 2 M Tris Base. Depth filtration was immediately performed using Millistak+ D0HC and X0HC pod filters (Millipore). The filtrate was further processed using a 6.7 L Capto Q (GE Healthcare) anion exchange column equilibrated in 25 mM Bis-Tris, pH 7.0. The column was loaded up to 150 g protein per liter of resin in non-binding mode. The flow-through product was filtered using a Viresolve Pro viral reduction filter then concentrated to 25 g/L. The material was buffer exchanged into a buffer. The purification procedure was performed on two different monoclonal antibody production runs and designated lots 17-0190 and 18-0146. Several vials from lot 17-0190 were designated 17-0190ARS for use as a reference standard.

12A.f. Surface plasmon resonance (SPR) binding analyses

12A.f.2. Anti-human capture monomeric Tau-binding assay

12A.f.2.i. Chip preparation

[0285] Reagent preparation. EDC [1-ethyl-3(3-dimethylaminopropyl)carbodiimide] and NHS (N-hydroxysuccinimide) were dissolved by adding 10.0 ml of Milli-Q water to each vial. Vials were capped tightly and vortexed until the solids were completely dissolved. EDC, NHS, and ethanolamine solutions were aliquoted separately into 0.5 ml aliquots in 7 mm plastic vials, capped, and stored frozen at -20°C. Anti-human IgG (Fc) from kit was centrifuged in microfuge briefly to collect antibody at bottom of tube. 15 µL anti-human IgG (Fc) was removed to a new 1.5 mL microfuge tube and diluted to 300 µL with 285 µL immobilization buffer. Sample was vortexed briefly to mix, then 70 µL was aliquoted to 4 separate 7 mm tubes and capped. 4 aliquots each of EDC, NHS, and ethanolamine were thawed, vortexed briefly to mix and displace any air bubbles trapped on tube walls, and placed in Reagent Rack 2.

[0286] 0.5 L of 1x HBS-P+ (Assay Running Buffer) was prepared by diluting 50 mL 10X HBS-P+ to 0.5 L with 450 mL Milli-Q® water in 1 L Pyrex bottle.

[0287] Preparation of instrument for assay. A 1 L bottle of Assay Running Buffer was attached to Buffer A line on BIAcore® T-100, an empty 2 L Pyrex bottle to BIAcore® T-100 waste line, and a 1 L Pyrex bottle filled with fresh 1 L Milli-Q® water to water line. A new CM5 chip was docked into the instrument.

[0288] Capture antibody immobilization. In BIAcore® T-100 Control software, a new Wizard Template was opened and “Immobilization” was selected. Chip type was set to “CM5”. Method was set to “Amine”. Ligand blanks were filled in as “anti-human”. Contact time was set to 360 sec for each flow cell and flow rate 5 µL/min. Following completion of these steps, assay was run.

12A.f.2.ii. Binding assay

[0289] Binding experiments were performed using a BIAcore™ T-100 instrument or a T-200 instrument. Running buffer used for the binding assay was HBS-P+/0.2% BSA. 7G6-HCzu25LCzu18 samples were diluted to 100 µg/mL, 100 µL final in Assay Running Buffer, then centrifuged at 18,000 x g for 10 min in microcentrifuge at ambient temperature. Dilution to

1 $\mu\text{g/mL}$ was done by removing 40 μL supernatant and diluting to 4.0 mL with Assay Running Buffer in labeled 5 mL tubes. 1 $\mu\text{g/mL}$ antibody solutions were transferred to labeled 1.5 mL capless plastic vials and capped with type 3 caps. Vials were vortexed briefly to remove any air bubbles adhered to tube walls or bottom and placed in Sample and Reagent Rack 1. 200 μL 1 $\mu\text{g/mL}$ solution of diluted reference standard antibody was transferred to a 7 mm plastic vial, capped, vortexed briefly to dislodge adhered air bubbles, and placed in Sample and Reagent Rack 1 (for chip conditioning cycles). Recombinant human wild-type 2N4R tau protein was diluted to 1 μM , 0.5 mL final in Assay Running Buffer (1 mg/mL stock is 21.7 μM). Sample was centrifuged at 18,000 $\times g$ for 10 min in microcentrifuge at ambient temperature and diluted to 100 nM by removing 400 μL supernatant and diluting to 4.0 mL with Assay Running Buffer in a labeled 5 mL tube. 100 nM solution was serially diluted 3-fold by removing 1333 μL 100 nM solution and diluting in 2667 μL Assay Running Buffer to a final volume of 4.0 mL (33.3 μL). Serial dilution was repeated 6 times, for a total of 8 dilutions (100 nM, 33.3 nM, 11.1 nM, 3.70 nM, 1.23 nM, 0.41 nM, 0.14 nM, and 0.046 nM tau). A 0 nM Tau protein solution was prepared by adding 3 mL Assay Running Buffer to labeled 5 mL tube. Analyte dilutions were transferred to labeled 4 mL plastic vials and capped with type 5 caps, vortexed briefly to remove any air bubbles adhered to tube walls or bottom, and placed in Sample and Reagent Rack 1. For chip conditioning analyte sample, 5 μL of 1 μM Tau protein solution supernatant was removed and diluted to 500 μL in Assay Buffer in a 7 mm plastic vial, capped, vortexed briefly to dislodge adhered air bubbles, and placed in Sample and Reagent Rack 1. Humanized antibodies were captured on flow cells 2, 3, and 4 sequentially at a flow rate of 10 $\mu\text{L/min}$ for a contact time of 36 sec. Dilutions of Tau protein were injected over all 4 flow cells at a flow rate of 30 $\mu\text{L/min}$ for a contact time of 300 sec. Dissociation was followed for 1800 sec. Following each cycle, the surface was regenerated by two sequential injections of 30 sec at 30 $\mu\text{L/min}$ of 3 M MgCl_2 over all four flow cells. After the run, kinetic data fitting was performed using a 1:1 Langmuir model.

12B. Results

[0290] The affinity of recombinant human wild-type 2N4R Tau protein to 7G6-HCzu25LCzu18 antibody was determined using an antibody-capture format assay. Following capture of 7G6-HCzu25LCzu18 antibody, human Tau protein was injected over the ligand surface for 300 sec, followed by observation and measurement of dissociation for 1800 sec. After each antibody capture, Tau protein binding, and dissociation cycle, the chip surface was regenerated to the anti-human antibody capture surface using 3M MgCl₂, as required by the manufacturer. Tau protein was analyzed in a concentration range from 100 nM to 0.046 nM (3-fold diluted). The assay was performed in multi-cycle mode, such that a dissociation was performed for each tau protein injection. Each ligand was analyzed on all three flow cells (fc2, fc3, and fc4) in triplicate, in order to eliminate any flow cell-specific effects.

[0291] Capture levels of each ligand on each flow cell (relative to fc1) were determined. These results are listed in Table 13:

Table 13 – Capture levels of 7G6-HCzu25-LCzu18 ligands

	fc2	fc3	fc4
7G6-HCzu25LCzu18, lot 17-0190	189.9	185.6	196.1
7G6-HCzu25LCzu18, lot 18-0146	177.0	173.7	183.1
7G6-HCzu25LCzu18, lot 17-0190ARS	161.7	158.1	166.7

Data are expressed in RU. Values represent averages of ligand capture levels for all relevant cycles. fc – flow cell

[0292] Captured ligand average levels were all between 158 RU and 196 RU. Only slight differences were observed between flow cells within a given ligand.

[0293] Binding data was double-referenced, meaning referenced to both fc1 with no ligand bound and to buffer analyte injections (0 nM Tau protein). Binding data was fitted to a 1:1 Langmuir binding model. This model is appropriate for the assay format, as bivalency of the antibody and resulting avidity effects are not relevant in an antibody capture format. Affinity data for each ligand on individual flow cells was averaged and standard deviation determined. These results are listed in Table 14:

Table 14 – Affinity constants for human Tau binding to 7G6-HCzu25LCzu18

	k_a ($M^{-1}sec^{-1}$)	k_d (sec^{-1})	K_D (M)
7G6-HCzu25LCzu18, lot 17-0190	$1.919 \pm 0.108 \times 10^6$	$1.256 \pm 0.022 \times 10^{-4}$	$6.565 \pm 0.493 \times 10^{-11}$
7G6-HCzu25LCzu18, lot 18-0146	$1.916 \pm 0.093 \times 10^6$	$1.259 \pm 0.027 \times 10^{-4}$	$6.587 \pm 0.460 \times 10^{-11}$
7G6-HCzu25LCzu18, lot 17-1090ARS	$1.914 \pm 0.027 \times 10^6$	$1.235 \pm 0.018 \times 10^{-4}$	$6.451 \pm 0.163 \times 10^{-11}$

Data are expressed as average $\pm$ standard deviation. Averages are from kinetic data from each flow cell.

[0294] No significant differences in on rate, off-rate, or affinity were observed between the two 7G6-HCzu25LCzu18 drug substance lots and 7G6-HCzu25LCzu18 reference standard.

Example 13: Fine epitope mapping of 7G6-HCzu8-LCzu6 and 7G6-HCzu25-LCzu18

[0295] Fine epitope mapping was performed for 7G6-HCzu8-LCzu6 and 7G6-HCzu25-LCzu18 antibodies as described in Example 3.

[0296] The fluorescent images of the chips and resulting intensity plots show that the 7G6-HCzu8-LCzu6 (Figure 26A) and 7G6-HCzu25/LCzu18 (Figure 26B) antibodies both bind to two major sites on the full length Tau protein, similar to the murine 7G6 antibody (see Figure 3). A stronger fluorescence intensity on the chip was observed generally for 7G6-HCzu25-LCzu18 resulting in some signs of signal saturation and therefore lack of true quantification for some but not all of the peptides. In this experiment, the data analysis software (PepSlide™ Analyser) identified the minimum binding sequence for 7G6-HCzu8-LCzu6 as KHVPGGG (SEQ ID NO: 1135) for the site within the second repeat (positions 298 to 304) and HVPGG (SEQ ID NO: 79) for the site within the fourth repeat (positions 362 to 366) of 2N4R protein. For 7G6-HCzu25-LCzu18, the software identified the minimum required sequence as HVPG (SEQ ID NO: 1133) for both binding sites.

[0297] Similar to murine 7G6, minor binding was observed at two additional sites: HQPGG (SEQ ID NO: 183) at amino acid positions 268 to 272 and HKPGG (SEQ ID NO: 182) at positions 330 to 334 for both 7G6-HCzu8-LCzu6 and 7G6-HCzu25-LCzu18 antibodies. Calculation of average signal intensities for peptides containing the HXPGG sequence (SEQ ID NO: 1136) demonstrated that the 7G6-HCzu8-LCzu6 human antibody showed a 108-fold or 104-fold preference in binding to the HVPGG site (SEQ ID NO: 79) normally contained within the second repeat region of full length 2N4R Tau compared to the HQPGG (SEQ ID NO: 183) (repeat region 1) or HKPGG (SEQ ID NO: 182) (repeat region 3) sequences, respectively.

Similarly, a 99-fold or 95-fold preference in 7G6-HCzu8-LCzu6 binding to the HVPGG (SEQ ID NO: 79) site normally contained within the fourth repeat region of full length 2N4R Tau compared to the HQPGG (SEQ ID NO: 183) (repeat region 1) or HKPGG (SEQ ID NO: 182) (repeat region 3) sequences, respectively, was observed. Identical data analysis for 7G6-HCzu25-LCzu18 demonstrated a 65-fold or 100-fold preference in binding to the HVPGG (SEQ ID NO: 79) site normally contained within the second repeat region of full length 4R Tau compared to the HQPGG (SEQ ID NO: 183) (repeat region 1) or HKPGG (SEQ ID NO: 182) (repeat region 3) sequences, respectively. Likewise, a 77-fold or 119-fold preference in 7G6-HCzu25-LCzu18 binding to the HVPGG (SEQ ID NO: 79) site normally contained within the fourth repeat region of full length 4R Tau compared to the HQPGG (SEQ ID NO: 183) (repeat region 1) or HKPGG (SEQ ID NO: 182) (repeat region 3) sequences, respectively, was observed.

Example 14: Epitope substitution scanning of 7G6-HCzu8-LCzu6 and 7G6-HCzu25-LCzu18

[0298] Epitope substitution scanning was performed for 7G6-HCzu8-LCzu6 and 7G6-HCzu25-LCzu18 antibodies as described in Example 4.

[0299] The substitution scanning showed that of the ¹HVPGG⁵ (SEQ ID NO: 79) sequence, both 7G6-HCzu8-LCzu6 and 7G6-HCzu25-LCzu18 antibodies require the ¹H, ³P and ⁴G residues with some substitution tolerability at ²V for peptide binding. These findings were similar to those observed for the murine 7G6 antibody (see Example 4). Some tolerability for substitution was also observed at the second glycine residue (⁵G) of the ¹HVPGG⁵ (SEQ ID NO: 79) sequence in this case. However, this residue was still able to exert considerable influence over the binding of 7G6-HCzu25-LCzu18 and 7G6-HCzu8-LCzu6 antibodies to the longer wild type peptide sequence. Together with Example 13, these results indicate that the HVPGG (SEQ ID NO: 79) sequence facilitates efficient binding of 7G6, 7G6-HCzu25-LCzu18 and 7G6-HCzu8-LCzu6 antibodies to 2N4R Tau at positions 299 to 303 and 362 to 366 within the second and fourth repeats, respectively.

Example 15: *In vitro* Tau aggregation with 7G6-HCzu25-LCzu18

Experiment 1

[0300] To determine whether 7G6-HCzu25-LCzu18 antibody could inhibit Tau aggregation *in vitro*, the antibody was tested in the assay described in Example 5 using the wild type Tau protein with minor modifications. The only difference was the control IgG used in this case was a human IgG1 antibody (BioXCell, catalogue number BE0297).

[0301] In this assay, 7G6-HCzu25-LCzu18 antibody was tested over a time course of several days. Figure 27 shows that 7G6-HCzu25-LCzu18 could effectively inhibit Tau aggregation *in vitro*. The effect was statistically significant (t-test) when comparing the IgG control and 7G6-HCzu25-LCzu18 for days 1, 2, 5 and 6 following incubation at 37 °C. No significance was observed on day 0 just after the reactions were initiated following heparin addition.

Experiment 2.

[0302] To confirm the humanized 7G6-HCzu25-LCzu18 antibody was comparable to the murine 7G6 antibody at inhibiting Tau aggregation *in vitro*, both antibodies were compared in the same *in vitro* Tau aggregation assay. The conditions used were identical to those in Experiment 1 of this Example with the exception that the same mouse IgG2b control antibody was used that was described in Example 5.

[0303] When both murine antibody 7G6 and humanized antibody 7G6-HCzu25-LCzu18 were tested according to the assay conditions provided in Example 5, both antibodies effectively inhibited Tau aggregation *in vitro*. As shown in Figure 28, the same effect size was seen between murine 7G6 and 7G6-HCzu25-LCzu18 antibodies.

Example 16: Cell-based Seeding Assay Using K18 Tau Fibril following Immunodepletion with 7G6-HCzu25-LCzu18

[0304] To determine whether immunodepletion of Tau seeds from cell culture medium could prevent further Tau aggregation within cells, the same HEK293 assay system as described in Example 6 was used. In this case however, a potent truncated form of Tau (K18) fibrils were used as Tau seeds rather than full length protein as described previously. The K18 fragment has been studied extensively and is normally expressed recombinantly as residues 244 to 372 of the full length 2N4R Tau protein. This fragment encodes the microtubule binding region of Tau and

has been reported to be more aggregate-prone than the full length protein (Shammas et al., Nature Comms., 6, Article number: 7025 (2015)) as well as having the ability to form potent seeds in cell-based assays (Kfoury et al., 2012, J. Biol. Chem., 287: 19440-19451).

Materials and Methods:

[0305] *Preparation of K18 fibrils.* Recombinant human Tau-441 (244-372; “K18”) (SignalChem) was dissolved in ultrapure water. Fibrils were generated by mixing together final concentrations of 40 $\mu\text{mol/L}$ K18 protein, 100 mmol/L sodium acetate (pH 7), 2 mmol/L DTT and 240 $\mu\text{g/mL}$ heparin. Reactions were agitated for three days at 37°C. Following incubation, the solution was centrifuged at 135,000 g for 20 minutes at room temperature. The supernatant was discarded, and the pellet was resuspended in 100 mmol/L sodium acetate (pH 7). Aggregated protein was sonicated briefly and then diluted with D-PBS (-) to a concentration of 50 $\mu\text{g/mL}$ and stored at -80°C.

[0306] *Preparation of immunodepleted and immunoprecipitated samples.* Immunoprecipitation of the prepared K18 fibrils was performed using the Immunoprecipitation Dynabeads® Protein G kit (ThermoFisher Scientific, catalogue number 10007D) as per the manufacturer’s instructions. Briefly, each immunoprecipitation used 1.5 mg of Dynabeads bound to either 3 or 0.3 μg of 7G6-HCzu25-LCzu18 antibody. Vehicle (no antibody) or 3 μg of commercially available human IgG1 antibody (Bio-Rad Laboratories, Inc.; catalog number HCA192) were included as controls. Antibody-bound (or vehicle-treated) beads were resuspended in 170 μL of buffer containing 0.2% BSA. The K18 fibril solution was then thawed, diluted to 10 $\mu\text{g/mL}$ in PBS, and added to the antibody-bound beads to give a final volume of 200 μL (containing 300 ng of K18 total). This gave final concentrations of either 15 or 1.5 $\mu\text{g/mL}$ of antibody in each immunoprecipitation reaction. Beads were incubated with the K18 fibrils for 20 minutes at room temperature with rotation and non-bound material was retained as the immunodepleted (ID) sample. Antibody-bound material was eluted in 20 μL of the buffer provided in the kit and also retained to provide the immunoprecipitated (IP) samples.

[0307] *Cell-based assay.* Polyethylenimine (PEI) solution was diluted in purified water to a final concentration of 0.1% and then used to coat a 96-well tissue culture plate at 37°C for at least one night. Plates were then washed twice with water before adding 150 μL of Dulbecco’s

modified Eagle's Medium (D-MEM) containing 10% fetal bovine serum and 1% penicillin/Streptomycin ("DMEM (+FBS, P/S)") medium to each well prior to conducting the assay.

[0308] Lenti-X 293T (Takar Bio Inc.) cells routinely maintained in D-MEM (+FBS, P/S) at 37°C with 5% CO₂ were transfected in suspension in the same media without antibiotics prior to Tau seed addition. For transfection, 7 µg of pcDNA3.1(+) (Invitrogen) mammalian expression vector containing cDNA encoding the mutant P301S 0N4R Tau isoform was mixed with LTX and PlusTM Reagent (Life Technologies, catalog number 15228-100) as per the manufacturer's recommendation. The resulting mixture was incubated for at least 25 minutes at room temperature before adding directly to a suspension of 6.0×10⁶ Lenti-X 293T cells at a density of 1.0×10⁵ cells/mL. Media was removed from the precoated plate and the treated cell suspension was dispensed at 150 µL per well (1.5×10⁴ cells/well) and incubated for 19 hours at 37 °C in a 5% CO₂ atmosphere.

[0309] Once thawed on ice, 30 µL of each ID sample was diluted into 420 µL of Opti-MEM[®] I Reduced-Serum Medium (ThermoFisher Scientific, catalog number 31985-062). For IP samples, solutions were also thawed on ice and 2 µL of each was diluted into 50 µL of Opti-MEM[®] I Reduced-Serum Medium. Then 2.5 µL of P3000 (Thermofisher Scientific, catalog number L3000-008) was added. In a separate tube, 22 µL of Lipofectamine[®] 3000 (Thermofisher Scientific, catalog number L3000-008) was diluted into 550 µL Opti-MEM[®] I Reduced-Serum Medium. Then, 52 µL of the diluted Lipofectamine 3000 solution was added to each IP sample containing the P3000 reagent.

[0310] Plated cells were washed twice and left in 75 µL of Opti-MEM[®] I Reduced-Serum Medium (ThermoFisher Scientific). An equal volume of diluted ID or IP sample as described above was added to each well and incubated for 44 hours at 37°C in a 5% CO₂ atmosphere. The experiment was performed in quadruplicate.

[0311] *Immunocytochemistry.* After two days of incubation, cells were fixed in 4% paraformaldehyde for 30 minutes at room temperature. Each well was washed 3 times with 100 µL of purified water and then left in 70 µL of Permeabilization/Blocking/DAPI staining buffer (Triton X-100 solution (final concentration: 0.2%) and Cellstain[®] DAPI solution (final

concentration: 0.1%; Dojindo) diluted in 5% BSA in TBS) was added to each well. The plate was covered and incubated for 30 minutes at room temperature with protection from light. After incubation, Permeabilization/Blocking/DAPI staining buffer was removed, and 80 μ L Thioflavin S (ThS) staining buffer (Thioflavin S dissolved in 50% Ethanol to a final concentration of 0.0003%) was added to each well and incubated for 40 minutes at room temperature. Then, each well was washed twice with 50% ethanol and replaced with 250 μ L of purified water.

[0312] *Imaging assay.* Fluorescence images of each well were obtained by an InCell® Analyzer 2200 (GE Healthcare) (ThS: Excitation [Ex]/Emission [Em] = 475/511 nm, DAPI: Ex/Em = 390/435 nm). Numbers of ThS and DAPI positive signal in each well were then analyzed using the InCell Developer Software (GE Healthcare).

[0313] *Data Analysis.* The ThS positive rate was calculated using the following formula:

$$\begin{aligned} \text{ThS positive rate} &= \text{ThS/DAPI} \\ &= \text{number of ThS positive signals / number of DAPI positive signals.} \end{aligned}$$

Then, the seeding effect of ID or IP samples were calculated using the following formulas (Software: TIBCO Spotfire):

The seeding effect of ID sample (% of control) = $T_1/C_1 \times 100$, where

T_1 : Average of ThS positive rate in the antibody treated ID sample, and

C_1 : Average of ThS positive rate in the buffer treated ID sample.

The seeding effect of IP sample (% of control) = $T_2/C_2 \times 100$, where

T_2 : Average of ThS positive rate in the antibody treated IP sample, and

C_2 : Average of ThS positive rate in the 7G6-HCzu25-LCzu18 antibody (15 μ g/mL)-treated IP sample.

[0314] Figure 29 shows the normalized ThS positive rate in the cell-based seeding assay after treatment of ID samples. 1.5 and 15 μ g/ml of 7G6-HCzu25-LCzu18 antibody removed the seeding effects of K18 fibril (>70% reduction vs human IgG1 kappa control). For

the IP samples, 7G6-HCzu25-LCzu18 antibody efficiently induced seeding effects in a concentration-dependent manner (data not shown).

Example 17: Intrahippocampal P301S Tau seed injection model with 7G6

Materials and Methods:

[0315] Tau seed was generated by mixing recombinant human 2N4R P301S Tau (40 $\mu\text{mol/L}$) and heparin (240 $\mu\text{g/mL}$), followed by an incubation step at 37°C for 48 to 96 hours in 100 mmol/L sodium acetate, pH7.0, containing 2 mmol/L Dithiothreitol (DTT). Aggregated Tau was collected by ultracentrifugation and resuspended in 100 mmol/L sodium acetate, pH7.0. The resulting fibrils were sonicated and used as seeds for injection.

[0316] 3 μL of Tau seed (1.5 mg/mL) or non-seed (100 mmol/L sodium acetate, pH7.0) was stereotactically injected into left hippocampus (A: +2.5, L: 2.0, V: 1.5) (Franklin and Paxinos, The Mouse Brain in Stereotaxic Coordinates Third Edition 2007, Elsevier USA) of 3- to 4-month-old Mouse/Thy-1hTau.P301S (CBA.C57BL/6) mice [homozygous human P301S Tau transgenic mouse (C57BL/6) generated previously (Allen et al., J Neurosci. 2002;22:9340–51)] using an UltraMicroPump III and Micro4 Controller (World Precision Instruments) at 0.5 $\mu\text{L/min}$ for 6 minutes. Mice were randomly divided into groups as shown in Table 15. Anti-human Tau mouse IgG2b monoclonal antibody, clone 7G6 or mouse IgG2b isotype control antibody (clone MPC11, BioXCell) in formulation buffer (25 mmol/L Sodium phosphate, 0.15 mol/L NaCl, pH6.5) were administered intraperitoneally to reach a dose of 40 mg/kg in the groups that had received seed. The same formulation buffer was administered to the non-seed group. Dosing was performed 6-16 hours before, and 1 and 2 weeks after Tau seed injection (total 3 times). The administration volume (10 mL/kg) was calculated from the body weight before administration.

Table 15. Treatment Groups

Study	Group No.	Treatment	Number of animals [‡]
Pharmacological	1	Non-seed + Vehicle	6

study	2	Tau seed + Control IgG	11
	3	Tau seed + 7G6	11

“Non-seed” represents injection of solution (100 mmol/L sodium acetate, pH7.0) into left hippocampus , and “Tau seed” represents injection of 1.5 mg/mL Tau seed solution into left hippocampus . Control IgG = Mouse IgG2b isotype control antibody, 7G6 = Anti-human tau mouse IgG2b monoclonal antibody.

[‡]Tissue from an additional five animals in the non-seed group and 11 animals for both treatment groups that received seed was processed by adding buffer containing sarkosyl to the tissue directly instead of RIPA buffer. These additional animals were therefore not included in the data analysis. A reduction in insoluble Tau (after extracting with buffer containing sarkosyl twice) was still observed, however, in these additional animals.

[0317] All mice were deeply anesthetized with a combination anesthetic (M/M/B: 0.3/4/5; prepared with 0.9 mg/kg of medetomidine, 12.0 mg/kg of midazolam, and 15 mg/kg of butorphanol), and plasma and cerebrospinal fluid (CSF) were collected. Then, the cortex and hippocampus from both sides (ipsilateral and contralateral) were separately dissected following intracardiac perfusion with saline. Brain tissues were immediately frozen in liquid nitrogen and stored at -80°C.

[0318] Dissected brain tissues were homogenized in 19 volumes (tissue weight/volume) of extraction buffer (“RIPA buffer”) containing 50 mmol/L Tris-HCl (pH7.5) (Invitrogen), 5 mmol/L EDTA (Nippon Gene), 1 mmol/L EGTA (Nacalai Tesque), 1% NP-40 Alternative (EMD Millipore), 0.25% Sodium Deoxycholate (Bio world), 0.1 mol/L NaCl, 0.5 mmol/L PMSF (Sigma Aldrich), 1 × PhosSTOP™ (Roche), and 1× Complete EDTA(-) (Roche). Homogenates were centrifuged at 163,000 g at 4°C for 20 minutes and the pellet was resuspended in 10 volumes (tissue weight/volume) of buffer containing 10 mmol/L Tris-HCl (pH7.5), 0.5 mol/L NaCl, 1 mmol/L EGTA, 10% sucrose (Wako Pure Chemical), and 1% sarkosyl prior to sonication. Sarkosyl-treated samples were incubated at 37°C for 60 minutes, and then centrifuged at 163,000 g at 4 °C for a further 20 minutes. Finally, 10 volumes of PBS (Gibco) was added to the pellet which was subsequently sonicated. This formed the sarkosyl-insoluble fraction.

[0319] The amount of Tau protein in the sarkosyl-insoluble fraction was quantified by Western blot analysis. Sarkosyl-insoluble fractions were solubilized in NuPAGE™ LDS sample buffer (Novex) and NuPAGE™ sample reducing agent (Invitrogen), heated at 80°C for 10

minutes, and separated using 12.5% polyacrylamide gels (DRC). Proteins were transferred to 0.2 µm PVDF membranes (Bio-Rad) and blots were blocked in 2.5% skimmed milk (Yukijirushi) in TBS (Takara) containing 0.05% Tween (Nacalai tesque) for 1 hour at room temperature. After blocking, blots were probed with the human-specific monoclonal anti-Tau antibody HT7 (1:1000, Thermo Fisher Scientific) in blocking buffer for 1 hour at room temperature. The blots were washed in TBS-T for 30 minutes and then incubated with HRP-conjugated anti-mouse IgG (1:2000, GE healthcare) for a further 1 hour at room temperature. Secondary antibody was removed and blots were washed as described above. Tau proteins were detected by chemiluminescent horseradish peroxidase (HRP) substrate (Merck Millipore) and quantified using the Fusion FX and FusionCapt version 16.15 (Vilber-Lourmat, France). To determine the amount of Tau, serial dilutions of Tau standards derived from the originating sarkosyl-insoluble fraction of P301S spinal cord (1, 2, 5, 10, 20 Arbitrary Unit [AU], 1 AU is equivalent to the band density of human Tau protein detected by HT7 antibody in sarkosyl insoluble fraction from 7 µg of spinal cord) were loaded onto each gel. The data calculated as less than 1 AU (detection limit) was expressed as 0.5 AU.

[0320] Data are expressed as the mean ±SEM. The differences in sarkosyl-insoluble Tau between the Non-seed, control IgG-treated and 7G6-treated groups were analyzed by 1-way analysis of variance (ANOVA) followed by Fisher's LSD test. A value of $P < 0.05$ (two sided) was considered statistically significant. Statistical analyses were performed using the GraphPad Prism version 7.02 (GraphPad Software).

RESULTS

[0321] The effect of 7G6 on sarkosyl-insoluble Tau induced by intra-hippocampal Tau seed injection was examined in both ipsilateral (injection side) and contralateral cortex and hippocampus, separately. As shown in Figures 30A-30D, 7G6 significantly suppressed the increase of sarkosyl-insoluble Tau in the contralateral hippocampus compared with control IgG (Figure 30A), but showed no significant effects in other regions (Figures 30B, 30C, and 30D). This suggests that 7G6 was able to prevent Tau transmission in this *in vivo* model.

Example 18: 7G6-HCzu25-LCzu18 Translational Biomarker Data

[0322] Male cynomolgus monkeys were treated with vehicle or 7G6-HCzu25-LCzu18 antibody (10, 30, and 100 mg/kg; 3 animals/dose) by intermittent intravenous administration once weekly for 4 weeks. MTBR-Tau (any isoform of full length or truncated Tau containing the MTBR) bound to 7G6-HCzu25-LCzu18 antibody ("Bound MTBR-Tau") and unbound form ("Free MTBR-Tau") in the cerebrospinal fluid ("CSF") collected from each monkey were separated by a Protein A column and analyzed by liquid chromatography coupled with mass spectrometry (LC/MS). LC/MS analysis was performed using UltiMate™ 3000 Nano LC system coupled to Orbitrap Fusion™ Lumos™ Tribrid™ mass spectrometer (Thermo Fisher Scientific, San Jose, CA) with needle column (3 µm C18 particle, 150 mm length, 100 µm inner diameter). A spray voltage of 2000 V was applied through a metallic tee connector. The flow rate was 500 nL/min. The mobile phases consisted of (A) 0.5% acetic acid in 4% acetonitrile and (B) 0.5% acetic acid in 80% acetonitrile and a multi-step linear gradient of 1 % to 1 % B for 5 min, 1 % to 37 % B for 15 min, 37 % to 68 % B for 5 min, 68 % to 99 % B for 1 min and 99 % to 99 % B for 4 min was employed to elute the analyte and then equilibrated by the initial condition, 1% B. A specific peptide containing 7G6-HCzu25-LCzu18 antibody epitope was measured by LC/MS as a proxy of MTBR-Tau. The amount of MTBR-Tau was expressed as the chromatographic peak area ratio of the specified peptide (Light) and its internal standard (Heavy), isotope-labelled peptide.

[0323] As shown in Figure 31A, the amount of bound MTBR-Tau in CSF increased with treatment of the 7G6-HCzu25-LCzu18 antibody in a dose-dependent manner, whereas the amount of free MTBR-Tau in monkey CSF decreased also with dose-dependency (Figure 31B). This suggests in vivo target engagement of the 7G6-HCzu25-LCzu18 antibody in monkey CSF.

[0324] 7G6-HCzu25-LCzu18 antibody was also spiked into human CSF at 10, 100, 500, 1000 or 2000 ng/mL. Then, MTBR-Tau bound by 7G6-HCzu25-LCzu18 was assayed by liquid chromatography coupled with mass spectrometry (LC/MS) in the same way as described above. As shown in Figure 32, the amount of the bound MTBR-Tau in human CSF increased by treatment of 7G6-HCzu25-LCzu18 antibody with dose-dependency. This data also indicates target engagement of 7G6-HCzu25-LCzu18 antibody for MTBR-Tau in human CSF.

Example 19: Measurement of Tau Uptake in CD32A overexpressing CHO cells

[0325] *Preparation of labelled Tau monomers and fibrils.* Wild type recombinant full length human 2N4R Tau aggregates were prepared from monomers as described for the P301S protein in Example 17. Prior to labelling, aggregates were sonicated to generate the fibrils used in the assay. Both Tau fibrils and monomers were fluorescently labelled using the DyLight™ 488 NHS-Ester kit (ThermoFisherScientific, Cat# 46403) according to the manufacturer's instructions with minor differences between the two forms of protein: 150 µL of Tau monomer (100 µM) was mixed with 100 µL of DyLight NHS Ester solution whereas 300 µL of Tau-441 fibril (587 µg/mL) was mixed with 66 µL of DyLight NHS Ester solution. Labelling was performed at room temperature for one hour. Excess unconjugated dye was removed with Pierce™ Dye Removal Columns (ThermoFisherScientific, Cat# 22858, lot# SL260099) according to the manufacturer's protocol using 125 µL of labelled Tau monomer or 122 µL of labelled fibrils. Final concentrations of labelled Tau monomers and fibrils were measured by bicinchoninic acid assay (BCA) assay, and stored at -80 °C.

[0326] *Cell-based assay.* Frozen CHO cells stably expressing CD32a (Fc gamma RIIA) were thawed rapidly in a 37°C water bath, and placed into CHO medium (RPMI 1640 Medium with 10% fetal bovine serum, L-Glutamine, Non-Essential Amino Acids, Sodium Pyruvate, and penicillin/Streptomycin). Cells were seeded at 1×10^4 cells/well (100 µL/well) in a 96-well assay plate (Costar, catalog no. 3603) and incubated for 24 hours at 37 °C in 5% CO₂ atmosphere. Labelled Tau monomers and fibrils were thawed on ice and diluted to concentrations of 1.5 µg/mL or 0.5 µg/mL respectively in assay buffer (RPMI 1640 media) (GIBCO, catalog no. 21875-034). Then, in a total volume of 60 µL, 7G6-HCzu25-LCzu18 antibody (final concentrations: 0.3 or 3 µg/mL), human IgG1 isotype control (BioXcell, catalog no. BE0297) (final concentration: 3 µg/mL) or vehicle (25 mM sodium phosphate buffer, pH 6.5, containing 150 mM NaCl) were added to either form of the protein and incubated at room temperature for one hour protected from light. CHO medium was removed from the plates and cells were pre-treated with 90 µL of assay buffer or a polyclonal antibody Fc receptor binding inhibitor (ThermoFisher Scientific, catalog no. 16-9161-71) diluted to 100 µg/mL also in assay buffer. Cells were then incubated for 30 min at 37 °C in 5% CO₂ atmosphere. Next, relevant wells received 10 µL of labelled Tau monomer or Tau fibril mixtures with or without antibody and

plates were incubated for a further 60 minutes again at 37 °C in a 5% CO₂ atmosphere. Each treatment was performed in quintuplicate wells. Six independent experiments were performed for Tau monomer uptake assays and five independent experiments were completed to measure Tau fibril uptake.

[0327] *Cell fixation and staining.* Following the final incubation period, cells were fixed in 4% paraformaldehyde for 30 min at room temperature. Each well was then washed with 100 µL of water and replaced by 70 µL of Hoechst staining buffer (Triton X-100 solution (final concentration: 0.2%) and Hoechst solution (final concentration: 0.02%)). The plate was covered and incubated for 30 minutes at room temperature with protection from light. The staining buffer was then removed and each well was washed twice more with 100 µL of water.

[0328] *Cell imaging.* Fluorescence images of each well were obtained using a Cellomics high content imaging system (ThermoFisherScientific). The total intensity of labelled Tau and the number of Hoechst positive cells in each well were recorded and analysed using the Thermo Scientific HCS Studio (ThermoFisherScientific) software.

[0329] *Data Analysis.* The mean of total intensity of Tau signal per cell was measured and the Tau uptake effect was calculated using the following formulas in the TIBCO spotfire software program:

Tau uptake effect (% of control) = $T_1/C_1 \times 100$, where

T_1 : Total intensity of DyLight 488 NHS conjugated Tau signal per cells in the antibody treated sample, and

C_1 : Total intensity of DyLight 488 NHS conjugated Tau signal per cells in the 7G6-HCzu25-LCzu18 (30 µg/mL) treated sample.

[0330] *Statistical Analysis.* Data are expressed as the mean ± SEM. Statistical analyses were performed using ONE-Way ANOVA test in the GraphPad Prism version 7.02 (GraphPad Software) **** $p < 0.0001$, ** $p < 0.01$, * $p < 0.05$.

[0331] Figures 33A and 33B show the efficacy of Tau monomer or fibril uptake, respectively, in CHO cells overexpressing CD32A. 7G6-HCzu25-LCzu18 antibody (3 µg/mL) significantly increased Tau monomer uptake compared to human IgG1 control (3 µg/mL) (Fig. 33A). Likewise, 7G6-HCzu25-LCzu18 antibody (0.3 and 3 µg/mL) also significantly increased Tau fibril uptake compared to human IgG1 control (3 µg/mL) (Fig. 33B). In both cases, FcR

inhibitor treatment significantly blocked the effect of 7G6-HCzu25-LCzu18 antibody-induced Tau uptake in this cell assay system.

What is Claimed:

1. A monoclonal antibody comprising a heavy chain and a light chain, or an antigen-binding fragment thereof, that specifically binds a human Tau, wherein:

the heavy chain comprises a heavy chain complementarity determining region 1 (HCDR1) comprising SEQ ID NO: 732, a heavy chain complementarity determining region 2 (HCDR2) comprising SEQ ID NO: 734, and a heavy chain complementarity determining region 3 (HCDR3) comprising SEQ ID NO: 736, and the light chain comprises a light chain complementarity determining region 1 (LCDR1) comprising SEQ ID NO: 846, a light chain complementarity determining region 2 (LCDR2) comprising SEQ ID NO: 848, and a light chain complementarity determining region 3 (LCDR3) comprising SEQ ID NO: 850 as defined according to the method of Kabat; or

the heavy chain comprises a HCDR1 comprising SEQ ID NO: 1002, a HCDR2 comprising SEQ ID NO: 1004, and a HCDR3 comprising SEQ ID NO: 1006 and the light chain comprises a LCDR1 comprising SEQ ID NO: 1116, a LCDR2 comprising SEQ ID NO: 1118, and a LCDR3 comprising SEQ ID NO: 1120 as defined by IMGT.

2. The monoclonal antibody or antigen-binding fragment according to claim 1, wherein the residue at position 49 of the light chain according to the method of Kabat is not cysteine.
3. The monoclonal antibody or antigen-binding fragment according to claim 2, wherein the residue at position 49 of the light chain according to the method of Kabat is serine.
4. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the residue at position 57 of the heavy chain according to the method of Kabat is not cysteine.
5. The monoclonal antibody or antigen-binding fragment according to claim 4, wherein the residue at position 57 of the heavy chain according to the method of Kabat is serine.

6. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the residue at position 34 of the light chain according to the method of Kabat is glutamate.
7. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the residue at position 36 of the light chain according to the method of Kabat is not phenylalanine.
8. The monoclonal antibody or antigen-binding fragment according to claim 7 wherein the residue at position 36 of the light chain according to the method of Kabat is tyrosine.
9. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the residue at position 46 of the light chain according to the method of Kabat is not arginine.
10. The monoclonal antibody or antigen-binding fragment according to claim 9 wherein the residue at position 46 of the light chain according to the method of Kabat is leucine.
11. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the residue at position 94 of the heavy chain according to the method of Kabat is not lysine.
12. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the residue at position 71 of the heavy chain according to the method of Kabat is not arginine.
13. The monoclonal antibody or antigen-binding fragment according to claim 12 wherein position 71 of the heavy chain according to the Kabat method is valine.
14. The monoclonal antibody or antigen-binding fragment according to claim 1, the antibody comprising:

a heavy chain variable domain (HCVD) comprising SEQ ID NO: 402 and a light chain variable domain (LCVD) comprising SEQ ID NO: 572.

15. The monoclonal antibody or antigen-binding fragment according to claim 1, wherein the antibody is a humanized antibody.
16. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the antibody is IgG1.
17. The monoclonal antibody or antigen-binding fragment according to claim 1 wherein the antibody binds monomeric wild-type human 2N4R Tau with a K_D of less than about 0.5 nM as measured by surface plasmon resonance.
18. The monoclonal antibody or antigen-binding fragment according to claim 1, wherein the antibody or antigen-binding fragment binds to human Tau at an epitope comprising the amino acid sequence HVPG (SEQ ID NO: 1133).
19. The monoclonal antibody or antigen-binding fragment according to claim 18, wherein the antibody or antigen-binding fragment is biepitopic and binds to human Tau at an epitope comprising the amino acid sequence HVPG (SEQ ID NO: 1133) within repeat region 2 or repeat region 4.
20. The monoclonal antibody or antigen-binding fragment according to claim 1, wherein the antibody or antigen-binding fragment binds to human Tau at an epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79).
21. The monoclonal antibody or antigen-binding fragment according to claim 20, wherein the antibody or antigen-binding fragment is biepitopic and binds to human Tau at an epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 2 or repeat region 4.
22. The monoclonal antibody or antigen-binding fragment according to claim 1, wherein the antibody or antigen-binding fragment binds human Tau at the epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 2 with a binding preference that is at least about 10-fold greater than binding at an epitope

comprising the amino acid sequence HKPGG (SEQ ID NO: 182) within repeat region 3 or than binding at an epitope comprising the amino acid sequence HQPGG (SEQ ID NO: 183) within repeat region 1, or wherein the antibody or antigen-binding fragment binds human Tau at the epitope comprising the amino acid sequence HVPGG (SEQ ID NO: 79) within repeat region 4 with a binding preference that is at least about 10-fold greater than binding at an epitope comprising the amino acid sequence HKPGG (SEQ ID NO: 182) within repeat region 3 or than binding at an epitope comprising the amino acid sequence HQPGG (SEQ ID NO: 183) within repeat region 1, as determined by a peptide binding assay.

23. A monoclonal antibody, or an antigen-binding fragment thereof, that specifically binds a human Tau, wherein the antibody is produced by the cell line having ATCC deposit number PTA-124524.
24. A pharmaceutical composition comprising the antibody or antigen-binding fragment of claim 1 and a pharmaceutically acceptable carrier.