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(71) **Applicant: ADIMAB, LLC** [US/US]; 7 Lucent Drive, Lebanon, New Hampshire 03766 (US).

(72) **Inventors: WALKER, Laura M.**; c/o Adimab, LLC, 7 Lucent Drive, Lebanon, New Hampshire 03766 (US). **PEJCHAL, Robert**; c/o Adimab, LLC, 7 Lucent Drive, Lebanon, New Hampshire 03766 (US). **KRAULAND, Eric**; c/o Adimab, LLC, 7 Lucent Drive, Lebanon, New Hampshire 03766 (US). **VASQUEZ, Maximiliano**; c/o Adimab, LLC, 7 Lucent Drive, Lebanon, New Hampshire 03766 (US). **LEUNG, Monica Wai Ling**; c/o Celgene Corporation, 86 Morris Avenue, Summit, New Jersey 07901 (US).

(74) **Agent: SAHR, Robert N.** et al.; Choate, Hall & Stewart LLP, Two International Place, Boston, Massachusetts 02110 (US).

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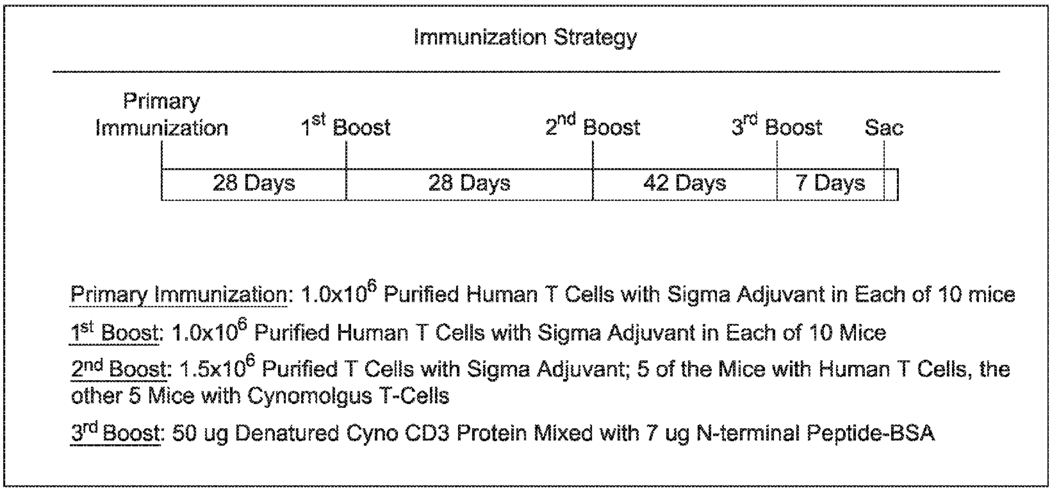
(54) **Title:** ANTI-CD3-BINDING DOMAINS AND ANTIBODIES COMPRISING THEM, AND METHODS FOR THEIR GENERATION AND USE



Primary Immunization: 1.0x10^6 Purified Human T Cells with Sigma Adjuvant in Each of 10 mice

1st Boost: 1.0x10^6 Purified Human T Cells with Sigma Adjuvant in Each of 10 Mice

2nd Boost: 1.5x10^6 Purified T Cells with Sigma Adjuvant; 5 of the Mice with Human T Cells, the other 5 Mice with Cynomolgus T-Cells

3rd Boost: 50 ug Denatured Cyno CD3 Protein Mixed with 7 ug N-terminal Peptide-BSA

Figure 1

(57) **Abstract:** Anti-CD3 binding domains and antibodies comprising them, including multispecific antibodies, with, inter alia, desirable T-cell activation and (re)directed target cell killing potency and developability, profiles are provided, as well as methods for their identification, isolation, and generation, and methods for their preparation and use. Reagents for identifying, isolating, selecting, generating and characterizing CD3 binding domains and antibodies comprising them are also provided.

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[Continued on next page]

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ANTI-CD3-BINDING DOMAINS AND ANTIBODIES COMPRISING THEM, AND METHODS FOR THEIR GENERATION AND USE

Cross Reference to Related Applications

[0001] This application claims priority to United States Provisional Application No. 62/503,315, filed on May 8, 2017, the entire content of which is incorporated herein by reference.

Sequence Listing

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created April 7, 2017, is named 2009186-0189_SL.TXT and is 2,923,505 bytes in size.

Field of the Invention

[0003] The invention relates, *inter alia*, to anti-Cluster of Differentiation 3 (CD3)-binding domains and antibodies comprising them, including multispecific and bispecific antibodies, and functional fragments thereof, and methods and reagents for their identification, isolation, preparation, and use. Reagents for identifying, isolating, selecting, generating and characterizing CD3 binding domains and antibodies comprising them are also provided.

Background of the Invention

[0004] All references cited herein, including without limitation patents, patent applications, and non-patent references and publications referenced throughout are hereby expressly incorporated by reference in their entireties for all purposes.

[0005] The body's immune system serves as a defense against infection, injury and cancer. Two separate but interrelated systems, humoral and cellular immune systems, work together to protect the body. The humoral system is mediated by soluble factors, named antibodies, which neutralize products recognized as being foreign by the body. In contrast, the cellular system involves cells, such as T cells and macrophages, which remove and neutralize foreign invaders.

[0006] The activation of T cells is important for the stimulation of immune responses. T cells exhibit immunological specificity and direct most of the cellular immune responses. Although T cells do not secrete antibodies, they are required for the secretion of antibodies by B lymphocytes. T cell activation requires the participation of a number of cell surface molecules, such as the T cell receptor complex, and CD4 or CD8 molecules. The antigen-specific T cell receptor (TcR) is composed of a disulfide-linked heterodimer, membrane glycoprotein with chains, alpha and beta (α and β), or gamma and delta (γ and δ). The TcR is non-covalently linked with a complex of invariant proteins, designated CD3.

[0007] The TcR confers antigen specificity and the CD3 structures transduce activation signals to T cells. The CD3 complex contains four subunits. They can contain two zeta subunits, one epsilon subunit and either a gamma or a delta subunit. Antigen binding leads to the cross-linking and activation of the TCR complex. T-cell receptor signaling leads to T-cell activation and IL-2 production and other cytokines in a complex process.

[0008] The ligand of the TcR is the MHC-peptide complex on the surface of target cells such as virus-infected cells. After the recognition of the MHC-peptide on the target cell, T cells can have a cytotoxic or an apoptotic effect on the target cell. Especially cytotoxic T cells (CD8 positive T cells) can have advantageous effects by directly removing virus-infected cells. This arm of the cellular immune response is particularly advantageous and is important for fighting virus infections and eliminating tumor cells.

[0009] Activation of the cytotoxic T cell may occur via direct binding of the CD3 antigen without the recognition of the MHC-peptide complex by the TcR. This alternative activation route can be achieved with anti-CD3 antibodies. Non-human monoclonal antibodies have been developed against some of the CD3 chains (subunits), as exemplified by the murine antibodies OKT3, SP34, UCHT1 or 64.1. (See e.g., June, et al., J. Immunol. 136:3945-3952 (1986); Yang, et al., J. Immunol. 137:1097-1100 (1986); and Hayward, et al., Immunol. 64:87-92 (1988)). Other CD3 antibodies are disclosed, for example, in U.S. Pat. Nos. 5,585,097; 5,929,212; 5,968,509; 6,706,265; 6,750,325; 7,381,803; 7,728,114. Bispecific antibodies with CD3 binding specificity are disclosed, for example, in U.S. Pat. Nos. 7,262,276; 7,635,472; and 7,862,813.

[0010] Many of these anti-CD3 antibodies bind the epsilon chain which leads to the development of highly activated T cells. Cancer immunotherapy with ordinary monoclonal antibodies does not typically activate T-lymphocytes sufficiently so as to elicit meaningful, targeted, pharmacologic activity towards the target cell type or tissue.

[0011] The recent development and use of multispecific antibodies, such as bispecific antibodies (bsAbs), to redirect effector T cells for the targeted killing of tumor cells has shown considerable promise both pre-clinically and clinically (see, e.g., Topp et al, 2012, Blood 120:5185-87; Bargou et al, 2008, Science 321:974-77). Many of the bispecific antibodies developed to date contain a first binding site specific to CD3 for T-cell recruitment and activation, and a second binding site for a targeted disease-associated antigen, such as CD19 (Bassan, 2012, Blood 120:5094-95). The bispecific antibody is thought to bring CD3$^+$ T cells into direct contact with targeted disease cells and induce cell-mediated cytotoxicity (Bassan, 2012). Anti-CD3 X anti-CD19 bispecific antibodies have been reported to produce a complete and durable molecular remission at very low concentrations in approximately 70% of adult patients with MRD$^+$ ALL (Topp et al, 2012, Blood 120:5185-87). Bispecific antibodies recognizing gliomas and the CD3 epitope on T cells have been successfully used in treating brain tumors in human patients (Nitta, et al. Lancet 1990; 355:368-371). In addition, CD3 x CD20 bispecific antibodies have been produced for clinical testing (US2015/0166661 and US2017/0202194), as well as CD3 x CLL-1 (US2016/0368994).

[0012] Leukocyte redirecting bsAbs are not limited to T cells. The bispecific killer engagers (BiKEs) comprising scFvs against the NK cell antigen CD16 and a tumor-associated antigen (e.g., CD19, CD22, CD33) have also shown potent anti-cancer activity (e.g., Miller, Hematology Soc Hematol Educ Program 2013:247-53). Other alternatives include trispecific killer engagers (TriKEs), such as anti-CD16 x anti-CD19 x anti-CD22 (Miller, 2013; Gleason et al, 2012, Mol Cancer Ther 11:2674-84). An anti-CD 16 x anti-CD33 BiKE was used to treat AML and myelodysplastic syndrome (Miller, 2013; Wiernik et al, 2013, Clin Cancer Res 19:3844-55). In refractory AML, a CD16 x CD33 BiTE led to potent tumor cell killing and cytokine production by NK cells. Inhibition of ADAM 17 enhanced the CD16 x CD33 BiKE response (Miller, 2013). Other trispecific, trivalent constructs, for example against CD16/CD19/HLA-DR, have been reported (Schubert et al, 2012, mAbs 4:45-56).

[0013] Numerous methods to produce bispecific antibodies are known (see, e.g. U.S. Patent No. 7,405,320). Bispecific antibodies can be produced by the quadroma method, which involves the fusion of two different hybridomas, each producing a monoclonal antibody recognizing a different antigenic site (Milstein and Cuello, Nature 1983; 305:537-540). The fused hybridomas are capable of synthesizing two different heavy chains and two different light chains, which can associate randomly to give a heterogeneous population of 10 different antibody structures of which only one of them, amounting to 1/8 of the total antibody molecules, will be bispecific, and therefore must be further purified from the other forms. Fused hybridomas are often less stable cytogenetically than the parent hybridomas, making the generation of a production cell line more problematic.

[0014] Another method for producing bispecific antibodies uses heterobifunctional cross-linkers to chemically tether two different monoclonal antibodies, so that the resulting hybrid conjugate will bind to two different targets (Staerz, et al. Nature 1985; 314:628-631; Perez, et al. Nature 1985; 316:354-356). Bispecific antibodies generated by this approach are essentially heteroconjugates of two IgG molecules, which diffuse slowly into tissues and are rapidly removed from the circulation. Bispecific antibodies can also be produced by reduction of each of two parental monoclonal antibodies to the respective half molecules, which are then mixed and allowed to reoxidize to obtain the hybrid structure (Staerz and Bevan. Proc Natl Acad Sci USA 1986; 83: 1453-1457). An alternative approach involves chemically cross-linking two or three separately purified Fab' fragments using appropriate linkers. All these chemical methods are undesirable for commercial development due to high manufacturing cost, laborious production process, extensive purification steps, low yields (<20%), and heterogeneous products.

[0015] Discrete VH and VL domains of antibodies produced by recombinant DNA technology may pair with each other to form a dimer (recombinant Fv fragment) with binding capability (U.S. Pat. No. 4,642,334). However, such non-covalently associated molecules are not sufficiently stable under physiological conditions to be of practical use. Cognate VH and VL domains can be joined with a peptide linker of appropriate composition and length (usually consisting of more than 12 amino acid residues) to form a single-chain Fv (scFv) with binding activity. Methods of manufacturing scFv-based agents of multivalency and multispecificity by varying the linker length were disclosed in U.S. Pat. No. 5,844,094, U.S. Pat. No. 5,837,242 and WO 98/44001. Common problems that have been frequently associated with generating scFv-based agents of multivalency and multispecificity are low expression levels, heterogeneous products, instability in solution leading to aggregates, instability in serum, and impaired affinity.

[0016] Several bispecific antibodies targeting CD3 and CD19 are in various stages of development and/or have been approved as therapeutics. An scFv-based bispecific antibody construct, known as BITE® (Bispecific T-cell Engager), employs a single polypeptide containing 2 antigen-binding specificities, each contributed by a cognate VH and VL, linked in tandem via a flexible linker (see, e.g., Nagorsen et al, 2009, Leukemia & Lymphoma 50:886-91; Amann et al, 2009, J Immunother 32:453-64; Baeuerle and Reinhardt, 2009, Cancer Res 69:4941-44). Another bispecific antibody called DART® (Dual-Affinity Re-Targeting) utilizes a disulfide-stabilized diabody design (see, e.g., Moore et al., 2011, Blood 117:4542-51; Veri et al, 2010, Arthritis Rheum 62: 1933-43). Both BITE® and DART® exhibit fast blood clearance due to their small size (~55 kDa), which requires frequent administration to maintain therapeutic levels of the bispecific antibodies.

[0017] SCORPION Therapeutics (Emergent Biosolutions, Inc., Seattle, Wash.) is a platform technology combining two antigen-binding domains in a single chain protein. One binding domain is on the C-terminus and a second binding domain on the N-terminus of an effector domain base on immunoglobulin Fc regions.

[0018] Tetravalent and bispecific antibody-like proteins are DVD-Igs which are engineered from two monoclonal antibodies (Wu, C. et al., Nature Biotechnology, 25, p 1290-1297, 2007). To construct the DVD-Ig molecule, the V domains of the two mAbs are fused in tandem by a short linker (TVAAP) (SEQ ID NO: 6714) with the variable domain of the first antibody light (VL) chain at the N terminus, followed by the other antibodies VL and Ck to form the DVD-Ig protein light chain. Similarly, the variable regions of the heavy (VH) chain of the two mAbs are fused in tandem by a short linker (ASTKGP) (SEQ ID NO: 6715) with the first antibody at the N terminus, followed by the other antibody and the heavy chain constant domains to form the DVD-Ig protein heavy chain (VH1/VL1). All light chain and heavy chain constant domains are preserved in the DVD-Ig design, as they are critical for the formation of a disulfide-linked full IgG-like molecule. Cotransfection of mammalian cells with expression vectors encoding the DVD-Ig light chain and heavy chain leads to the secretion of a single species of an

IgG-like molecule with molecular weight of approximately 200 kDa. This molecule has now four binding sites, 2 from each mAb.

[0019] Bispecific antibodies have shown considerable benefits over monospecific antibodies for the treatment and the detection of cancer. Broad commercial application of bispecific antibodies has been hampered by the lack of efficient/low-cost production methods, the lack of stability of bispecific polypeptides and the lack of long half-lives in humans. A large variety of methods have been developed over the last decades to produce bispecific monoclonal antibodies (BsMAB).

[0020] However, although many candidate clinical and therapeutic antibodies have been found in early discovery efforts which display exquisite selectivity and high potency towards numerous targets of interest, a large proportion of these antibodies have nonetheless subsequently been discovered through downstream development and clinical efficacy activities to suffer from undesirable characteristics such as: promiscuity of binding, polyspecific binding (also termed herein and throughout, “polyspecificity”), off-target binding; nonspecific binding; poor expression levels or profiles in eukaryotic host cells, such as mammalian host cells and yeast cells; poor chemical and physical properties, such as poor stability during storage (e.g., poor/low “shelf-life” stability), poor (low) solubility, poor (high) viscosity, propensity to aggregate, and the like; and poor clinical and biophysical profiles, such as poor pharmacokinetic profiles, poor pharmacodynamic profiles, fast or poor in vivo clearance rates, short circulation half-life, and the like; thereby requiring the termination of further therapeutic development of such candidate antibodies. Additionally, it has been observed that antibodies derived from display technologies represent a historical minority of all clinical and marketed antibodies, a trend which is believed by many to be due, at least in part, to promiscuity of binding, poor PK profiles, and poor CMC characteristics - liabilities which are further postulated to be largely due to a lack of suitable means and methods by which undevelopable antibodies may be detected and/or counter-selected against when screening for antibodies using display technologies (see, e.g., Meninger 2012; available at hyper-text transfer protocol: proteins-congress.com/wordpress/wp-content/uploads/2012/01/Trends-in-Therapeutic-Monoclonal-Antibody-Discovery-Technology.pdf).

[0021] The art has developed certain techniques and assays to assess many of the aforementioned developability characteristics for discovered antibodies in the context of downstream development activities ("post-discovery antibodies"), such as CIC, SIC, BVP-ELISA, TMA, and other assays; however, such assays are typically not amenable to their incorporation into high-throughput early polypeptide and antibody discovery platforms, such as antibody display platforms. Furthermore, assessment of these attributes typically requires milligram to gram quantities of protein, thus often imposing a de facto limitation on the number of leads that can be pragmatically considered for development, and consequently reducing the likelihood of program success. Consequently, significant resources are often expended attempting to fix poorly behaving lead candidates with few backups available in later stages of development.

[0022] In recognition of this bottleneck, considerable efforts have been made to develop assays with lower material requirements and to bring developability assessments further upstream in the development process (Esfandiary *et al.*, 2013, Protein Eng Des Sel 26 (10): 663-670, 2013; Sathish *et al.*, 2013, Nat Rev Drug Discov. 12(4):306-24). A number of such assays are directed at predicting antibody solubility and aggregation behavior of identified, lead candidates. Self-interaction chromatography (SIC) and cross-interaction chromatography (CIC) are column based, low-to-medium throughput assays that correlate with and thus predict antibody solubility at relatively low concentration (Ahamed *et al.*, 2005, J Biol Chem 280(37):32090-100; Jacobs *et al.*, Pharm Res 27:65-71, 2010; Spencer et al., Mabs 4(3)319-325, 2012). A longer retention time on such SIC or CIC columns suggests interaction with antibodies coupled to the column, and is correlated to poor solubility (Jacobs et al., 2010). Sule and co-workers reported a medium throughput gold nanoparticle assay to predict solubility at very low concentration and further broadened the assay scope to be compatible with complex cell culture media (Sule *et al.*, Biophys J 101(7):1749-1757, 2011; Mol Pharmaceutics 10(4):1322-1331, 2013).

[0023] As mentioned above, polyspecificity is a highly undesirable property that has been linked to poor antibody pharmacokinetics (Wu *et al.*, J Mol Biol 368:652-665, 2007; Hötzel *et al.*, 2012, MAbs 4(6):753-760). Certain polyspecificity assays have been reported in the art to serve as medium-throughput substitutes for broad panel tissue immunohistochemistry. Wardemann and colleagues have reported an enzyme-linked immunosorbent assay (ELISA) method using LPS, Insulin, dsDNA, and ssDNA to study polyreactivity in natural antibody repertoires over the course of B-cell maturation (Wardemann *et al.*, 2003, Science 301(5638):1374-7). Protein biochips in which a diverse set of proteins are spotted onto an array for high-throughput ELISAs are another type of screening tool. A chip with ~400 different human proteins from Protagen (Dortmund, Germany) has been reported to compare favorably with IHC staining analysis (Lueking *et al.*, 2008, Bio Techniques 45(4):Pi-Pv), as well as a measure of off-target binding of clinically approved TNF-alpha inhibitors (Feyen *et al.*, Anal Bioanal Chem 391:1713-1720, 2008). More recently, Frese *et al.* reported on a 384-well assay that measures polyreactivity to 32 test proteins, termed Protein Panel Profiling or *3P* (Frese *et al.*, 2013, MAbs 5:2, 279-287). Using this assay, the authors showed that FDA-approved therapeutic antibodies show a highly specific profile to the 32 test proteins and apply it to screen candidates from a phage selection process. These particular polyreactivity profiling assays have not yet been correlated with downstream development issues such as solubility, expression, and stability. A recent advance in this area was reported by Hötzel *et al.* 2012 MAbs 4(6):753-760), in which a baculovirus particle (BVP) ELISA was shown to predict faster antibody non-target mediated clearance *in vivo*, while traditional biophysical properties such as Size Exclusion Chromatography retention time, Hydrophobic Interaction Chromatography elution time, Fv charge, and pI did not (Hötzel, *et al.*, 2012_MAbs 4(6):753-760). Recently, reagents, methods, and means to assess, predict, select and enrich for developable therapeutic antibodies, and ultimately to generate and obtain developable antibodies, for example from antibody libraries, were disclosed (see, e.g., WO2014/179363).

[0024] While the CD3-targeting approach has shown considerable promise, a common side effect of certain T-cell immunostimulatory therapies is the associated production of cytokines, often leading to toxic cytokine release syndrome (CRS), also known as cytokine storm or cytokine release crisis. Because the anti-CD3 binding domain of the bispecific antibody engages all T cells, the high cytokine-producing CD4+ T cell subset is recruited. Moreover, the CD4+ T cell subset includes regulatory T cells, whose recruitment and expansion can potentially lead to immune suppression and have a negative impact on long-term tumor suppression.

[0025] Cell proliferative disorders, such as cancer, are characterized by the uncontrolled growth of cell subpopulations. They are the leading cause of death in the developed world and the second leading cause of death in developing countries, with over 12 million new cancer cases diagnosed and 7 million cancer deaths occurring each year. The National Cancer Institute estimates that greater than half a million Americans will die of cancer in 2013, accounting for nearly one out of every four deaths in the country. As the elderly population has grown, the incidence of cancer has concurrently risen, as the probability of developing cancer is more than two-fold higher after the age of seventy. Cancer care thus represents a significant and ever-increasing societal burden. There is, therefore a need for the provision for CD3 binding domains, and antibodies comprising them (including multispecific antibodies), which display desirable developability and/or CRS risk profiles and are safe and efficacious in, for example, binding specifically to CD3 expressed on T-cells, activating T-cells, (re)-directing the activated T-cells to kill target cells, and doing this with diminished risk of eliciting cytokine release syndrome (also known as cytokine storm or cytokine release crisis).

Summary of the Invention

[0026] It has now been discovered, and is disclosed herein and throughout, a large series of CD3 binding domains and antibodies comprising them, and methods of preparing and using them. Members of this large series of CD3 binding domains collectively display a broad range of desirable properties, including, e.g.,: broad of affinities for CD3 epsilon; cross-reactivity towards both human CD3 ("Hu CD3") and cynomolgus CD3 ("Cy CD3"); as well as desirable developability profiles and/or cytokine release syndrome (CRS) risk profiles, which for many of the CD3 binding domains disclosed herein are observed to be superior to the developability profiles of other anti-CD3 antibodies (e.g., I2C; SP34 ; 38E4; CAB21609_A01, CAB21609_B01, CAB21609_C01,CAB21609_D01 as disclosed herein as well as in Yang et al., J Immunol, Vol 137, pages 1097-1100 (August 4, 1986); US 2014/008295; and WO 2015/095392).

[0027] Advantageously, the CD3 binding domains may be incorporated into essentially any antibody format, including immunoglobulin formats (e.g., IgG, IgM, IgA, IgE, and isotypes thereof), and multispecific (including bispecific) formats. Exemplary multispecific formats that are amenable for incorporation of the inventive CD3 binding domains include, e.g.: Fab-Fc-scFv ("bottle-opener") (XENCOR), Mab-scFv (XENCOR), Mab-Fv (XENCOR), Dual scFv (XENCOR), central Fv (XENCOR), central scFv (XENCOR), one-arm central scFv (XENCOR), Fab-Fab (XENCOR), Fab-Fv (XENCOR), mAb-Fv (XENCOR), mAb-Fab (XENCOR), DART (MACROGENICS), BiTE (AMGEN/MICROMET), KiTE, common light chain-IgG

(GENENTECH), TandAb (AFFIMED) Cross-Mab (ROCHE), SEED (EMD SERONO), BEAT (GLENMARK), TrioMab (TRION PHARMA/FRESENIUS BIOTECH), DuetMab (MEDIMMUNE), and others, as disclosed, e.g., in (WO 95/09917; WO 2008/119566; WO 2008/119567; WO2011/121110; WO 2010/037835; WO 2007/042261; WO 2007/110205; WO 2011/121110; WO 2012/055961; WO 2012/16067; WO 2016/086189; WO 2016/182751; WO 2015/006749; WO 2014/049003; WO 2013/177101; WO 2015/128509; US 7,951,917; US 2009/0252729; US 2014/0348839; US 7,183,076; Mazor et al., *Mabs*, Vol. 7, pages 377-389 (2015); Muda et al., *Protein Engineering, Designe, & Selection*, Vol. 24, pages 447-454 (2011); and Del Bano et al., *Antibodies*, Vol. 5, pages 1-23 (2016).

[0028] As the inventive CD3 binding domains and antibodies comprising them collectively possess a broad range of affinity for cell-surface expressed CD3 and a broad range of T-cell activation and (re)directed target cell killing potency, and are further amenable to essentially any multispecific (including bispecific) antibody format of any valency of interest, the inventive CD3 antibodies may be selected and incorporated into therapeutic molecules designed to target almost any cell type, tissue type, and physiological compartment, and thus may serve as components of therapeutic molecules designed to address almost any disease type or disease state.

[0029] In certain embodiments, the invention provides CD3 binding domains and antibodies comprising them that bind to CD3 (e.g., CD3ε and/or CD3γ).

[0030] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them are provided which display an enhanced developability profile relative to other CD3 binding domains (or antibodies comprising them). In certain embodiments, the inventive CD3 binding domains and antibodies comprising them are provided which display an enhanced developability profile relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab 366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0031] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them display a developability score of: between about 0 MFI and about 500 MFI; between about 0 MFI and about 450 MFI; between about 0 MFI and about 400 MFI; between about 0 MFI and about 350 MFI; between about 0 MFI and about 300 MFI; between about 0

MFI and about 250 MFI; between about 0 MFI and about 200 MFI; between about 0 MFI and about 150 MFI; between about 0 MFI and about 100 MFI; between about 0 MFI and about 50 MFI; between about 200 MFI and 500 MFI; between about 200 MFI and about 450 MFI; between about 200 MFI and about 400 MFI; between about 200 MFI and about 350 MFI; between about 200 MFI and about 300 MFI; between about 200 MFI and about 250 MFI; between about 100 MFI and about 450 MFI; between about 100 MFI and about 400 MFI; between about 100 MFI and about 350 MFI; between about 100 MFI and about 300 MFI; between about 100 MFI and about 250 MFI; between about 100 MFI and about 200 MFI; or between about 100 MFI and about 150 MFI.

[0032] In other embodiments, the inventive CD3 binders and antibodies comprising them display a normalized developability score of between about 0.0 and about 0.6; between about 0.0 and about 0.57; between about 0.0 and about 0.55; between about 0.0 and about 0.53; between about 0.0 and about 0.51; between about 0.0 and about 0.49; between about 0.0 and about 0.47; between about 0.0 and about 0.45; between about 0.0 and about 0.43; between about 0.0 and about 0.41; between about 0.0 and about 0.39; between about 0.0 and about 0.37; between about 0.0 and about 0.35; between about 0.0 and about 0.33; between about 0.0 and about 0.31; between about 0.0 and about 0.29; between about 0.0 and about 0.27; between about 0.0 and about 0.25; between about 0.0 and about 0.23; between about 0.0 and about 0.21; between about 0.0 and about 0.19; between about 0.0 and about 0.17; between about 0.0 and about 0.15; between about 0.0 and about 0.13; between about 0.0 and about 0.11; between about 0.0 and about 0.09; between about 0.0 and about 0.07; or between about 0.0 and about 0.05.

[0033] In certain embodiments, the developability profile and/or developability score for the inventive CD3 binders and antibodies comprising them is obtained by performing a PSR assay; an SCP assay; AS-CINS; a BVP assay; an ELISA; a DSF assay; a Tm assay; a HIC assay; a CIC assay; or combinations thereof.

[0034] In other embodiments, the inventive CD3 binding domains and antibodies comprising them elicit potent T cell activation or T cell killing while displaying a decreased propensity to elicit cytokine production to levels capable of inducing cytokine release syndrome. In certain embodiments, at least one cytokine for which cytokine production levels are measured in order to assess the propensity to elicit cytokine production levels capable of inducing cytokine release syndrome is selected from the group consisting of: Interleukin 6 (IL-6); Interleukin 12 (IL-12); tumor necrosis factor alpha (TNFa); (TGFb); Interleukin 2 (IL-2); and Interferon gamma (IFNg).

[0035] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them elicit T cell activation or T cell killing while displaying a decreased propensity to elicit cytokine production to levels capable of inducing cytokine release relative to that observed one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab 366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2. In certain embodiments, at least one cytokine for which cytokine production levels are measured in order to assess the propensity to elicit cytokine production levels capable of inducing cytokine release syndrome is selected from the group consisting of: Interleukin 6 (IL-6); Interleukin 12 (IL-12); tumor necrosis factor alpha (TNFa); (TGFb); Interleukin 2 (IL-2); and Interferon gamma (IFNg).

[0036] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them display a cytokine release syndrome risk profile that is indicative of decreased risk of eliciting cytokine release syndrome (CRS). In other embodiments, the inventive CD3 binding domains and antibodies comprising them display a cytokine release syndrome risk profile that is indicative of decreased risk of eliciting cytokine release syndrome (CRS) when compared to the cytokine release syndrome risk profile assessed for one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab 366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0037] In certain embodiments, the invention provides an antibody comprising a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH3 is not 100% identical to the CDRH3 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0038] In certain embodiments, the invention provides an antibody comprising a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH2 is not 100% identical to the CDRH2 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0039] In certain embodiments, the invention provides an antibody comprising a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH1 is not 100% identical to the CDRH1 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0040] In certain embodiments, the invention provides an antibody comprising a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL3 is not 100% identical to the CDRL3 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0041] In certain embodiments, the invention provides an antibody comprising a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL2 is not 100% identical to the CDRL2 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0042] In certain embodiments, the invention provides an antibody comprising a CDRL1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL1 is not 100% identical to the CDRL1 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0043] In certain embodiments, the invention provides an antibody comprising a heavy chain (HC) that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; an HC selected from the group consisting of the HCs of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the HC is not 100% identical to the HC of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0044] In certain embodiments, the invention provides an antibody comprising a light chain (LC) that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; an LC selected from the group consisting of the LCs of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the LC is not 100% identical to the LC of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0045] In certain embodiments, the invention provides an antibody comprising a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the neither the CDRH3, CDRH2, nor the CHRH1 is 100% identical to the CHRH3, CDRH2, or CDRH1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0046] In certain embodiments, the invention provides an antibody comprising a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and a CDRL1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical; to a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the neither the CDRL3, CDRL2, nor the CHRL1 is 100% identical to the CHRL3, CDRL2, or CDRL1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0047] In certain embodiments, the invention provides an antibody comprising a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and a CDRL1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the neither the CDRH3, CDRH2, CDRH1, CDRL3, CDHL2, nor the CHRL1 is 100% identical to the CHRH3, CDRH2, CDRH1, CDRL3, CDHL2, or the CDRL1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0048] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-15512; ADI-15516; and ADI-16513; as provided in Table 2.

[0049] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-18562; ADI-18564; ADI-18565; ADI-18566; ADI-18567; ADI-18568; ADI-18570; ADI-18571; ADI-18572; ADI-18573; ADI-18563; ADI-18569; ADI-18574; ADI-18575; ADI-18576; ADI-18578; ADI-18579; ADI-18580; ADI-18581; ADI-18582; ADI-18584; ADI-18585; ADI-18577; ADI-18583; ADI-18588; ADI-18589; ADI-18590; ADI-18591; ADI-18593; ADI-18594; ADI-18595;

ADI-18596; ADI-18597; ADI-18592; ADI-18587; ADI-18586; and; ADI-16606; as provided in Table 2.

[0050] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-18576; ADI-20820; ADI-20578; ADI-20571; ADI-21097; ADI-20577; ADI-20576; ADI-20568; ADI-20582; ADI-20575; ADI-20567; ADI-20574; ADI-20573; ADI-20579; ADI-18565; ADI-20818; ADI-20587; ADI-20588; ADI-20589; ADI-20590; ADI-20594; ADI-20596; ADI-20599; ADI-20605; ADI-20607; ADI-20608; and ADI-20609; as provided in Table 2.

[0051] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-16606; ADI-20587; ADI-20607; ADI-20590; ADI-28708; ADI-28709; ADI-28710; ADI-21943; ADI-28711; ADI-28712; ADI-28713; ADI-28714; ADI-28715; ADI-21944; ADI-28716; ADI-21945; ADI-21946; ADI-28717; ADI-21947; ADI-28718; ADI-28719; ADI-28720; ADI-28721; ADI-28722; ADI-28723; ADI-28724; ADI-28725; ADI-28726; ADI-28727; ADI-28728; ADI-28729; ADI-28730; ADI-28731; ADI-28732; ADI-28733; ADI-28734; ADI-28735; ADI-28736; ADI-28737; ADI-28738; ADI-28739; ADI-28740; ADI-28741; ADI-28742; ADI-28743; ADI-21948; ADI-21949; ADI-28744; ADI-21950; ADI-28745; ADI-28746; ADI-28747; ADI-28748; ADI-21951; ADI-21952; ADI-28749; ADI-28750; ADI-28751; ADI-21953; ADI-28752; ADI-21954; ADI-28753; ADI-28754; ADI-28755; ADI-28756; ADI-28757; ADI-28758; ADI-28759; ADI-28760; ADI-28761; ADI-28762; ADI-28763; ADI-28764; ADI-28765; ADI-28766; ADI-28767; ADI-28768; ADI-21955; ADI-28769; ADI-28770; ADI-21956; ADI-28771; ADI-28772; ADI-28773; ADI-28774; and ADI-28775; as provided in Table 2.

[0052] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-21959; ADI-21963; ADI-21965; ADI-21967; ADI-21970; ADI-21971; ADI-21972; ADI-21973; ADI-21974; ADI-21975; ADI-21976; ADI-21977; ADI-21978; ADI-21979; ADI-21943; ADI-21944; ADI-21945; ADI-21946; ADI-21947; ADI-21948; ADI-21949; ADI-21950; ADI-21951; ADI-21952; ADI-21953; ADI-21954; ADI-21955; and ADI-21956; as provided in Table 2.

[0053] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-21952;

ADI-22523; ADI-24403; ADI-24404; ADI-24405; ADI-24407; ADI-24408; ADI-24409; ADI-24410; ADI-24411; ADI-24412; ADI-24413; ADI-24414; ADI-24415; ADI-24416; ADI-24417; ADI-24418; ADI-24434; ADI-24435; ADI-24436; ADI-24437; ADI-24438; ADI-24439; ADI-24440; ADI-24441; ADI-24442; ADI-24443; ADI-24444; ADI-24445; ADI-24446; ADI-24449; ADI-24388; ADI-24389; ADI-24390; ADI-24391; ADI-24392; ADI-24393; ADI-24394; ADI-24395; ADI-24396; ADI-24397; ADI-24398; ADI-24399; ADI-24400; ADI-24401; ADI-24402; ADI-24419; ADI-24420; ADI-24421; ADI-24422; ADI-24423; ADI-24424; ADI-24425; ADI-24426; ADI-24427; ADI-24428; ADI-24429; ADI-24430; ADI-24431; ADI-24432; ADI-24433; ADI-24447; and ADI-24448; as provided in Table 2.

[0054] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-23652; ADI-23653; ADI-23654; ADI-23655; ADI-23656; ADI-23657; ADI-23658; ADI-23651; ADI-23644; ADI-23645; ADI-23646; ADI-23647; ADI-23648; ADI-23649; ADI-23650; ADI-23667; ADI-23668; ADI-23669; ADI-23670; ADI-23671; ADI-23672; ADI-23673; ADI-23659; ADI-23660; ADI-23661; ADI-23663; ADI-23664; ADI-23639; ADI-23641; ADI-23642; ADI-23640; ADI-23643; ADI-21952; ADI-23633; ADI-23634; ADI-23635; ADI-23636; ADI-23637; ADI-23638; ADI-23632; and ADI-23629; as provided in Table 2.

[0055] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26909; ADI-26910; ADI-26912; ADI-26913; ADI-26915; ADI-26916; ADI-26917; ADI-26918; ADI-26919; ADI-26920; ADI-26921; ADI-26924; ADI-26925; ADI-26927; ADI-26928; ADI-26929; ADI-26930; ADI-26932; ADI-26933; ADI-26938; ADI-26939; ADI-26940; ADI-26941; ADI-26942; ADI-26943; ADI-26944; ADI-26945; ADI-26950; ADI-26954; ADI-23672; ADI-23673; ADI-23664; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26968; ADI-26969; ADI-26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; ADI-26994; and ADI-26995; as provided in Table 2.

[0056] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26910; ADI-26913; ADI-26915; ADI-26919; ADI-26920; ADI-26921; ADI-26943; ADI-26954; ADI-21952; ADI-26955; ADI-26956; ADI-26962; ADI-26978; ADI-26983; and ADI-26994; as provided in Table 2.

[0057] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: ADI-15512; ADI-16513; ADI-15516; ADI-18565; ADI-18589; ADI-18585; ADI-18590; ADI-18576; ADI-20568; ADI-20580; ADI-21978; ADI-22523; ADI-25133; and ADI-26906.

[0058] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: ADI-16606; ADI-29601; ADI-29602; ADI-29603; ADI-20587; ADI-20607; ADI-20590; ADI-21952; ADI-23633; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26961; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26967; ADI-26968; ADI-26969; ADI-26970; ADI-26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; and ADI-26994.

[0059] In certain embodiments either alone or in combination with other embodiments of the invention, the inventive CD3 binding domains and antibodies comprising them display a decreased propensity for degradation relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab 366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0060] In certain embodiments either alone or in combination with other embodiments of the invention, the inventive CD3 binding domains and antibodies comprising them display a decreased CRS risk profile relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab 366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0061] In certain embodiments either alone or in combination with other embodiments, provided are CD3 binding domains and antibodies comprising them display a decreased propensity for degradation relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab 366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0062] In certain embodiments and/or in combination with any of the embodiments disclosed herein and throughout, provided are CD3 binding domains and antibodies comprising them that are humanized. In certain embodiments, such CD3 binding domains comprise CDRs of such other embodiments, and further comprise an acceptor human framework, e.g., a human immunoglobulin framework or a human consensus framework.

[0063] In certain embodiments and/or in combination with any of the embodiments disclosed herein and throughout provided are CD3 binding domains and antibodies comprising them comprising a VH as in any of the embodiments provided herein and throughout, and a VL as in any of the embodiments provided herein and throughout, wherein one or both of the variable domain sequences include post-translational modifications.

[0064] In a further aspect of the invention, provided are CD3 binding domains and antibodies comprising them that bind to the same epitope as a CD3 binding domain provided in the other embodiments disclosed therein and throughout.

[0065] In certain embodiments, CD3 binding domains and/or antibodies comprising them have a CD3 dissociation constant (Kd) of ≤ 1 μM, ≤ 100 nM, ≤ 10 nM, ≤ 1 nM, ≤ 0.1 nM, ≤ 0.01 nM, or ≤ 0.001 nM (e.g., 10^{-8}M or less, e.g., from 10^{-8}M to 10^{-13}M, e.g., from 10^{-9}M to 10^{-13} M).

[0066] In a further aspect of the invention, CD3 binding domains and antibodies comprising them comprise a multispecific antibody. In a further aspect of the invention, CD3 binding domains and antibodies comprising them comprise a bispecific antibody.

[0067] In a further aspect of the invention, CD3 binding domains and antibodies comprising them comprise at least a second antigen binding domain that specifically binds to an oncology target; an immune-oncology target; a neurodegenerative disease target; an autoimmune disorder target; an infectious disease target; a metabolic disease target; a cognitive disorder target; a blood-brain barrier target; or a blood disease target.

[0068] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody wherein the multispecific antibody comprises a second binding domain having specificity for a second antigen selected from the group consisting of: 0772P (CA125, MUC16; Genbank accession no. AF36148); adipophilin (perilipin-2, Adipose differentiation-related protein, ADRP, ADFP, MGC10598; NCBI Reference Sequence: NP—001113.2); AIM-2 (Absent In Melanoma 2, PYHIN4, Interferon-Inducible Protein AIM2; NCBI Reference Sequence: NP—004824.1); ALDH1 A1 (Aldehyde Dehydrogenase 1 Family, Member A1, ALDH1, PUMB1, Retinaldehyde Dehydrogenase 1, ALDC, ALDH-E1, ALHDII, RALDH 1, EC 1.2.1.36, ALDH11, HEL-9, HEL-S-53e, HEL12, RALDH1, Acetaldehyde Dehydrogenase 1, Aldehyde Dehydrogenase 1, Soluble, Aldehyde Dehydrogenase, Liver Cytosolic, ALDH Class 1, Epididymis Luminal Protein 12, Epididymis Luminal Protein 9, Epididymis Secretory Sperm Binding Protein Li 53e, Retinal Dehydrogenase 1, RaIDH1, Aldehyde Dehydrogenase Family 1 Member A1, Aldehyde Dehydrogenase, Cytosolic, EC 1.2.1; NCBI Reference Sequence: NP—000680.2); alpha-actinin-4 (ACTN4, Actinin, Alpha 4, FSGS1, Focal Segmental Glomerulosclerosis 1, Non-Muscle Alpha-Actinin 4, F-Actin Cross-Linking Protein, FSGS, ACTININ-4, Actinin Alpha4 Isoform, alpha-actinin-4; NCBI Reference Sequence: NP—004915.2); alpha-fetoprotein (AFP, HPAFP, FETA, alpha-1-fetoprotein, alpha-fetoglobulin, Alpha-1-fetoprotein, Alpha-fetoglobulin, HP; GenBank: AAB58754.1); Amphiregulin (AREG, SDGF, Schwannoma-Derived Growth Factor, Colorectum Cell-Derived Growth Factor, AR, CRDGF; GenBank: AAA51781.1); ARTC1 (ART1, ADP-Ribosyltransferase 1, Mono(ADP-Ribosyl)Transferase 1, ADP-Ribosyltransferase C2 And C3 Toxin-Like 1, ART2, CD296, RT6, ADP-Ribosyltransferase 2, GPI-Linked NAD(P)(+)-Arginine ADP-Ribosyltransferase 1, EC 2.4.2.31, CD296 Antigen; NP); ASLG659; ASPHD1 (Aspartate Beta-Hydroxylase Domain Containing 1, Aspartate Beta-Hydroxylase Domain-Containing Protein 1, EC 1.14.11., GenBank: AAI44153.1); B7-H4 (VTCN1, V-Set Domain Containing T Cell Activation Inhibitor 1, B7H4, B7 Superfamily Member 1, Immune Costimulatory Protein B7-H4, B7h.5, T-Cell Costimulatory Molecule B7x, B7S1, B7X, VCTN1, H4, B7 Family Member, PRO1291, B7 Family Member, H4, T Cell Costimulatory Molecule B7x, V-Set Domain-Containing T-Cell Activation Inhibitor 1, Protein B7S1; GenBank:

AAZ17406.1); BAFF-R (TNFRSF13C, Tumor Necrosis Factor Receptor Superfamily, Member 13C, BAFFR, B-Cell-Activating Factor Receptor, BAFF Receptor, BLyS Receptor 3, CVID4, BROMIX, CD268, B Cell-Activating Factor Receptor, prolixin, Tumor Necrosis Factor Receptor Superfamily Member 13C, BR3, CD268 Antigen; NCBI Reference Sequence: NP—443177.1); BAGE-1; BCLX (L); BCR-ABL fusion protein (b3a2); beta-catenin (CTNNB1, Catenin (Cadherin-Associated Protein), Beta 1, 88 kDa, CTNNB, MRD19, Catenin (Cadherin-Associated Protein), Beta 1 (88kD), armadillo, Catenin Beta-1; GenBank: CAA61107.1); BING-4 (WDR46, WD Repeat Domain 46, C6orf11, BING4, WD Repeat-Containing Protein BING4, Chromosome 6 Open Reading Frame 11, FP221, UTP7, WD Repeat-Containing Protein 46; NP); BMPR1 B (bone morphogenetic protein receptor-type IB, Genbank accession no. NM—00120; NP); B-RAF (Brevican (BCAN, BEHAB, Genbank accession no. AF22905); Brevican (BCAN, Chondroitin Sulfate Proteoglycan 7, Brain-Enriched Hyaluronan-Binding Protein, BEHAB, CSPG7, Brevican Proteoglycan, Brevican Core Protein, Chondroitin Sulfate Proteoglycan BEHAB; GenBank: AAH27971.1); CALCA (Calcitonin-Related Polypeptide Alpha, CALC1, Calcitonin 1, calcitonin, Alpha-Type CGRP, Calcitonin Gene-Related Peptide I, CGRP-I, CGRP, CGRP1, CT, KC, Calcitonin/Calcitonin-Related Polypeptide, Alpha, katacalcin; NP); CASP-5 (CASP5, Caspase 5, Apoptosis-Related Cysteine Peptidase, Caspase 5, Apoptosis-Related Cysteine Protease, Protease ICH-3, Protease TY, ICE(rel)-111, ICE(rel)III, ICEREL-III, ICH-3, caspase-5, TY Protease, EC 3.4.22.58, ICH3, EC 3.4.22; NP); CASP-8; CD19 (CD19-B-lymphocyte antigen CD19 isoform 2 precursor, B4, CVID3 [Homo sapiens], NCBI Reference Sequence: NP—001761.3); CD20 (CD20-B-lymphocyte antigen CD20, membrane-spanning 4-domains, subfamily A, member 1, B1,Bp35,CD20,CVID5,LEU-16,MS4A2,S7; NCBI Reference Sequence: NP—690605.1); CD21 (CD21 (CR2 (Complement receptor or C3DR (C3d/Epstein Barr virus receptor) or Hs.73792 Genbank accession no. M2600); (CD22 (B-cell receptor CD22-B isoform, BL-CAM, Lyb-8, LybB, SIGLEC-2, FLJ22814, Genbank accession No. AK02646); CD22; CD33 (CD33 Molecule, CD33 Antigen (Gp67), Sialic Acid Binding Ig-Like Lectin 3, Sialic Acid-Binding Ig-Like Lectin 3, SIGLEC3, gp67, SIGLEC-3, Myeloid Cell Surface Antigen CD33, p67, Siglec-3, CD33 Antigen; GenBank: AAH28152.1); CD45; CD70 (CD70-tumor necrosis factor (ligand) superfamily, member 7; surface antigen CD70; Ki-24 antigen; CD27 ligand; CD27-L; tumor necrosis factor ligand superfamily member 7; NCBI Reference Sequence for species homo sapiens: NP—001243.1); CD72 (CD72 (B-cell differentiation antigen CD72, Lyb-; 359 aa, μl: 8.66, MW: 40225, TM: 1 [P] Gene Chromosome: 9p13.3, Genbank accession No. NP—001773.); CD79a (CD79a (CD79A, CD79a, immunoglobulin-associated alpha, a B cell-specific protein that covalently interacts with Ig beta (CD79B) and forms a complex on the surface with Ig M molecules, transduces a signal involved in B-cell differentiation), μl: 4.84, MW: 25028 TM: 2 [P] Gene Chromosome: 19q13.2, Genbank accession No. NP—001774.1); CD79b (CD79b (CD79B, CD79b, IGb (immunoglobulin-associated beta), B29, Genbank accession no. NM—000626 or 1103867); Cdc27 (Cell Division Cycle 27, D0S1430E, D17S978E, Anaphase Promoting Complex Subunit 3, Anaphase-Promoting Complex Subunit 3, ANAPC3, APC3, CDC27Hs, H-NUC, CDC27 Homolog, Cell Division Cycle 27 Homolog (S. Cerevisiae), HNUC, NUC2, Anaphase-Promoting Complex, Protein 3, Cell Division Cycle 27 Homolog, Cell Division Cycle Protein 27 Homolog, Nuc2 Homolog; GenBank: AAH11656.1); CDK4 (Cyclin-Dependent Kinase 4, Cell Division Protein Kinase 4, PSK-J3, EC 2.7.11.22, CMM3, EC 2.7.11; NCBI Reference Sequence: NP—000066.1); CDKN2A (Cyclin-Dependent Kinase Inhibitor 2A, MLM, CDKN2, MTS1, Cyclin-Dependent Kinase Inhibitor 2A (Melanoma, P16, Inhibits CDK4), Cyclin-Dependent Kinase 4 Inhibitor A, Multiple Tumor Suppressor 1, CDK4I, MTS-1, CMM2, P16, ARF, INK4, INK4A, P14, P14ARF, P16-INK4A, P16INK4, P16INK4A, P19, P19ARF, TP16, CDK4 Inhibitor P16-INK4, Cell Cycle Negative Regulator Beta, p14ARF, p16-INK4, p16-INK4a, p16INK4A, p19ARF; NP); CEA; CLL1 (CLL-1 (CLEC12A, MICL, and DCAL, encodes a member of the C-type lectin/C-type lectin-like domain (CTL/CTLD) superfamily. Members of this family share a common protein fold and have diverse functions, such as cell adhesion, cell-cell signaling, glycoprotein turnover, and roles in inflammation and immune response. The protein encoded by this gene is a negative regulator of granulocyte and monocyte function. Several alternatively spliced transcript variants of this gene have been described, but the full-length nature of some of these variants has not been determined. This gene is closely linked to other CTL/CTLD superfamily members in the natural killer gene complex region on chromosome 12p13 (Drickamer, K Curr. Opin. Struct. Biol. 9:585-90 [1999]; van Rhenen, A, et al., Blood 110:2659-66 [2007]; Chen C H, et al. Blood 107:1459-67 [2006]; Marshall A S, et al. Eur. J. Immunol. 36:2159-69 [2006]; Bakker A B, et al Cancer Res. 64:8443-50 [2004]; Marshall A S, et al J. Biol. Chem. 279:14792-80, 2004. CLL-1 has been shown to be a type II transmembrane receptor comprising a single C-type lectin-like domain (which is not predicted to bind either calcium or sugar), a stalk region, a transmembrane domain and a short cytoplasmic tail containing an ITIM motif.); CLPP (Caseinolytic Mitochondrial Matrix Peptidase Proteolytic Subunit, Endopeptidase Clp, EC 3.4.21.92, PRLTS3, ATP-Dependent Protease ClpAP (*E. coli*), ClpP (Caseinolytic Protease, ATP-Dependent, Proteolytic Subunit, *E. coli*) Homolog, ClpP Caseinolytic Peptidase, ATP-Dependent, Proteolytic Subunit Homolog (*E. coli*), ClpP Caseinolytic Protease, ATP-Dependent, Proteolytic Subunit Homolog (*E. coli*), human, Proteolytic Subunit, ATP-Dependent Protease ClpAP, Proteolytic Subunit, Human, ClpP Caseinolytic Peptidase ATP-Dependent, Proteolytic Subunit, ClpP Caseinolytic Peptidase, ATP-Dependent, Proteolytic Subunit Homolog, ClpP Caseinolytic Protease, ATP-Dependent, Proteolytic Subunit Homolog, Putative ATP-Dependent Clp Protease Proteolytic Subunit, Mitochondrial; NP); COA-1; CPSF; CRIPTO (CRIPTO (CR, CR1, CRGF, CRIPTO, TDGF1, teratocarcinoma-derived growth factor, Genbank accession no. NP—003203 or NM—00321); Cw6; CXCR5 CXCR5 (Burkitt's lymphoma receptor 1, a G protein-coupled receptor that is activated by the CXCL13 chemokine, functions in lymphocyte migration and humoral defense, plays a role in HIV-2 infection and perhaps development of AIDS, lymphoma, myeloma, and leukemia); 372 aa, μl: 8.54 MW: 41959 TM: 7 [P] Gene Chromosome: 11q23.3, Genbank accession No. NP—001707.); CXORF61 CXORF61—chromosome X open reading frame 61[Homo sapiens], NCBI Reference Sequence: NP—001017978.1); cyclin D1 (CCND1, BCL1, PRAD1, D11S287E, B-Cell CLL/Lymphoma 1, B-Cell Lymphoma 1 Protein, BCL-1 Oncogene, PRAD1 Oncogene, Cyclin D1 (PRAD1: Parathyroid Adenomatosis 1), G1/S-Specific Cyclin D1, Parathyroid Adenomatosis 1, U21B31, G1/S-Specific Cyclin-D1, BCL-1; NCBI Reference Sequence: NP—444284.1); Cyclin-A1 (CCNA1, CT146, Cyclin A1; GenBank: AAH36346.1); dek-can fusion protein; DKK1 (Dickkopf WNT Signaling Pathway Inhibitor 1, SK, hDkk-1, Dickkopf (Xenopus Laevis) Homolog 1, Dickkopf 1 Homolog (Xenopus Laevis), DKK-1, Dickkopf 1 Homolog, Dickkopf Related Protein-1, Dickkopf-1 Like, Dickkopf-Like Protein 1, Dickkopf-Related Protein 1, Dickkopf-1, Dkk-1; GenBank: AAQ89364.1); DR1 (Down-Regulator Of Transcription 1, TBP-Binding (Negative Cofactor 2), Negative Cofactor 2-Beta, TATA-Binding Protein-Associated Phosphoprotein, NC2, NC2-BETA, Protein Dr1, NC2-beta, Down-Regulator Of Transcription 1; NCBI Reference Sequence: NP—001929.1); DR13 (Major Histocompatibility Complex, Class II, DR Beta 1, HLA-DR1B, DRw10, DW2.2/DR2.2, SS1, DRB1, HLA-DRB, HLA Class II Histocompatibility Antigen, DR-1 Beta Chain, Human Leucocyte Antigen DRB1, Lymphocyte

Antigen DRB1, MHC Class II Antigen, MHC Class II HLA-DR Beta 1 Chain, MHC Class II HLA-DR-Beta Cell Surface Glycoprotein, MHC Class II HLA-DRw10-Beta, DR-1, DR-12, DR-13, DR-14, DR-16, DR-4, DR-5, DR-7, DR-8, DR-9, DR1, DR12, DR13, DR14, DR16, DR4, DR5, DR7, DRB, DR9, DRw11, DRw8, HLA-DRB2, Clone P2-Beta-3, MHC Class II Antigen DRB1*1, MHC Class II Antigen DRB1*10, MHC Class II Antigen DRB1*11, MHC Class II Antigen DRB1*12, MHC Class II Antigen DRB1*13, MHC Class II Antigen DRB1*14, MHC Class II Antigen DRB1*15, MHC Class II Antigen DRB1*16, MHC Class II Antigen DRB1*3, MHC Class II Antigen DRB1*4, MHC Class II Antigen DRB1*7, MHC Class II Antigen DRB1*8, MHC Class II Antigen DRB1*9; NP); E16 (E16 (LAT1, SLC7A5, Genbank accession no. NM—00348); EDAR (EDAR— tumor necrosis factor receptor superfamily member EDAR precursor, EDA-A1 receptor; downless homolog; ectodysplasin-A receptor; ectodermal dysplasia receptor; anhidrotic ectodysplasin receptor 1, DL; ECTD10A; ECTD10B; ED1R; ED3; ED5; EDA-A1R; EDA1R; EDA3; HRM1 [Homo sapiens]; NCBI Reference Sequence: NP—071731.1); EFTUD2 (Elongation Factor Tu GTP Binding Domain Containing 2, Elongation Factor Tu GTP-Binding Domain-Containing Protein 2, hSNU114, SNU114 Homolog, U5 SnRNP-Specific Protein, 116 KDa, MFDGA, KIAA0031, 116 KD, U5 SnRNP Specific Protein, 116 KDa U5 Small Nuclear Ribonucleoprotein Component, MFDM, SNRNP116, Snrp116, Snu114, U5-116KD, SNRP116, U5-116 KDa; GenBank: AAH02360.1); EGFR (Epidermal Growth Factor Receptor, ERBB, Proto-Oncogene C-ErbB-1, Receptor Tyrosine-Protein Kinase ErbB-1, ERBB1, HER1, EC 2.7.10.1, Epidermal Growth Factor Receptor (Avian Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog), Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog (Avian), PIG61, Avian Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog, Cell Growth Inhibiting Protein 40, Cell Proliferation-Inducing Protein 61, mENA, EC 2.7.10; GenBank: AAH94761.1); EGFR-G719A; EGFR-G719C; EGFR-G719S; EGFR-L858R; EGFR-L861 Q; EGFR-57681; EGFR-T790M; Elongation factor 2 (EEF2, Eukaryotic Translation Elongation Factor 2, EF2, Polypeptidyl-TRNA Translocase, EF-2, SCA26, EEF-2; NCBI Reference Sequence: NP—001952.1); ENAH (hMena) (Enabled Homolog (Drosophila), MENA, Mammalian Enabled, ENA, NDPP1, Protein Enabled Homolog; GenBank: AAH95481.1)—results for just “ENAH” not “ENAH (hMena)”; EpCAM (Epithelial Cell Adhesion Molecule, M4S1, MIC18, Tumor-Associated Calcium Signal Transducer 1, TACSTD1, TROP1, Adenocarcinoma-Associated Antigen, Cell Surface Glycoprotein Trop-1, Epithelial Glycoprotein 314, Major Gastrointestinal Tumor-Associated Protein GA733-2, EGP314, KSA, DIAR5, HNPCC8, Antigen Identified By Monoclonal Antibody AUA1, EGP-2, EGP40, ESA, KS1/4, MK-1, Human Epithelial Glycoprotein-2, Membrane Component, Chromosome 4, Surface Marker (35kD Glycoprotein), EGP, Ep-CAM, GA733-2, M1S2, CD326 Antigen, Epithelial Cell Surface Antigen, hEGP314, KS 1/4 Antigen, ACSTD1; GenBank: AAH14785.1); EphA3 (EPH Receptor A3, ETK1, ETK, TYRO4, HEK, Eph-Like Tyrosine Kinase 1, Tyrosine-Protein Kinase Receptor ETK1, EK4, EPH-Like Kinase 4, EC 2.7.10.1, EPHA3, HEK4, Ephrin Type-A Receptor 3, Human Embryo Kinase 1, TYRO4 Protein Tyrosine Kinase, hEK4, Human Embryo Kinase, Tyrosine-Protein Kinase TYRO4, EC 2.7.10; GenBank: AAH63282.1); EphB2R; Epiregulin (EREG, ER, proepiregulin; GenBank: AAI36405.1); ETBR (EDNRB, Endothelin Receptor Type B, HSCR2, HSCR, Endothelin Receptor Non-Selective Type, ET-B, ET-BR, ETRB, ABCDS, WS4A, ETB, Endothelin B Receptor; NP); ETV6-AML1 fusion protein; EZH2 (Enhancer Of Zeste Homolog 2 (Drosophila), Lysine N-Methyltransferase 6, ENX-1, KMT6 EC 2.1.1.43, EZH1, WVS, Enhancer Of Zeste (Drosophila) Homolog 2, ENX1, EZH2b, KMT6A, WVS2, Histone-Lysine N-Methyltransferase EZH2, Enhancer Of Zeste Homolog 2, EC 2.1.1; GenBank: AAH10858.1); FcRH1 (FCRL1, Fc Receptor-Like 1, FCRH1, Fc Receptor Homolog 1, FcR-Like Protein 1, Immune Receptor Translocation-Associated Protein 5, IFGP1, IRTA5, hIFGP1, IFGP Family Protein 1, CD307a, Fc Receptor-Like Protein 1, Immunoglobulin Superfamily Fc Receptor, Gp42, FcRL1, CD307a Antigen; GenBank: AAH33690.1); FcRH2 (FCRL2, Fc Receptor-Like 2, SPAP1, SH2 Domain-Containing Phosphatase Anchor Protein 1, Fc Receptor Homolog 2, FcR-Like Protein 2, Immunoglobulin Receptor Translocation-Associated Protein 4, FCRH2, IFGP4, IRTA4, IFGP Family Protein 4, SPAP1A, SPAP1 B, SPAP1C, CD307b, Fc Receptor-Like Protein 2, Immune Receptor Translocation-Associated Protein 4, Immunoglobulin Superfamily Fc Receptor, Gp42, SH2 Domain Containing Phosphatase Anchor Protein 1, FcRL2, CD307b Antigen; GenBank: AAQ88497.1); FcRH5 (FCRL5, Fc Receptor-Like 5, IRTA2, Fc Receptor Homolog 5, FcR-Like Protein 5, Immune Receptor Translocation-Associated Protein 2, BXMAS1, FCRH5, CD307, CD307e, PRO820, Fc Receptor-Like Protein 5, Immunoglobulin Superfamily Receptor Translocation Associated 2 (IRTA2), FCRL5, CD307e Antigen; GenBank: AAI01070.1); FLT3-ITD; FN1(Fibronectin 1, Cold-Insoluble Globulin, FN, Migration-Stimulating Factor, CIG, FNZ, GFND2, LETS, ED-B, FINC, GFND, MSF, fibronectin; GenBank: AAI43764.1); G250 (MN, CAIX, Carbonic Anhydrase IX, Carbonic Dehydratase, RCC-Associated Protein G250, Carbonate Dehydratase IX, Membrane Antigen MN, Renal Cell Carcinoma-Associated Antigen G250, CA-IX, P54/58N, pMW1, RCC-Associated Antigen G250, Carbonic Anhydrase 9; NP);—alias results for “G250” not “G250/MN/CAIX”; GAGE-1,2,8; GAGE-3,4,5,6,7; GDNF-Ra1 (GDNF family receptor alpha 1; GFRA1; GDNFR; GDNFRA; RETL1; TRNR1; RET1 L; GDNFR-alpha1; GFR-ALPHA-; U95847; BC014962; NM—145793 NM—005264); GEDA (Genbank accession No. AY26076); GFRA1—GDNF family receptor alpha-1; GDNF receptor alpha-1; GDNFR-alpha-1; GFR-alpha-1; RET ligand 1; TGF-beta-related neurotrophic factor receptor 1 [Homo sapiens]; ProtKB/Swiss-Prot: P56159.2; glypican-3 (GPC3, Glypican 3, SDYS, Glypican Proteoglycan 3, Intestinal Protein OCI-5, GTR2-2, MXR7, SGBS1, DGSX, OCI-5. SGB, SGBS, Heparan Sulphate Proteoglycan, Secreted Glypican-3, OCI5; GenBank: AAH35972.1); GnTVf; gp100 (PMEL, Premelanosome Protein, SILV, D12S53E, PMEL17, SIL, Melanocyte Protein Pmel 17, Melanocytes Lineage-Specific Antigen GP100, Melanoma-Associated ME20 Antigen, Silver Locus Protein Homolog, ME20-M, ME20M, P1, P100, Silver (Mouse Homolog) Like, Silver Homolog (Mouse), ME20, SI, Melanocyte Protein Mel 17, Melanocyte Protein PMEL, Melanosomal Matrix Protein17, Silver, Mouse, Homolog Of; GenBank: AAC60634.1); GPC; GPNMB (Glycoprotein (Transmembrane) Nmb, Glycoprotein NMB, Glycoprotein Nmb-Like Protein, osteoactivin, Transmembrane Glycoprotein HGFIN, HGFIN, NMB, Transmembrane Glycoprotein, Transmembrane Glycoprotein NMB; GenBank: AAH32783.1); GPR172A (G protein-coupled receptor 172A; GPCR41; FLJ11856; D15Ertd747e); NP—078807.1; NM—024531.3); GPR19 (G protein-coupled receptor 19; Mm.478; NP—006134.1; NM—006143.2); GPR54 (KISS1 receptor; KISS1R; GPR54; HOT7T175; AXOR1; NP—115940.2; NM—032551.4); HAVCR1 (Hepatitis A Virus Cellular Receptor 1, T-Cell Immunoglobulin Mucin Family Member 1, Kidney Injury Molecule 1, KIM-1, KIM1, TIM, TIM-1, TIM1, TIMD-1, TIMD1, T-Cell Immunoglobulin Mucin Receptor 1, T-Cell Membrane Protein 1, HAVCR, HAVCR-1, T Cell Immunoglobin Domain And Mucin Domain Protein 1, HAVcr-1, T-Cell Immunoglobulin And Mucin Domain-Containing Protein 1; GenBank: AAH13325.1); HER2 (ERBB2, V-Erb-B2 Avian Erythroblastic Leukemia Viral Oncogene Homolog 2, NGL, NEU, Neuro/Glioblastoma Derived Oncogene Homolog, Metastatic Lymph Node Gene 19 Protein, Proto-Oncogene C-ErbB-2, Proto-Oncogene Neu, Tyrosine Kinase-Type Cell Surface Receptor HER2, MLN 19, p185erbB2, EC 2.7.10.1, V-Erb-

B2 Avian Erythroblastic Leukemia Viral Oncogene Homolog 2 (Neuro/Glioblastoma Derived Oncogene Homolog), CD340, HER-2, HER-2/neu, TKR1, C-Erb B2/Neu Protein, herstatin, Neuroblastoma/Glioblastoma Derived Oncogene Homolog, Receptor Tyrosine-Protein Kinase ErbB-2, V-Erb-B2 Erythroblastic Leukemia Viral Oncogene Homolog 2, Neuro/Glioblastoma Derived Oncogene Homolog, MLN19, CD340 Antigen, EC 2.7.10; NP); HER-2/neu—alias of above; HERV-K-MEL; HLA-DOB (Beta subunit of MHC class II molecule (la antigen) that binds peptides and presents them to CD4+ T lymphocytes); 273 aa, μl: 6.56, MW: 30820.TM: 1 [P] Gene Chromosome: 6p21.3, Genbank accession No. NP—002111); hsp70-2 (HSPA2, Heat Shock 70 kDa Protein 2, Heat Shock 70kD Protein 2, HSP70-3, Heat Shock-Related 70 KDa Protein 2, Heat Shock 70 KDa Protein 2; GenBank: AAD21815.1); IDO1 (Indoleamine 2,3-Dioxygenase 1, IDO, INDO, Indoleamine-Pyrrole 2,3-Dioxygenase, IDO-1, Indoleamine-Pyrrole 2,3 Dioxygenase, Indolamine 2,3 Dioxygenase, Indole 2,3 Dioxygenase, EC 1.13.11.52; NCBI Reference Sequence: NP—002155.1); IGF2B3; IL13Ralpha2 (IL13RA2, Interleukin 13 Receptor, Alpha 2, Cancer/Testis Antigen 19, Interleukin-13-Binding Protein, IL-13R-alpha-2, IL-13RA2, IL-13 Receptor Subunit Alpha-2, IL-13R Subunit Alpha-2, CD213A2, CT19, IL-13R, IL13BP, Interleukin 13 Binding Protein, Interleukin 13 Receptor Alpha 2 Chain, Interleukin-13 Receptor Subunit Alpha-2, IL13R, CD213a2 Antigen; NP); IL20Rα; Intestinal carboxyl esterase; IRTA2 (alias of FcRH5); Kallikrein 4 (KLK4, Kallikrein-Related Peptidase 4, PRSS17, EMSP1, Enamel Matrix Serine Proteinase 1, Kallikrein-Like Protein 1, Serine Protease 17, KLK-L1, PSTS, AI2A1, Kallikrein 4 (Prostase, Enamel Matrix, Prostate), ARM1, EMSP, Androgen-Regulated Message 1, Enamel Matrix Serine Protease 1, kallikrein, kallikrein-4, prostase, EC 3.4.21.-, Prostase, EC 3.4.21; GenBank: AAX30051.1); KIF20A (Kinesin Family Member 20A, RAB6KIFL, RAB6 Interacting, Kinesin-Like (Rabkinesin6), Mitotic a; LAGE-1; LDLR-fucosyltransferase AS fusion protein; Lengsin (LGSN, Lengsin, Lens Protein With Glutamine Synthetase Domain, GLULD1, Glutamate-Ammonia Ligase Domain-Containing Protein 1, LGS, Glutamate-Ammonia Ligase (Glutamine Synthetase) Domain Containing 1, Glutamate-Ammonia Ligase (Glutamine Synthase) Domain Containing 1, Lens Glutamine Synthase-Like; GenBank: AAF61255.1); LGR5 (leucine-rich repeat-containing G protein-coupled receptor 5; GPR49, GPR6; NP—003658.1; NM—003667.2; LY64 (Lymphocyte antigen 64 (RP10, type I membrane protein of the leucine rich repeat (LRR) family, regulates B-cell activation and apoptosis, loss of function is associated with increased disease activity in patients with systemic lupus erythematosis); 661 aa, μl: 6.20, MW: 74147 TM: 1 [P] Gene Chromosome: 5q12, Genbank accession No. NP—005573.; Ly6E (lymphocyte antigen 6 complex, locus E; Ly67, RIG-E,SCA-2, TSA-; NP—002337.1; NM—002346.2); Ly6G6D (lymphocyte antigen 6 complex, locus G6D; Ly6-D, MEGT; NP—067079.2; NM—021246.2); LY6K (lymphocyte antigen 6 complex, locus K; LY6K; HSJ001348; FLJ3522; NP—059997.3; NM—017527.3); LyPD1-LY6/PLAUR domain containing 1, PHTS [Homo sapiens], GenBank: AAH17318.1); MAGE-A1 (Melanoma Antigen Family A, 1 (Directs Expression Of Antigen MZ2-E, MAGE1, Melanoma Antigen Family A 1, MAGEA1, Melanoma Antigen MAGE-1, Melanoma-Associated Antigen 1, Melanoma-Associated Antigen MZ2-E, Antigen MZ2-E, Cancer/Testis Antigen 1.1, CT1.1, MAGE-1 Antigen, Cancer/Testis Antigen Family 1, Member 1, Cancer/Testis Antigen Family 1, Member 1, MAGE1A; NCBI Reference Sequence: NP—004979.3); MAGE-A10 (MAGEA10, Melanoma Antigen Family A, 10, MAGE10, MAGE-10 Antigen, Melanoma-Associated Antigen 10, Cancer/Testis Antigen 1.10, CT1.10, Cancer/Testis Antigen Family 1, Member 10, Cancer/Testis Antigen Family 1, Member 10; NCBI Reference Sequence: NP—001238757.1); MAGE-A12 (MAGEA12, Melanoma Antigen Family A, 12, MAGE12, Cancer/Testis Antigen 1.12, CT1.12, MAGE12F Antigen, Cancer/Testis Antigen Family 1, Member 12, Cancer/Testis Antigen Family 1, Member 12, Melanoma-Associated Antigen 12, MAGE-12 Antigen; NCBI Reference Sequence: NP—001159859.1); MAGE-A2 (MAGEA2, Melanoma Antigen Family A, 2, MAGE2, Cancer/Testis Antigen 1.2, CT1.2, MAGEA2A, MAGE-2 Antigen, Cancer/Testis Antigen Family 1, Member 2, Cancer/Testis Antigen Family 1, Member 2, Melanoma Antigen 2, Melanoma-Associated Antigen 2; NCBI Reference Sequence: NP—001269434.1); MAGE-A3 (MAGEA3, Melanoma Antigen Family A, 3, MAGE3, MAGE-3 Antigen, Antigen MZ2-D, Melanoma-Associated Antigen 3, Cancer/Testis Antigen 1.3, CT1.3, Cancer/Testis Antigen Family 1, Member 3, HIPS, HYPD, MAGEA6, Cancer/Testis Antigen Family 1, Member 3; NCBI Reference Sequence: NP—005353.1); MAGE-A4 (MAGEA4, Melanoma Antigen Family A, 4, MAGE4, Melanoma-Associated Antigen 4, Cancer/Testis Antigen 1.4, CT1.4, MAGE-4 Antigen, MAGE-41 Antigen, MAGE-X2 Antigen, MAGE4A, MAGE4B, Cancer/Testis Antigen Family 1, Member 4, MAGE-41, MAGE-X2, Cancer/Testis Antigen Family 1, Member 4; NCBI Reference Sequence: NP—001011550.1); MAGE-A6 (MAGEA6, Melanoma Antigen Family A, 6, MAGE6, MAGE-6 Antigen, Melanoma-Associated Antigen 6, Cancer/Testis Antigen 1.6, CT1.6, MAGE3B Antigen, Cancer/Testis Antigen Family

1, Melanoma Antigen Family A 6, Member 6, MAGE-3b, MAGE3B, Cancer/Testis Antigen Family 1, Member 6; NCBI Reference Sequence: NP—787064.1); MAGE-A9 (MAGEA9, Melanoma Antigen Family A, 9, MAGE9, MAGE-9 Antigen, Melanoma-Associated Antigen 9, Cancer/Testis Antigen 1.9, CT1.9, Cancer/Testis Antigen Family 1, Member 9, Cancer/Testis Antigen Family 1, Member 9, MAGEA9A; NCBI Reference Sequence: NP—005356.1); MAGE-C1 (MAGEC1, Melanoma Antigen Family C, 1, Cancer/Testis Antigen 7.1, CT7.1, MAGE-C1 Antigen, Cancer/Testis Antigen Family 7, Member 1, CT7, Cancer/Testis Antigen Family 7, Member 1, Melanoma-Associated Antigen C1; NCBI Reference Sequence: NP—005453.2); MAGE-C2 (MAGEC2, Melanoma Antigen Family C, 2, MAGEE1, Cancer/Testis Antigen 10, CT10, HCA587, Melanoma Antigen, Family E, 1, Cancer/Testis Specific, Hepatocellular Carcinoma-Associated Antigen 587, MAGE-C2 Antigen, MAGE-E1 Antigen, Hepatocellular Cancer Antigen 587, Melanoma-Associated Antigen C2; NCBI Reference Sequence: NP—057333.1); mammaglobin-A (SCGB2A2, Secretoglobin, Family 2A, Member 2, MGB1, Mammaglobin 1, UGB2, Mammaglobin A, mammaglobin-A, Mammaglobin-1, Secretoglobin Family 2A Member 2; NP); MART2 (H HAT, Hedgehog Acyltransferase, SKI1, Melanoma Antigen Recognized By T-Cells 2, Skinny Hedgehog Protein 1, Skn, Melanoma Antigen Recognized By T Cells 2, Protein-Cysteine N-Palmitoyltransferase HHAT, EC 2.3.1.-; GenBank: AAH39071.1); M-CSF (CSF1, Colony Stimulating Factor 1 (Macrophage), MCSF, CSF-1, lanimostim, Macrophage Colony-Stimulating Factor 1, Lanimostim; GenBank: AAH21117.1); MCSP (SMCP, Sperm Mitochondria-Associated Cysteine-Rich Protein, MCS, Mitochondrial Capsule Selenoprotein, HSMCSGEN1, Sperm Mitochondrial-Associated Cysteine-Rich Protein; NCBI Reference Sequence: NP—109588.2); XAGE-1b/GAGED2a; WT1 (Wilms Tumor 1, WAGR, GUD, WIT-2, WT33, Amino-Terminal Domain Of EWS, NPHS4, Last Three Zinc Fingers Of The DNA-Binding Domain Of WT1, AWT1, Wilms Tumor Protein, EWS-WT1; GenBank: AAB33443.1); VEGF; Tyrosinase (TYR; OCAIA; OCA1A; tyrosinase; SHEP; NP—000363.1; NM—000372.4; GenBank: AAB60319.1); TrpM4 (BR22450, FLJ20041, TRPM4, TRPM4B, transient receptor potential cation channel, subfamily M, member 4, Genbank accession no. NM—01763); TRP2-INT2; TRP-2; TRP-1/gp75 (Tyrosinase-Related Protein 1, 5,6-Dihydroxyindole-2-Carboxylic Acid Oxidase, CAS2, CATB, TYRP, OCAS, Catalase B, b-PROTEIN, Glycoprotein 75, EC 1.14.18., Melanoma Antigen Gp75, TYRP1, TRP, TYRRP, TRP1, SHEP11, DHICA Oxidase, EC 1.14.18, GP75, EC 1.14.18.1;

Triosephosphate isomerase (Triosephosphate isomerase 1, TPID, Triose-Phosphate Isomerase, HEL-S-49, TIM, Epididymis Secretory Protein Li 49, TPI, Triosephosphate Isomerase, EC 5.3.1.1; TRAG-3 (CSAG Family Member 2, Cancer/Testis Antigen Family 24, CSAG3B, Member 2, CSAG Family Member 3B, Cancer/Testis Antigen Family 24 Member 2, Cancer/Testis Antigen 24.2, Chondrosarcoma-Associated Gene 2/3 Protein, Taxol-Resistant-Associated Gene 3 Protein, Chondrosarcoma-Associated Gene 2/3 Protein-Like, CT24.2, Taxol Resistance Associated Gene 3, TRAG-3, CSAG3A, TRAG3;); TMEM46 (shisa homolog 2 (Xenopus laevis); SHISA; NP—001007539.1; NM—001007538.1; TMEM118 (ring finger protein, transmembrane2; RNFT2; FLJ1462; NP—001103373.1; NM—001109903.1; TMEFF1 (transmembrane protein with EGF-like and two follistatin-like domains 1; Tomoregulin-; H7365; C9orf2; C9ORF2; U19878; X83961; NM—080655; NM—003692; TGF-betaRII (TGFBR2, Transforming Growth Factor, Beta Receptor II (70/80 kDa), TGFbeta-RII, MFS2, tbetaR-II, TGFR-2, TGF-Beta Receptor Type IIB, TGF-Beta Type II Receptor, TGF-Beta Receptor Type-2, EC 2.7.11.30, Transforming Growth Factor Beta Receptor Type IIC, AAT3, TbetaR-II, Transforming Growth Factor, Beta Receptor II (70-80kD), TGF-Beta Receptor Type II, FAA3, Transforming Growth Factor-Beta Receptor Type II, LDS1 B, HNPCC6, LDS2B, LDS2, RITC, EC 2.7.11, TAAD2; TENB2 (TMEFF2, tomoregulin, TPEF, HPP1, TR, putative transmembrane proteoglycan, related to the EGF/heregulin family of growth factors and follistatin); 374 aa, NCBI Accession: AAD55776, AAF91397, AAG49451, NCBI RefSeq: NP—057276; NCBI Gene: 23671; OMIM: 605734; SwissProt Q9UIK5; Genbank accession No. AF179274; AY358907, CAF85723, CQ782436; TAG-2; TAG-1 (Contactin 2 (Axonal), TAG-1, AXT, Axonin-1 Cell Adhesion Molecule, TAX, Contactin 2 (transiently Expressed), TAXI, Contactin-2, Axonal Glycoprotein TAG-1, Transiently-Expressed Axonal Glycoprotein, Transient Axonal Glycoprotein, Axonin-1, TAX-1, TAG1, FAMES; PRF: 444868); SYT-SSX1 or -SSX2 fusion protein; survivin; STEAP2 (HGNC 8639, IPCA-1, PCANAP1, STAMP1, STEAP2, STMP, prostate cancer associated gene 1, prostate cancer associated protein 1, six transmembrane epithelial antigen of prostate 2, six transmembrane prostate protein, Genbank accession no. AF45513; STEAP1 (six transmembrane epithelial antigen of prostate, Genbank accession no. NM—01244; SSX-4; SSX-2 (SSX2, Synovial Sarcoma, X Breakpoint2, X Breakpoint 2, SSX, X Breakpoint 2B, Cancer/Testis Antigen 5.2, X-Chromosome-Related 2, Tumor Antigen HOM-MEL-40, CT5.2, HD21, Cancer/Testis Antigen Family 5, HOM-MEL-40, Isoform B, Cancer/Testis Antigen Family 5 member 2a, member 2a, Protein SSX2, Sarcoma, Sarcoma, Synovial, X-Chromosome-Related 2, synovial, Synovial Sarcoma, X Breakpoint 2B, Synovial Sarcomam, SSX2A; Sp17; SOX10 (SRY (Sex Determining Region Y)-Box 10, mouse, PCWH, DOM, WS4, WS2E, WS4C, Dominant Megacolon, mouse, Human Homolog Of, Dominant Megacolon, SRY-Related HMG-Box Gene 10, Human Homolog Of, transcription Factor SOX-10; GenBank: CAG30470.1); SNRPD1 (Small Nuclear Ribonucleoprotein D1, Small Nuclear Ribonucleoprotein D1, Polypeptide 16 kDa, Polypeptide (16kD), SNRPD, HsT2456, Sm-D1, SMD1, Sm-D Autoantigen, Small Nuclear Ribonucleoprotein D1 Polypeptide 16 kDa Pseudogene, SnRNP Core Protein D1, Small Nuclear Ribonucleoprotein Sm D1; SLC35D3 (Solute Carrier Family 35, Member D3, FRCL1, Fringe Connection-Like Protein 1, bA55K22.3, Frc, Fringe-Like 1, Solute Carrier Family 35 Member D3; NCBI GenBank: NC—000006.11 NC—018917.2 NT—025741.16); SIRT2 (Sirtuin 2, NAD-Dependent Deacetylase Sirtuin-2, SIRL2, Silent Information Regulator 2, Regulatory Protein SIR2 Homolog 2, Sir2-Related Protein Type 2, SIR2-Like Protein 2, Sirtuin Type 2, Sirtuin (Silent Mating Type Information Regulation 2 Homolog) 2 (S. cerevisiae), Sirtuin-2, Sirtuin (Silent Mating Type Information Regulation 2, S. cerevisiae, Homolog) 2, EC 3.5.1., SIR2; GenBank: AAK51133.1); Sema 5b (FLJ10372, KIAA1445, Mm.42015, SEMA5B, SEMAG, Semaphorin 5b Hlog, sema domain, seven thrombospondin repeats (type 1 and type 1-like), Transmembrane Domain™ and short cytoplasmic domain, (semaphorin) 5B, Genbank accession no. AB04087; secernin 1 (SCRN1, SES1, KIAA0193, secerin-1; GenBank: EAL24458.1); SAGE (SAGE1, Sarcoma Antigen 1, Cancer/Testis Antigen 14, CT14, Putative Tumor Antigen; NCBI Reference Sequence: NP—061136.2); RU2AS (KAAG1, Kidney Associated Antigen 1, RU2AS, RU2 Antisense Gene Protein, Kidney-Associated Antigen 1; GenBank: AAF23613.1); RNF43-E3 ubiquitin-protein ligase RNF43 precursor [Homo sapiens], RNF124; URCC; NCBI Reference Sequence: NP—060233.3; RhoC (RGS5 (Regulator Of G-Protein Signaling 5, MSTP032, Regulator Of G-Protein Signalling 5, MSTP092, MST092, MSTP106, MST106, MSTP129, MST129; GenBank: AAB84001.1); RET (ret proto-oncogene; MEN2A; HSCR1; MEN2B; MTC1; PTC; CDHF12; Hs.168114; RET51; RET-ELE; NP—066124.1; NM—020975.4); RBAF600 (UBR4, Ubiquitin Protein Ligase E3 Component N-Recognin 4, Zinc Finger, UBR1 Type 1, ZUBR1, E3 Ubiquitin-Protein Ligase UBR4, RBAF600, 600 KDa Retinoblastoma Protein-Associated Factor, Zinc Finger UBR1-Type Protein 1, EC 6.3.2., N-recognin-4, KIAA0462, p600, EC 6.3.2, KIAA1307;

GenBank: AAL83880.1); RAGE-1 (MOK, MOK Protein Kinase, Renal Tumor Antigen, RAGE, MAPK/MAK/MRK Overlapping Kinase, Renal Tumor Antigen 1, Renal Cell Carcinoma Antigen, RAGE-1, EC 2.7.11.22, RAGE1; UniProtKB/Swiss-Prot: Q9UQ07.1); RAB38/NY-MEL-1 (RAB38, NY-MEL-1, RAB38, Member RAS Oncogene Family, Melanoma Antigen NY-MEL-1, Rab-Related GTP-Binding Protein, Ras-Related Protein Rab-38, rrGTPbp; GenBank: AAH15808.1); PTPRK (DJ480J14.2.1 (Protein Tyrosine Phosphatase, Receptor Type, K R-PTP-KAPPA, Protein Tyrosine Phosphatase Kappa, Protein Tyrosine Phosphatase Kappa), Protein Tyrosine Phosphatase, Receptor Type, K, Protein-Tyrosine Phosphatase Kappa, Protein-Tyrosine Phosphatase, Receptor Type, Kappa, R-PTP-kappa, Receptor-Type Tyrosine-Protein Phosphatase Kappa, EC 3.1.3.48, PTPK; GenBank: AAI44514.1); PSMA; PSCA hIg(2700050C12Rik, C530008016Rik, RIKEN cDNA 2700050C12, RIKEN cDNA 2700050C12 gene, Genbank accession no. AY358628); PSCA (Prostate stem cell antigen precursor, Genbank accession no. AJ29743; PRDX5 (Peroxiredoxin 5, EC 1.11.1.15, TPx Type VI, B166, Antioxidant Enzyme B166, HEL-S-55, Liver Tissue 2D-Page Spot 71 B, PMP20, Peroxisomal Antioxidant Enzyme, PRDX6, Thioredoxin Peroxidase PMP20, PRXV, AOEB166, Epididymis Secretory Protein Li 55, Alu Co-Repressor 1, Peroxiredoxin-5, Mitochondrial, Peroxiredoxin V, prx-V, Thioredoxin Reductase, Prx-V, ACR1, Alu Corepressor, PLP; GenBank: CAG33484.1); PRAME (Preferentially Expressed Antigen In Melanoma, Preferentially Expressed Antigen Of Melanoma, MAPE, 01P-4, OIPA, CT130, Cancer/Testis Antigen 130, Melanoma Antigen Preferentially Expressed In Tumors, Opa-Interacting Protein 4, Opa-Interacting Protein 01P4; GenBank: CAG30435.1); pml-RARalpha fusion protein; PMEL17 (silver homolog; SILV; D12S53E; PMEL17; SI; SIL); ME20; gp10 BC001414; BT007202; M32295; M77348; NM—006928; PBF (ZNF395, Zinc Finger Protein 395, PRF-1, Huntington disease regulatory, HD Gene Regulatory Region-Binding Protein, Region-Binding Protein 2, Protein 2, Papillomavirus Regulatory Factor 1, HD-Regulating Factor 2, Papillomavirus-Regulatory Factor, PRF1, HDBP-2, Si-1-8-14, HDBP2, Huntington'S Disease Gene Regulatory Region-Binding Protein 2, HDRF-2, Papillomavirus Regulatory Factor PRF-1, PBF; GenBank: AAH01237.1); PAX5 (Paired Box 5, Paired Box Homeotic Gene 5, BSAP, Paired Box Protein Pax-5, B-Cell Lineage Specific Activator, Paired Domain Gene 5, Paired Box Gene 5 (B-Cell Lineage Specific Activator Protein), B-Cell-Specific Transcription Factor, Paired Box Gene 5 (B-Cell Lineage Specific Activator); PAP (REG3A, Regenerating Islet-Derived 3 Alpha, INGAP, PAP-H, Hepatointestinal Pancreatic Protein, PBBCGF, Human Proislet Peptide, REG-Ill, Pancreatitis-Associated Protein 1, Regi, Reg III-Alpha, hepatocarcinoma-intestine-pancreas, Regenerating Islet-Derived Protein III-Alpha, Pancreatic Beta Cell Growth Factor, HIP, PAP Homologous Protein, HIP/PAP, Proliferation-Inducing Protein 34, PAP1, Proliferation-Inducing Protein 42, REG-3-alpha, Regenerating Islet-Derived Protein 3-Alpha, Pancreatitis-Associated Protein; GenBank: AAH36776.1); p53 (TP53, Tumor Protein P53, TPR53, P53, Cellular Tumor Antigen P53, Antigen NY-CO-13, Mutant Tumor Protein 53, Phosphoprotein P53, P53 Tumor Suppressor, BCC7, Transformation-Related Protein 53, LFS1, tumor Protein 53, Li-Fraumeni Syndrome, Tumor Suppressor P53; P2X5 (Purinergic receptor P2X ligand-gated ion channel 5, an ion channel gated by extracellular ATP, may be involved in synaptic transmission and neurogenesis, deficiency may contribute to the pathophysiology of idiopathic detrusor instability); 422 aa), µl: 7.63, MW: 47206 TM: 1 [P] Gene Chromosome: 17p13.3, Genbank accession No. NP—002552.; OGT (0-Linked N-Acetylglucosamine (GlcNAc) Transferase, O-GlcNAc Transferase P110 Subunit, 0-Linked N-Acetylglucosamine (GlcNAc) Transferase (UDP-N-Acetylglucosamine:Polypeptide-N-Acetylglucosaminyl Transferase, UDP-N-Acetylglucosamine-Peptide N-Acetylglucosaminyltransferase 110 KDa Subunit, UDP-N-Acetylglucosamine:Polypeptide-N-Acetylglucosaminyl Transferase, Uridinediphospho-N-Acetylglucosamine:Polypeptide Beta-N-Acetylglucosaminyl Transferase, O-GlcNAc Transferase Subunit P110, EC 2.4.1.255, 0-Linked N-Acetylglucosamine Transferase 110 KDa Subunit, EC 2.4.1, HRNT1, EC 2.4.1.186, 0-GLCNAC; GenBank: AAH38180.1); 0A1 (Osteoarthritis QTL 1, OASD; GenBank: CAA88742.1); NY-ESO-1/LAGE-2 (Cancer/Testis Antigen 1 B, CTAG1 B, NY-ESO-1, LAGE-2, ESO1, CTAG1, CTAG, LAGE2B, Cancer/Testis Antigen 1, Autoimmunogenic Cancer/Testis Antigen NY-ESO-1, Ancer Antigen 3, Cancer/Testis Antigen 6.1, New York Esophageal Squamous Cell Carcinoma 1, L Antigen Family Member 2, LAGE2, CT6.1, LAGE2A; GenBank: AAI30365.1); NY-BR-1 (ANKRD30A, Ankyrin Repeat Domain 30A, Breast Cancer Antigen NY-BR-1, Serologically Defined Breast Cancer Antigen NY-BR-1, Ankyrin Repeat Domain-Containing Protein 30A; NCBI Reference Sequence: NP—443723.2); N-ras (NRAS, Neuroblastoma RAS Viral (V-Ras) Oncogene Homolog, NRAS1, Transforming Protein N-Ras, GTPase NRas, ALPS4, N-Ras Protein Part 4, NS6, Oncogene Homolog, HRAS1; GenBank: AAH05219.1); NFYC (Nuclear Transcription Factor Y, Gamma, HAP5, HSM, Nuclear Transcription Factor Y Subunit C, Transactivator HSM-1/2, CCAAT Binding Factor

Subunit C, NF-YC, CCAAT Transcription Binding Factor Subunit Gamma, CAAT Box DNA-Binding Protein Subunit C, Histone H1 Transcription Factor Large Subunit 2A, CBFC, Nuclear Transcription Factor Y Subunit Gamma, CBF-C, Transactivator HSM-1, H1TF2A, Transcription Factor NF-Y, C Subunit; neo-PAP (PAPOLG, Poly(A) Polymerase Gamma, Neo-Poly(A) Polymerase, Nuclear Poly(A) Polymerase Gamma, Polynucleotide Adenylyltransferase Gamma, SRP RNA 3′ Adenylating Enzyme/Pap2, PAP-gamma, Neo-PAP, SRP RNA 3′-Adenylating Enzyme, PAP2, EC 2.7.7.19, PAPG; NCBI Reference Sequence: NP—075045.2); NCA (CEACAM6, Genbank accession no. M1872); Napi3b (NAPI-3B, NPTIIb, SLC34A2, solute carrier family 34 (sodium phosphate), member 2, type II sodium-dependent phosphate transporter 3b, Genbank accession no. NM—00642); Myosin class I; MUM-3; MUM-2 (TRAPPC1, Trafficking Protein Particle Complex 1, BETS, BETS Homolog, MUM2, Melanoma Ubiquitous Mutated 2, Multiple Myeloma Protein 2, Trafficking Protein Particle Complex Subunit 1; MUM-1f; Mucin (MUC1, Mucin 1, Cell Surface Associated, PEMT, PUM, CA 15-3, MCKD1, ADMCKD, Medullary Cystic Kidney Disease 1 (Autosomal Dominant), ADMCKD1, Mucin 1, Transmembrane, CD227, Breast Carcinoma-Associated Antigen DF3, MAM6, Cancer Antigen 15-3, MCD, Carcinoma-Associated Mucin, MCKD, Krebs Von Den Lungen-6, MUC-1/SEC, Peanut-Reactive Urinary Mucin, MUC1/ZD, Tumor-Associated Epithelial Membrane Antigen, DF3 Antigen, Tumor-Associated Mucin, episialin, EMA, H23 Antigen, H23AG, Mucin-1, KL-6, Tumor Associated Epithelial Mucin, MUC-1, Episialin, PEM, CD227 Antigen; UniProtKB/Swiss-Prot: P15941.3); MUCSAC (Mucin SAC, Oligomeric Mucus/Gel-Forming, Tracheobronchial Mucin′ MUC5, TBM, Mucin 5, Subtypes A And C, Tracheobronchial/Gastric, leB, Gastric Mucin, Mucin SAC, Oligomeric Mucus/Gel-Forming Pseudogene, Lewis B Blood Group Antigen, LeB, Major Airway Glycoprotein, MUC-SAC, Mucin-5 Subtype AC, Tracheobronchial; MUC1 (Mucin 1, Cell Surface Associated, PEMT, PUM, CA 15-3, MCKD1, ADMCKD, Medullary Cystic Kidney Disease 1 (Autosomal Dominant), ADMCKD1, Mucin 1, Transmembrane, CD227, Breast Carcinoma-Associated Antigen DF3, MAM6, Cancer Antigen 15-3, MCD, Carcinoma-Associated Mucin, MCKD, Krebs Von Den Lungen-6, MUC-1/SEC, Peanut-Reactive Urinary Mucin, MUC-1/X, Polymorphic Epithelial Mucin, MUC1/ZD, Tumor-Associated Epithelial Membrane Antigen, DF3 Antigen, Tumor-Associated Mucin, episialin, EMA, h23 Antigen, H23AG, mucin-1, KL-6, Tumor Associated Epithelial Mucin, MUC-1, Episialin, PEM, CD227 Antigen; MSG783 (RNF124, hypothetical protein FLJ20315, Genbank accession no. NM-01776; MRP4-multidrug resistance-associated protein 4 isoform 3, MOAT-B; MOATB [Homo sapiens]; NCBI Reference Sequence: NP—001288758.1; MPF (MPF, MSLN, SMR, megakaryocyte potentiating factor, mesothelin, Genbank accession no. NM—00582; MMP-7 (MMP7, matrilysin, MPSL1, matrin, Matrix Metalloproteinase 7 (Matrilysin, Uterine), Uterine Matrilysin, Matrix Metalloproteinase-7, EC 3.4.24.23, Pump-1 Protease, Matrin, Uterine Metalloproteinase, PUMP1, MMP-7, EC 3.4.24, PUMP-1; GenBank: AAC37543.1); MMP-2 (MMP2, Matrix Metallopeptidase 2 (Gelatinase A, 72 kDa Gelatinase, 72 kDa Type IV Collagenase), MONA, CLG4A, Matrix Metalloproteinase 2 (Gelatinase A, 72kD Gelatinase, 72kD Type IV Collagenase), CLG4, 72 kDa Gelatinase, 72 kDa Type IV Collagenase), Matrix Metalloproteinase-2, MMP-II, 72 KDa Gelatinase, Collagenase Type IV-A, MMP-2, Matrix Metalloproteinase-II, TBE-1, Neutrophil Gelatinase, EC 3.4.24.24, EC 3.4.24; GenBank: AAH02576.1); and Meloe.

[0069] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody wherein the multispecific antibody comprises a second binding domain having specificity for a second antigen selected from the group consisting of: 17-IA, 4-1BB, 4Dc, 6- keto-PGFla, 8-iso-PGF2a, 8-oxo-dG, Al Adenosine Receptor, A33, ACE, ACE-2, Activin, Activin A, Activin AB, Activin B, Activin C, Activin RIA, Activin RIA ALK-2, Activin RIB ALK-4, Activin RIIA, Activin RUB, ADAM, ADAM10, ADAM12, ADAM15, ADAM17/TACE, ADAM8, ADAM9, ADAMTS, ADAMTS4, ADAMTS5, Addressins, aFGF, ALCAM, ALK, ALK-1, ALK-7, alpha-l-antitrypsin, alpha-V/beta-1 antagonist, ANG, Ang, APAF-1, APE, APJ, APP, APRIL, AR, ARC, ART, Artemin, anti-Id, ASPARTIC, Atrial natriuretic factor, av/b3 integrin, Axl, b2M, B7-1, B7-2, B7-H, B-lymphocyte Stimulator (BlyS), BACE, BACE-1, Bad, BAFF, BAFF-R, Bag-1, BAK, Bax, BCA-1, BCAM, Bel, BCMA, BDNF, b-ECGF, bFGF, BID, Bik, BIM, BLC, BL-CAM, BLK, BMP, BMP-2 BMP-2a, BMP-3 Osteogenin, BMP-4 BMP-2b, BMP-5, BMP-6 Vgr-1, BMP-7 (OP-1), BMP-8 (BMP-8a, OP-2), BMPR, BMPR-IA (ALK-3), BMPR-IB (ALK-6), BRK-2, RPK-1, BMPR-II (BRK-3), BMPs, b- NGF, BOK, Bombesin, Bone-derived neurotrophic factor, BPDE, BPDE-DNA, BTC, complement factor 3 (C3), C3a, C4, C5, C5a, CIO, CA125, CAD-8, Calcitonin, cAMP, carcinoembryonic antigen (CEA), carcinoma-associated antigen, Cathepsin A, Cathepsin B, Cathepsin C/DPPI, Cathepsin D, Cathepsin E, Cathepsin H, Cathepsin L, Cathepsin O, Cathepsin S, Cathepsin V, Cathepsin X/Z/P, CBL, CCI, CCK2, CCL, CCLl, CCLll, CCL12, CCL13, CCL 14, CCL15, CCL16, CCLl 7, CCL18, CCL19, CCL2, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CCL3, CCL4, CCL5, CCL6, CCL7, CCL8, CCL9/10, CCR, CCR1, CCR10, CCR10, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CD1, CD2, CD4, CD5, CD6, CD7, CD8, CD10, CDlla, CDllb, CDllc, CD13, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD27L, CD28, CD29, CD30, CD30L, CD32, CD33 (p67 proteins), CD34, CD38, CD40, CD40L, CD44, CD45, CD46, CD49a, CD52, CD54, CD55, CD56, CD61, CD64, CD66e, CD74, CD80 (B7-1), CD89, CD95, CD123, CD137, CD138, CD140a, CD146, CD147, CD148, CD152, CD164, CEACAM5, CFTR, cGMP, CINC, Clostridium botulinum toxin, Clostridium perfringens toxin, CKb8-l, CLC, CMV, CMV UL, CNTF, CNTN-1, COX, C-Ret, CRG-2, CT-1, CTACK, CTGF, CTLA-4, CX3CL1, CX3CR1, CXCL, CXCLl, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9, CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CXCR, CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, cytokeratin tumor-associated antigen, DAN, DCC, DcR3, DC-SIGN, Decay accelerating factor, des(l-3)-IGF-I (brain IGF-1), Dhh, digoxin, DNAM-1, Dnase, Dpp, DPPIV/CD26, Dtk, ECAD, EDA, EDA-A1, EDA-A2, EDAR, EGF, EGFR (ErbB-1), EMA, EMMPRIN, EN A, endothelin receptor, Enkephalinase, eNOS, Eot, eotaxinl, EpCAM, Ephrin B2/ EphB4, EPO, ERCC, E-selectin, ET-1, Factor Ila, Factor VII, Factor VIIIc, Factor IX, fibroblast activation protein (FAP), Fas, FcRl, FEN-1, Ferritin, FGF, FGF-19, FGF-2, FGF3, FGF-8, FGFR, FGFR-3, Fibrin, FL, FLIP, Flt-3, Flt-4, Follicle stimulating hormone, Fractalkine, FZD1, FZD2, FZD3, FZD4, FZD5, FZD6, FZD7, FZD8, FZD9, FZD10, G250, Gas 6, GCP-2, GCSF, GD2, GD3, GDF, GDF-1, GDF-3 (Vgr-2), GDF-5 (BMP-14, CDMP- 1), GDF-6 (BMP-13, CDMP-2), GDF-7 (BMP-12, CDMP-3), GDF-8 (Myostatin), GDF-9, GDF- 15 (MIC-1), GDNF, GDNF, GFAP, GFRa-1, GFR-alphal, GFR-alpha2, GFR-alpha3, GITR, Glucagon, Glut 4, glycoprotein Ilb/IIIa (GP Ilb/IIIa), GM-CSF, gpl30, gp72, GRO, Growth hormone releasing factor, Hapten (NP-cap or NIP-cap), HB-EGF, HCC, HCMV gB envelope glycoprotein, HCMV) gH envelope glycoprotein, HCMV UL, Hemopoietic growth factor (HGF), Hep B gpl20, heparanase, Her2, Her2/neu (ErbB-2), Her3 (ErbB-3), Her4 (ErbB-4), herpes simplex virus (HSV) gB glycoprotein, HSV gD glycoprotein, HGFA, High molecular weight melanoma-associated antigen (HMW-MAA), HIV gpl20, HIV IIIB gp 120 V3 loop, HLA, HLA-DR, HM1.24, HMFG PEM, HRG, Hrk, human cardiac myosin, human cytomegalovirus (HCMV), human growth hormone (HGH),

HVEM, 1-309, IAP, ICAM, ICAM-1, ICAM-3, ICE, ICOS, IFNg, Ig, IgA receptor, IgE, IGF, IGF binding proteins, IGF-1R, IGFBP, IGF-I, IGF-II, IL, IL-1, IL-1R, IL-2, IL-2R, IL-4, IL-4R, IL-5, IL-5R, IL-6, IL-6R, IL-8, IL- 9, IL-10, IL-12, IL-13, IL-15, IL-18, IL-18R, IL-23, interferon (INF)-alpha, INF-beta, INF- gamma, Inhibin, iNOS, Insulin A-chain, Insulin B-chain, Insulin-like growth factor 1, integrin alpha2, integrin alpha3, integrin alpha4, integrin alpha4/betal, integrin, alpha4/beta7, integrin alpha5 (alphaV), integrin alpha5/betal, integrin alpha5/beta3, integrin alpha6, integrin betal, integrin beta2, interferon gamma, IP-10, 1-TAC, JE, Kallikrein 2, Kallikrein 5, Kallikrein 6, , Kallikrein 11, Kallikrein 12, Kallikrein 14, Kallikrein 15, Kallikrein LI, Kallikrein L2, Kallikrein L3, Kallikrein L4, KC, KDR, Keratinocyte Growth Factor (KGF), laminin 5, LAMP, LAP, LAP (TGF- 1), Latent TGF-1, Latent TGF-1 bpl, LBP, LDGF, LECT2, Lefty, Lewis-Y antigen, Lewis-Y related antigen, LFA-1, LFA-3, Lfo, LIF, LIGHT, lipoproteins, LIX, LKN, Lptn, L-Selectin, LT-a, LT-b, LTB4, LTBP-1, Lung surfactant, Luteinizing hormone, Lymphotoxin Beta Receptor, Mac-1, MAdCAM, MAG, MAP2, MARC, MCAM, MCAM, MCK-2, MCP, M-CSF, MDC, Mer, METALLOPROTEASES, MGDF receptor, MGMT, MHC (HLA-DR), MIF, MIG, MIP, MIP-1-alpha, MK, MMAC1, MMP, MMP-1, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-2, MMP-24, MMP- 3, MMP-7, MMP-8, MMP-9, MPIF, Mpo, MSK, MSP, mucin (Mucl), MUC18, Muellerian- inhibitin substance, Mug, MuSK, NAIP, NAP, NCAD, N-Cadherin, NCA 90, NCAM, NCAM, Neprilysin, Neurotrophin-3,-4, or -6, Neurturin, Neuronal growth factor (NGF), NGFR, NGF-beta, nNOS, NO, NOS, Npn, NRG-3, NT, NTN, OB, OGG1, OPG, OPN, OSM, OX40L, OX40R, pl50, p95, PADPr, Parathyroid hormone, PARC, PARP, PBR, PBSF, PCAD, P-Cadherin, PCNA, PDGF, PDGF, PDK-1, PECAM, PEM, PF4, PGE, PGF, PGI2, PGJ2, PIN, PLA2, placental alkaline phosphatase (PLAP), P1GF, PLP, PP14, Proinsulin, Prorelaxin, Protein C, PS, PSA, PSCA, prostate specific membrane antigen (PSMA), PTEN, PTHrp, Ptk, PTN, R51, RANK, RANKL, RANTES, RANTES, Relaxin A-chain, Relaxin B-chain, renin, respiratory syncytial virus (RSV) F, RSV Fgp, Ret, Rheumatoid factors, RLIP76, RPA2, RSK, S100, SCF/KL, SDF-1, SERINE, Serum albumin, sFRP-3, Shh, SIGIRR, SK-1, SLAM, SLPI, SMAC, SMDF, SMOH, SOD, SPARC, Stat, STEAP, STEAP-II, TACE, TACI, TAG-72 (tumor-associated glycoprotein-72), TARC, TCA-3, T-cell receptors (e.g., T-cell receptor alpha/beta), TdT, TECK, TEM1, TEM5, TEM7, TEM8, TERT, testicular PLAP-like alkaline phosphatase, TfR, TGF, TGF-alpha, TGF-beta, TGF-beta Pan Specific, TGF-beta RI (ALK-5), TGF-beta RII, TGF-beta Rllb, TGF-beta RIII, TGF-betal, TGF-beta2, TGF-beta3, TGF-beta4, TGF-beta5, Thrombin, Thymus Ck-1, Thyroid stimulating hormone, Tie, TIMP, TIQ, Tissue Factor, TMEFF2, Tmpo, TMPRSS2, TNF, TNF-alpha, TNF-alpha beta, TNF-beta2, TNFc, TNF-RI, TNF-RII, TNFRSF10A (TRAIL Rl Apo-2, DR4), TNFRSFIOB (TRAIL R2 DR5, KILLER, TRICK-2A, TRICK-B), TNFRSF10C (TRAIL R3 DcRl, LIT, TRID), TNFRSF10D (TRAIL R4 DcR2, TRUNDD), TNFRSF11A (RANK ODF R, TRANCE R), TNFRSFllB (OPG OCIF, TR1), TNFRSF12 (TWEAK R FN14), TNFRSF13B (TACI), TNFRSF13C (BAFF R), TNFRSF14 (HVEM ATAR, HveA, LIGHT R, TR2), TNFRSF16 (NGFR p75NTR), TNFRSF17 (BCMA), TNFRSF18 (GITR AITR), TNFRSF19 (TROY TAJ, TRADE), TNFRSF19L (RELT), TNFRSFIA (TNF RI CD120a, p55-60), TNFRSFIB (TNF RII CD120b, p75-80), TNFRSF26 (TNFRH3), TNFRSF3 (LTbR TNF RIII, TNFC R), TNFRSF4 (OX40 ACT35, TXGP1 R), TNFRSF5 (CD40 p50), TNFRSF6 (Fas Apo-1, APT1, CD95), TNFRSF6B (DcR3 M68, TR6), TNFRSF7 (CD27), TNFRSF8 (CD30), TNFRSF9 (4-lBB CD137, ILA), TNFRSF21 (DR6), TNFRSF22 (DcTRAIL R2 TNFRH2), TNFRST23 (DcTRAIL Rl TNFRH1), TNFRSF25 (DR3 Apo-3, LARD, TR-3, TRAMP, WSL-1), TNFSF10 (TRAIL Apo-2 Ligand, TL2), TNFSF11 (TRANCE/RANK Ligand ODF, OPG Ligand), TNFSF12 (TWEAK Apo-3 Ligand, DR3 Ligand), TNFSF13 (APRIL TALL2), TNFSF13B (BAFF BLYS, TALL1, THANK, TNFSF20), TNFSF14 (LIGHT HVEM Ligand, LTg), TNFSF15 (TL1A/VEGI), TNFSF18 (GITR Ligand AITR Ligand, TL6), TNFSFIA (TNF-a Conectin, DIF, TNFSF2), TNFSF1B (TNF-b LTa, TNFSF1), TNFSF3 (LTb TNFC, p33), TNFSF4 (OX40 Ligand gp34, TXGP1), TNFSF5 (CD40 Ligand CD154, gp39, HIGM1, IMD3, TRAP), TNFSF6 (Fas Ligand Apo-1 Ligand, APT1 Ligand), TNFSF7 (CD27 Ligand CD70), TNFSF8 (CD30 Ligand CD153), TNFSF9 (4-lBB Ligand CD137 Ligand), TP-1, t-PA, Tpo, TRAIL, TRAIL R, TRAIL-R1, TRAIL-R2, TRANCE, transferring receptor, TRF, Trk, TROP-2, TSG, TSLP, tumor-associated antigen CA 125, tumor-associated antigen expressing Lewis Y related carbohydrate, TWEAK, TXB2, Ung, uPAR, uPAR-1, Urokinase, VCAM, VCAM-1, VECAD, VE-Cadherin, VE-cadherin-2, VEFGR-1 (flt-1), VEGF, VEGFR, VEGFR-3 (flt-4), VEGI, VIM, Viral antigens, VLA, VLA-1, VLA-4, VNR integrin, von Willebrands factor, WIF- 1, WNT1, WNT2, WNT2B/13, WNT3, WNT3A, WNT4, WNT5A, WNT5B, WNT6, WNT7A, WNT7B, WNT8A, WNT8B, WNT9A, WNT9A, WNT9B, WNT10A, WNT10B, WNT11, WNT16, XCL1, XCL2, XCR1, XCR1, XEDAR, XIAP, XPD, CTLA4 (cytotoxic T lymphocyte antigen-4), PD1 (programmed cell death protein 1), PD-L1 (programmed cell death ligand 1), LAG-3 (lymphocyte activation gene-3), TIM-3 (T cell immunoglobulin and mucin protein-3), receptors for hormones, and growth factors.

[0070] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody wherein the multispecific antibody comprises a second binding domain having specificity for a second antigen selected from the group consisting of: BCMA, CTLA4 (cytotoxic T lymphocyte antigen-4), PD1 (programmed cell death protein 1), PD-L1 (programmed cell death ligand 1), LAG-3 (lymphocyte activation gene-3), TIM-3, CD20, CD2, CD19, Her2, EGFR, EpCAM, FcyRIIIa (CD16), FcyRIIa (CD32a), FcyRIIb (CD32b), FcyRI (CD64), Toll-like receptors (TLRs), TLR4, TLR9, cytokines, IL-2, IL-5, IL-13, IL-6, IL-17, IL-12, IL-23, TNFa, TGFb, cytokine receptors, IL-2R, chemokines, chemokine receptors, growth factors, VEGF, and HGF.

[0071] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise at least a second antigen binding domain that specifically binds to an antigen, wherein said antibody comprises a multispecific format selected from the group consisting of: Fab-Fc-scFv, “bottle-opener”, Mab-scFv, Mab-Fv, Dual scFv, central Fv, central scFv, one-arm central scFv, Fab-Fab, Fab-Fv, mAb-Fv, mAb-Fab, DART, BiTE, common light chain-IgG, TandAb, Cross-Mab, SEED, BEAT, TrioMab, and DuetMab.

[0072] In certain embodiments are provided isolated nucleic acid sequences encoding the inventive CD3 binding domains and antibodies comprising them.

[0073] In certain embodiments are provided expression vectors comprising nucleic acid sequences encoding the inventive CD3 binding domains and antibodies comprising them.

[0074] In certain embodiments are provided host cells transfected, transformed, or transduced with a nucleic acid sequences encoding the inventive CD3 binding domains and antibodies comprising them.

[0075] In certain embodiments are provided host cells transfected, transformed, or transduced with vectors encoding the inventive CD3 binding domains and antibodies comprising them.

[0076] In certain embodiments are provided pharmaceutical compositions comprising one or more of the inventive CD3 binding domains and antibodies comprising them.

[0077] In certain embodiments are provided pharmaceutical compositions comprising one or more of the inventive CD3 binding domains and antibodies comprising them and a pharmaceutically acceptable carrier and/or excipient.

[0078] In certain embodiments are provided pharmaceutical compositions comprising one or more nucleic acids encoding one or more of the inventive CD3 binding domains and antibodies comprising them.

[0079] In certain embodiments are provided pharmaceutical compositions comprising one or more vectors encoding one or more of the inventive CD3 binding domains and antibodies comprising them and a pharmaceutically acceptable carrier and/or excipient.

[0080] In certain embodiments are provided methods of treating or delaying the progression of a disorder in a mammal in need of such treating, the methods comprising adimistering one or more of the inventive CD3 binding domains and antibodies comprising them, wherein the disorder is decreased or ameliorated as a result of said administering. In certain embodiments are provided methods of preventing or decreasing risk of developing a disorder in a mammal by administering one or more of the inventive CD3 binding domains and antibodies comprising them, wherein the disorder is prevented as a result of said administering. In certain embodiments are provided methods of treating a disorder in a mammal in need of such treating, wherein the disorder comprises a proliferative disorder, an oncological disorder, an immuno-oncological disorder, a neurological disorder, a neurodegenerative disorder, or an autoimmune disorder, comprising administering one or more of the inventive CD3 binding domains and antibodies comprising them, wherein the disorder is decreased or ameliorated as a result of said administering. In certain embodiments such methods further comprise administering to the mammal an additional therapeutic agent. In certain embodiments such mammal is a human.

[0081] In certain embodiments is provided a heterodimeric CD3 fusion protein comprising: a first polypeptide chain comprising a CD3 epsilon polypeptide fused to a first Fc region; and a second polypeptide chain comprising CD3 delta polypeptide fused to a second Fc region. In certain embodiments, the CD3 epsilon polypeptide comprises a human CD3 epsilon polypeptide and the CD3 delta polypeptide comprises a human CD3 delta polypeptide. In certain embodiments, the CD3 epsilon polypeptide is a human CD3 epsilon polypeptide and the CD3 delta polypeptide is a human CD3 delta polypeptide. In certain embodiments, the CD3 epsilon polypeptide comprises a cynomolgus CD3 epsilon polypeptide and the CD3 delta polypeptide comprises a cynomolgus CD3 delta polypeptide. In certain embodiments the CD3 epsilon polypeptide is a cynomolgus CD3 epsilon polypeptide and the CD3 delta polypeptide is a cynomolgus CD3 delta polypeptide. In certain embodiments the first polypeptide of the heterodimeric CD3 fusion protein comprises the following amino acid sequence: QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6716); and the second polypeptide chain comprises the following amino acid sequence: FKIPIEELEDRVFVNCNTSITWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRMCQSCVELDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6717). In certain embodiments the first polypeptide of the heterodimeric CD3 fusion protein comprises the following amino acid sequence: QDGNEEMGSITQTPYQVSISGTTVILTCSQHLGSEAQWQHNGKNKEDSGDRLFLPEFSEMEQSGYYVCYPRGSNPEDASHHLYLKARVCENCMEMDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6718); and the second polypeptide chain comprises the following amino acid sequence: FKIPVEELEDRVFVKCNTSVTWVEGTVGTLLTNNTRLDLGKRILDPRGIYRCNGTDIYKDKESAVQVHYRMCQNCVELDPGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL

HNHYTQKSLSLSPGK (SEQ ID NO: 6719). In certain embodiments are provided uses of such heterodimeric CD3 fusion proteins in identifying, isolating, selecting, generating, and/or characterizing CD3 binding domains and antibodies comprising them.

Detailed Description of the Invention

[0082] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used herein, the term "about," when used in reference to a particular recited numerical value, means that the value may vary from the recited value by no more than 1 %. For example, as used herein, the expression "about 100" includes 99 and 101 and all values in between (e.g., 99.1, 99.2, 99.3, 99.4, etc.).

[0083] It is understood that aspects and embodiments of the invention described herein include “comprising,” “consisting,” and “consisting essentially of” aspects and embodiments.

[0084] “Cluster of Differentiation 3” or ”CD3”, generally refers to any native CD3 from any vertebrate source, including mammals such as primates (e.g., humans) and rodents (e.g., mice and rats), unless otherwise indicated, including, for example, CD3ε, CD3γ, CD3α, and CD3β chains. The term encompasses “full-length,” unprocessed CD3 (e.g., unprocessed or unmodified CD3ε or CD3γ), as well as any form of CD3 that results from processing in the cell. The term also encompasses naturally occurring variants of CD3, including, for example, splice variants or allelic variants. CD3 includes, for example, human CD3ε protein (NCBI RefSeq No. NP_000724), which is 207 amino acids in length, and human CD3γ protein (NCBI RefSeq No. NP_000064), which is 182 amino acids in length. The term also refers to either the human or cynomolgus CD3epsilon protein, the amino acid sequence for which is depcted, for example in Figure 18 herein. “CD3εN27” and “CD3εN13” refer to the N-terminal 27 amino acids and the N-terminal 13 amino acids, respectively, of CD3, and optionally containing chemical modifications or cojugations made thereto.

[0085] The “class” of an antibody refers to the type of constant domain or constant region possessed by its heavy chain. There are five major classes of antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG_1,

IgG_2, IgG_3, IgG_4, IgA_1, and IgA_2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α, δ, ε, γ, and μ, respectively.

[0086] The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents a cellular function and/or causes cell death or destruction. Cytotoxic agents include, but are not limited to, radioactive isotopes (e.g., At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32}, Pb^{212} and radioactive isotopes of Lu); chemotherapeutic agents or drugs (e.g., methotrexate, adriamicin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents); growth inhibitory agents; enzymes and fragments thereof such as nucleolytic enzymes; antibiotics; toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof; and the various antitumor or anticancer agents disclosed below.

[0087] A "disorder" refers to any condition or disease that would benefit from treatment including, but not limited to, chronic and acute disorders or diseases including those pathological conditions which predispose a mammal to the disorder in question.

[0088] The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder comprises cancer. In one embodiment, the cell proliferative disorder comprises a tumor.

[0089] The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include, but not limited to, squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer and gastrointestinal stromal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, superficial spreading melanoma, lentigo maligna melanoma, acral lentiginous melanomas, nodular melanomas, multiple myeloma and B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); hairy cell leukemia; chronic myeloblastic leukemia; and post-transplant lymphoproliferative disorder (PTLD), as well as abnormal vascular proliferation associated with phakomatoses, edema (such as that associated with brain tumors), Meigs' syndrome, brain, as well as head and neck cancer, and associated metastases. In certain embodiments, cancers that are amenable to treatment by the antibodies of the invention include breast cancer, colorectal cancer, rectal cancer, non-small cell lung cancer, glioblastoma, non-Hodgkins lymphoma (NHL), renal cell cancer, prostate cancer, liver cancer, pancreatic cancer, soft-tissue sarcoma, kaposi's sarcoma, carcinoid carcinoma, head and neck cancer, ovarian cancer, mesothelioma, and multiple myeloma. In some embodiments, the cancer is selected from: small cell lung cancer, gliblastoma, neuroblastomas, melanoma, breast carcinoma, gastric cancer, colorectal cancer (CRC), and hepatocellular carcinoma. Yet, in some embodiments, the cancer is selected from: non-small cell lung cancer, colorectal cancer, glioblastoma and breast carcinoma, including metastatic forms of those cancers. In other embodiments, the cancer is selected from a class of mature B-Cell cancers excluding Hodgkin's Lymphoma but including germinal-center B-cell-like (GCB) DLBCL, activated B-cell-like (ABC) DLBCL, follicular lymphoma (FL), mantle cell lymphoma (MCL), acute myeloid leukemia (AML), chronic lymphoid leukemia (CLL), marginal zone lymphoma (MZL), small lymphocytic leukemia (SLL), lymphoplasmacytic lymphoma (LL), Waldenstrom macroglobulinemia (WM), central nervous system lymphoma (CNSL), Burkitt's lymphoma (BL), B-cell prolymphocytic leukemia, Splenic marginal zone lymphoma, Hairy cell leukemia, Splenic lymphoma/leukemia, unclassifiable, Splenic diffuse red pulp small B-cell lymphoma, Hairy cell leukemia variant, Waldenström macroglobulinemia, Heavy chain diseases, a Heavy chain disease, γ Heavy chain disease, μ Heavy chain disease, Plasma cell myeloma, Solitary plasmacytoma of bone, Extraosseous plasmacytoma, Extranodal marginal zone lymphoma of mucosa-associated lymphoid tissue (MALT lymphoma), Nodal marginal zone lymphoma, Pediatric nodal marginal zone lymphoma, Pediatric follicular lymphoma, Primary cutaneous follicle centre lymphoma, T-cell/histiocyte rich large B-cell lymphoma, Primary DLBCL of the CNS, Primary cutaneous DLBCL, leg type, EBV-positive DLBCL of the elderly, DLBCL associated with chronic inflammation, Lymphomatoid granulomatosis, Primary mediastinal (thymic) large B-cell lymphoma, Intravascular large B-cell lymphoma, ALK-positive large B-cell lymphoma, Plasmablastic lymphoma, Large B-cell lymphoma arising in HHV8-associated multicentric Castleman disease, Primary effusion lymphoma: B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma and Burkitt lymphoma, and B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma and classical Hodgkin lymphoma.

[0090] Ther term “tumor” as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. The terms “cancer”, “cancerous”, “cell proliferative disorder”, “proliferative disorder” and “tumor” are not mutually exclusive as referred to herein.

[0091] The term “tumor antigen” as used herein, may be understood as those antigens that are presented on tumor cells. These antigens can be presented on the cell surface with an extracellular part, which is often combined with a transmembrane and cytoplasmic part of the molecule. These antigens can sometimes be presented only by tumor cells and never by the normal ones. Tumor antigens can be exclusively expressed on tumor cells or might represent a tumor specific mutation compared to normal cells. In this case, they are called tumor-specific antigens. More common are tumor antigens that are presented by tumor cells and normal cells, and they are called tumor-associated antigens. These tumor-associated antigens can be overexpressed compared to normal cells or are accessible for antibody binding in tumor cells due to the less compact structure of the tumor tissue compared to normal tissue.

[0092] The term "EC_{50}" refers to the "half maximal effective concentration", which value measures the effectiveness of compound (e.g. an anti-CD3 bonding domain-comprising antibody) towards a biological or biochemical utility. This quantitative measure indicates the quantity or concentration required for a particular compound or antibody to elicit a given biological process to half of the maximal response.

[0093] “Effector functions” refer to those biological activities attributable to the Fc region of an antibody, which vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation.

[0094] An “effective amount” of a compound, for example, an anti-CD3 antibody of the invention or a composition (e.g., pharmaceutical composition) thereof, is at least the minimum amount required to achieve the desired therapeutic or prophylactic result, such as a measurable improvement or prevention of a particular disorder (e.g., a cell proliferative disorder, e.g., cancer). An effective amount herein may vary according to factors such as the disease state, age, sex, and weight of the patient, and the ability of the antibody to elicit a desired response in the individual. An effective amount is also one in which any toxic or detrimental effects of the treatment are outweighed by the therapeutically beneficial effects. For prophylactic use, beneficial or desired results include results such as eliminating or reducing the risk, lessening the severity, or delaying the onset of the disease, including biochemical, histological and/or behavioral symptoms of the disease, its complications and intermediate pathological phenotypes presenting during development of the disease. For therapeutic use, beneficial or desired results include clinical results such as decreasing one or more symptoms resulting from the disease, increasing the quality of life of those suffering from the disease, decreasing the dose of other medications required to treat the disease, enhancing effect of another medication such as via targeting, delaying the progression of the disease, and/or prolonging survival. In the case of cancer or tumor, an effective amount of the drug may have the effect in reducing the number of cancer cells; reducing the tumor size; inhibiting (i.e., slow to some extent or desirably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and desirably stop) tumor metastasis; inhibiting to some extent tumor growth; and/or relieving to some extent one or more of the symptoms associated with the disorder. An effective amount can be administered in one or more administrations. For purposes of this invention, an effective amount of drug, compound, or pharmaceutical composition is an amount sufficient to accomplish prophylactic or therapeutic treatment either directly or indirectly. As is understood in the clinical context, an effective amount of a drug, compound, or pharmaceutical composition may or may not be achieved in conjunction with another drug, compound, or pharmaceutical composition.

Thus, an "effective amount" may be considered in the context of administering one or more therapeutic agents, and a single agent may be considered to be given in an effective amount if, in conjunction with one or more other agents, a desirable result may be or is achieved.

[0095] The term "Fc region" herein is used to define a C-terminal region of an immunoglobulin heavy chain that contains at least a portion of the constant region. The term includes native sequence Fc regions and variant Fc regions. In one embodiment, a human IgG heavy chain Fc region extends from Cys226, or from Pro230, to the carboxyl-terminus of the heavy chain. However, the C-terminal lysine (Lys447) of the Fc region may or may not be present. Unless otherwise specified herein, numbering of amino acid residues in the Fc region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991.

[0096] "Framework" or "FR" refers to variable domain residues other than complementary determining region (CDR) residues. The FR of a variable domain generally consists of four FR domains: FR1, FR2, FR3, and FR4. Accordingly, the CDR and FR sequences generally appear in the following sequence in VH (or VL): FR1-H1(L1)-FR2-H2(L2)-FR3-H3(L3)-FR4.

[0097] The terms "full-length antibody," "intact antibody," and "whole antibody" are used herein interchangeably to refer to an antibody having a structure substantially similar to a native antibody structure or having heavy chains that contain an Fc region as defined herein.

[0098] A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell either in vitro or in vivo. In one embodiment, growth inhibitory agent is growth inhibitory antibody that prevents or reduces proliferation of a cell expressing an antigen to which the antibody binds. In another embodiment, the growth inhibitory agent may be one which significantly reduces the percentage of cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in Mendelsohn and Israel, eds., The Molecular Basis of Cancer, Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami et al. (W.B. Saunders, Philadelphia, 1995), e.g., p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, RHONE-POULENC RORER), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, BRISTOL-MYERS SQUIBB). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

[0099] A phrase that includes an antigen and the term, "-positive", such as "HER2-positive", means that a disease, condition, or disorder is characterized, inter alia, by higher than normal levels of the referenced antigen or target. In certain embodiments, the antigen or target comprises a moiety that is expressed or otherwise present on cancer cells at a level that is higher than on normal cells.

[0100] The terms "host cell," "host cell line," and "host cell culture" are used interchangeably and refer to cells into which exogenous nucleic acid has been introduced, including the progeny of such cells. Host cells include "transformants" and "transformed cells," which include the primary transformed cell and progeny derived therefrom without regard to the number of passages. Progeny may not be completely identical in nucleic acid content to a parent cell, but may contain mutations. Mutant progeny that have the same function or biological activity as screened or selected for in the originally transformed cell are included herein.

[0101] A "human antibody" is one which possesses an amino acid sequence which corresponds to that of an antibody produced by a human or a human cell or derived from a non-human source that utilizes human antibody repertoires or other human antibody-encoding sequences. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues. Human antibodies can be produced using various techniques known in the art, including phage-display libraries. Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991). Also available for the preparation of human monoclonal antibodies are methods described in Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985); Boerner et al., J. Immunol.

147(1):86-95 (1991). See also van Dijk and van de Winkel, Curr. Opin. Pharmacol., 5: 368-74 (2001). Human antibodies can be prepared by administering the antigen to a transgenic animal that has been modified to produce such antibodies in response to antigenic challenge, but whose endogenous loci have been disabled, e.g., immunized xenomice (see, e.g., U.S. Pat. Nos. 6,075,181 and 6,150,584 regarding XENOMOUSE technology). See also, for example, Li et al., Proc. Natl. Acad. Sci. USA, 103:3557-3562 (2006) regarding human antibodies generated via a human B-cell hybridoma technology. The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human mAbs of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs and in particular CDR3. However, the term "human antibody", as used herein, is not intended to include mAbs in which CDR sequences derived from the germline of another mammalian species (e.g., mouse), have been grafted onto human FR sequences.

[0102] A “human consensus framework” is a framework which represents the most commonly occurring amino acid residues in a selection of human immunoglobulin VL or VH framework sequences. Generally, the selection of human immunoglobulin VL or VH sequences is from a subgroup of variable domain sequences. Generally, the subgroup of sequences is a subgroup as in Kabat et al., Sequences of Proteins of Immunological Interest, Fifth Edition, NIH Publication 91-3242, Bethesda Md. (1991), vols. 1-3. In one embodiment, for the VL, the subgroup is subgroup kappa I as in Kabat et al., supra. In one embodiment, for the VH, the subgroup is subgroup III as in Kabat et al., supra.

[0103] A “humanized antibody” refers to an antibody comprising amino acid residues from non-human CDRs and amino acid residues from human FRs. In certain embodiments, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the (e.g., CDRs) correspond to those of a non-human antibody, and all or substantially all of the FRs correspond to those of a human antibody. A humanized antibody optionally may comprise at least a portion of an antibody constant region derived from a human antibody. A humanized form of an antibody, e.g., a non-human antibody, refers to an antibody that has undergone humanization.

[0104] An “immunoconjugate” is an antibody conjugated to one or more heterologous molecule(s), including but not limited to a cytotoxic agent.

[0105] A “subject” or an “individual” is a mammal. Mammals include, but are not limited to, domesticated animals (e.g., cows, sheep, cats, dogs, and horses), primates (e.g., humans and non-human primates such as monkeys), rabbits, and rodents (e.g., mice and rats). In certain embodiments, the subject or individual is a human.

[0106] An “isolated antibody” is one which has been separated from a component of its natural environment. In some embodiments, an antibody is purified to greater than 95% or 99% purity as determined by, for example, electrophoretic (e.g., SDS-PAGE, isoelectric focusing (IEF), capillary electrophoresis) or chromatographic (e.g., ion exchange or reverse phase HPLC). For review of methods for assessment of antibody purity, see, e.g., Flatman et al., J. Chromatogr. B 848:79-87 (2007).

[0107] An “isolated nucleic acid” refers to a nucleic acid molecule that has been separated from a component of its natural environment. An isolated nucleic acid includes a nucleic acid molecule contained in cells that ordinarily contain the nucleic acid molecule, but the nucleic acid molecule is present extrachromosomally or at a chromosomal location that is different from its natural chromosomal location.

[0108] The term “monoclonal antibody” or “mAb” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical and/or bind the same epitope, except for possible variant antibodies, e.g., containing naturally occurring mutations or arising during production of a monoclonal antibody preparation, such variants generally being present in minor amounts. In contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. Thus, the modifier “monoclonal” indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by a variety of techniques, including but not limited to the hybridoma method, recombinant DNA methods, phage-display methods, and methods utilizing transgenic animals containing all or part of the human immunoglobulin loci, such methods and other exemplary methods for making monoclonal antibodies being described herein.

[0109] The term "pharmaceutical formulation" or "pharmaceutical composition" refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein, such as the inventive CD3 binding domains and antibodies comprsising them, to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered.

[0110] A "pharmaceutically acceptable carrier" refers to an ingredient in a pharmaceutical formulation, other than an active ingredient, which is nontoxic to a subject. A pharmaceutically acceptable carrier includes, but is not limited to, a buffer, excipient, stabilizer, or preservative.

[0111] By the phrase "therapeutically effective amount" is meant an amount that produces the desired effect for which it is administered. The exact amount will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (see, for example, Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding).

[0112] An "immune response" or "immunological response" as used herein, in a subject refers to the development of a humoral immune response, a cellular- immune response, or a humoral and a cellular immune response to an antigen/immunogen. A "humoral immune response" refers to one that is at least in part mediated by antibodies. A "cellular immune response" is one mediated by T-lymphocytes or other white blood cells or both, and includes the production of cytokines, chemokines and similar molecules produced by activated T-cells, white blood cells, or both. Immune responses can be determined using standard immunoassays and neutralization assays, which are known in the art.

[0113] "Immunogenicity", as used herein, refers to the capability of a protein or polypeptide to elicit an immune response directed specifically against a bacteria or virus that causes the identified disease.

[0114] As used herein, “treatment” (and grammatical variations thereof such as “treat” or “treating”) refers to clinical intervention in an attempt to alter the natural course of the individual being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include, but are not limited to, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. In some embodiments, antibodies of the invention are used to delay development of a disorder or disease or to slow the progression of a disorder or disease.

[0115] As used herein, “delaying progression” of a disorder or disease means to defer, hinder, slow, retard, stabilize, and/or postpone development of the disease or disorder (e.g., a cell proliferative disorder, e.g., cancer). This delay can be of varying lengths of time, depending on the history of the disease and/or individual being treated. As is evident to one skilled in the art, a sufficient or significant delay can, in effect, encompass prevention, in that the individual does not develop the disease. For example, a late stage cancer, such as development of metastasis, may be delayed.

[0116] By “reduce” or “inhibit” is meant the ability to cause an overall decrease, for example, of 20% or greater, of 50% or greater, or of 75%, 85%, 90%, 95%, or greater. In certain embodiments, reduce or inhibit can refer to the effector function of an antibody that is mediated by the antibody Fc region, such effector functions specifically including complement-dependent cytotoxicity (CDC), antibody-dependent cellular cytotoxicity (ADCC), and antibody-dependent cellular phagocytosis (ADCP).

[0117] As used herein, the terms "prevent," "preventing," and "prevention" refer to the prevention or inhibition of the development or onset of a disorder or disease.

[0118] As used herein, the terms “ameliorate” and “alleviate” refer to a reduction or diminishment in the severity a condition or any symptoms thereof.

[0119] The term "antibody" herein is used in the broadest sense and encompasses various antibody structures, including but not limited to monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments so long as they exhibit the desired antigen-binding activity. With regard to multispecific antibodies, such antibodies comprise at least two different antigen binding domains which recognized and specifically bind to at least two different antigens. With regard to bispecific antibodies, such antibodies comprise two different antigen binding domains which recognized and specifically bind to at least two different antigens. A "different antigen" or "different antigens" may refer to different and/or distinct proteins, polypeptides, or molecules; as well as different and/or distinct epitopes, which epitopes may be contained within one protein, polypeptide, or other molecule. Unless specifically indicated otherwise, the term "antibody," as used herein, shall also be understood to encompass, in addition to the above, antibody molecules comprising two immunoglobulin heavy chains and two immunoglobulin light chains (i.e., "full antibody molecules") as well as antigen-binding fragments thereof. The terms "antigen-binding portion" of an antibody, "antigen-binding fragment" of an antibody, and the like, as used herein, include any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex.

[0120] An "antibody" and "antibodies" may also refer to immunoglobulin molecules comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains interconnected by disulfide bonds (i.e., "full antibody molecules"), as well as multimers thereof (e.g. IgM) or antigen-binding fragments thereof. Each heavy chain is comprised of a heavy chain variable region ("VH") and a heavy chain constant region (comprised of domains C_H1, C_H2 and C_H3). Each light chain is comprised of a light chain variable region ("VL") and a light chain constant region ("CL"). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In certain embodiments of the invention, the FRs of the antibody (or antigen binding fragment thereof) may be identical to the human germline sequences, or may be naturally or artificially modified. An amino acid consensus sequence may be defined based on a side-by-side analysis of two or more CDRs. Accordingly, the CDRs in a heavy chain are designated "CHRH1", "CDRH2", and "CDRH3", respectively, and the CDRs in a light chain are designated "CDRL1", "CDRL2", and "CDRL3".

[0121] An "antibody fragment" refers to a molecule other than an intact antibody that comprises a portion of an intact antibody that binds the antigen to which the intact antibody binds. Examples of antibody fragments include but are not limited to Fv, Fab, Fab', Fab'-SH , F(ab') 2; diabodies ; linear antibodies; single-chain antibody molecules (e.g. scFv) ; and multispecific antibodies formed from antibody fragments.

[0122] By "binding domain" or "antigen binding domain" is meant a part of an antibody, compound, or a molecule that specifically binds to a target epitope, antigen, ligand, or receptor. Binding domains include but are not limited to antibodies (e.g., monoclonal, polyclonal, recombinant, humanized, and chimeric antibodies), antibody fragments or portions thereof (e.g., Fab fragments, Fab'$_2$, scFv antibodies, Fv fragments, SMIP, domain antibodies, diabodies, minibodies, scFv-Fc, affibodies, nanobodies, and VH and/or VL domains of antibodies) , receptors, ligands, aptamers, and other molecules having an identified binding partner.

[0123] An "affinity matured antibody" refers to an antibody with one or more alterations in one or more complementary determining regions (CDRs), compared to a parent antibody which does not possess such alterations, such alterations resulting in an improvement in the affinity of the antibody for antigen. Substitution of one or more CDR residues or omission of one or more CDRs is also possible. Antibodies have been described in the scientific literature in which one or two CDRs can be dispensed with for binding. Padlan et al. (1995 FASEB J. 9:133-139) analyzed the contact regions between antibodies and their antigens, based on published crystal structures, and concluded that only about one fifth to one third of CDR residues actually contact the antigen. Padlan also found many antibodies in which one or two CDRs had no amino acids in contact with an antigen (see also, Vajdos et al. 2002 J Mol Biol 320:415-428). CDR residues not contacting antigen can be identified based on previous studies (for example residues H60-H65 in CDRH2 are often not required), from regions of Kabat CDRs lying outside Chothia CDRs, by molecular modeling and/or empirically. If a CDR or residue(s) thereof is omitted, it is usually substituted with an amino acid occupying the corresponding position in another human antibody sequence or a consensus of such sequences. Positions for substitution within CDRs and amino acids to substitute can also be selected empirically.

[0124] Fully human monoclonal antibodies as disclosed herein may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The present invention includes antibodies, and antigen-binding fragments thereof, which are derived from any of the amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are mutated to the corresponding residue(s) of the germline sequence from which the antibody was derived, or to the corresponding residue(s) of another human germline sequence, or to a conservative amino acid substitution of the corresponding germline residue(s) (such sequence changes are referred to herein collectively as "germline mutations"). A person of ordinary skill in the art, starting with the heavy and light chain variable region sequences disclosed herein, can easily produce numerous antibodies and antigen-binding fragments which comprise one or more individual germline mutations or combinations thereof. In certain embodiments, all of the framework and/or CDR residues within the V_H and/or V_L domains are mutated back to the residues found in the original germline sequence from which the antibody was derived. In other embodiments, only certain residues are mutated back to the original germline sequence, e.g., only the mutated residues found within the first 8 amino acids of FR1 or within the last 8 amino acids of FR4, or only the mutated residues found within CDR1, CDR2 or CDR3. In other embodiments, one or more of the framework and/or CDR residue(s) are mutated to the corresponding residue(s) of a different germline sequence (i.e., a germline sequence that is different from the germline sequence from which the antibody was originally derived). Furthermore, the antibodies of the present invention may contain any combination of two or more germline mutations within the framework and/or CDR regions, e.g., wherein certain individual residues are mutated to the corresponding residue of a particular germline sequence while certain other residues that differ from the original germline sequence are maintained or are mutated to the corresponding residue of a different germline sequence. Once obtained, antibodies and antigen-binding fragments that contain one or more germline mutations can be easily tested for one or more desired property such as, improved binding specificity, increased binding affinity, improved or enhanced antagonistic or agonistic biological properties (as the case may be), reduced immunogenicity, etc. Antibodies and antigen-binding fragments obtained in this general manner are encompassed within the present invention.

[0125] The present invention also includes fully monoclonal antibodies comprising variants of any of the CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes antibodies having CDR amino acid sequences with, e.g., 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the CDR amino acid sequences disclosed herein.

[0126] The terms “anti-CD3 antibody”, “anti-CD3 binding domain-comprising antibody”, “an antibody that binds to CD3”, “a CD3 binding domain”, “an antibody comprising a CD3 binding domain”, and the like refer to an antibody (or a CD3 binding domain) that is capable of binding CD3 with sufficient affinity and/or specificity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting CD3. In one embodiment, the extent of binding of an anti-CD3 antibody to an unrelated, non-CD3 protein is less than about 10% of the binding of the antibody to CD3 as measured, e.g., by one of a variety of solution and surface based affinity measurement methodologies and instrumentation, such as, e.g., biolayer interferometry (BLI), surface plasmon resonance (SPR), solution equilibrium based kinetic exclusion assays, KinExA direct association, assays using FORTEBIO instruments and reagents, such as Octet RED 384 and HTX BLI-based instruments, enzyme-linked immunosorbent assays (ELISA), and radioimmunoassay (RIA) (see, e.g., Estep et al, *MAbs*, Vol. 5, pages 270-278 (2013); Yu et al., *J Biomol Screen*, Vol. 21, pages 88-95 (2016)). In certain embodiments, an antibody that binds to CD3 has a dissociation constant (Kd) of < 1mM, < 100 nM, < 10 nM, < 1 nM, < 0.1 nM, < 0.01 nM, or < 0.001 nM (e.g. 10^{-8} M or less, e.g. from 10^{-8} M to 10^{-13} M, e.g., from 10^{-9} M to 10^{-13} M). In certain embodiments, an anti-CD3 antibody binds to an epitope of CD3 that is conserved among CD3 from different species.

[0127] The term “developable” refers to extent to which one or more polypeptides in a plurality of polypeptides possess desirable characteristics, such as, e.g.: desirable expression, for example, in mammalian cells; solubility; viscosity; aggregation; chemical and/or physical stability; desirable “shelf-life”; melting temperature; pharmacokinetic profiles; circulation half-life; and clearance characteristics. Such characteristics may serve as indicia, independently, as combinations of sub-sets of such indicia, or in totality, for the likelihood that such one or more polypeptides may be successfully developed as a therapeutic candidate, and ultimately an approved drug. Accordingly, as understood in the art, generally, polypeptides with desirable developability characteristics possess, e.g., relatively high solubility, relatively low viscosity, relatively low propensity for aggregation, relatively high chemical stability, relatively high physical stability, relatively long "shelf life", relatively high melting temperature, relatively long circulation half-life, relatively long clearance time, and the like. Polypeptides with undesirable developability characteristics possess, e.g., relatively low solubility, relatively high viscosity, relatively high propensity for aggregation, relatively poor chemical stability, relatively poor physical stability, relatively short "shelf life", relatively low melting temperature, relatively short circulation half-life, relatively short clearance time, and the like.

[0128] Methods and assays which may be employed to ascertain the degree to which polypeptides, such as the inventive CD3 binding domains and antibodies comprising them, possess such desirable (or undesirable, as the case may be) developability characteristics are available in the art, and include, for example; those disclosed in WO 2014/179363 and Xu et al., *Protein Eng Des Sol*, Vol. 26, pages 663-670 (2013); SMP and SCP assays and the like cross interaction chromatography (CIC); self-interaction chromatography (SIC); dynamic light scattering; size exclusion chromatography (SEC), dynamic light scattering (DLS) spectroscopy; photon correlation spectroscopy; quasi-elastic light scattering, circular dichroism (CD), viscosity measurements; whole cell binding; tissue micro array methodologies; BVP ELISA assays; AC-SINS assays (Liu et al; *MAbs*, Vol. 6, pages 483-492 (2014); differential scanning calorimetry; and the like (see, e.g., He et al., *J. Pharm. Sci.*, Vol. 100(4), pp. 1330-1340 (2011); Wagner et al., *Pharm. Develop. & Technol* (posted online 2012; hyper-text transfer protocol: informahealthcare.com/doi/abs/10.3109/10837450.2011.649851); Hotzel et al., *mAbs*, Vol. 4(6), pages 753-7601 (2012); Weiqiang et al., *J. Pharm. Sci.*, Vol. 101(5), pp. 1701-1720 (2012); Banks et al., *J. Pharm. Sci.*, Vol. 101(8), pp. 2720-2732 (2012); Lie et al., *J. Pharm. Sci.*, Vol. 94(9), pp. 1928-1948 (2005); and Payne et al., *Biopolymers*, Vol. 85(5), pp. 527-533 (2006)).

[0129] Furthermore polypeptides, such as the inventive CD3 binding domains and antibodies comprising them selected or identified as possessing enhanced developability are referred to as "developable". Polypeptides that are detected in accordance with the disclosed and claimed methods as possessing decreased developability are so detected by virtue of their interaction with the disclosed and claimed PSRs, and as such are referred to as "polyspecific" polypeptides. Such polyspecific polypeptides are further referred to as relatively "undevelopable" or relatively "non-developable" polypeptides.

[0130] Any means for detecting an interaction between one or more polypeptides and a moiety with which the one or more polypeptide interacts may be employed in accordance with the disclosed and claimed methods. Exemplary such means include, e.g.: flow cytometry; magnetic-activated cell sorting (MAGS); fluorescence assisted cell sorting (FACS); immunohistochemistry; column and/or affinity chromatography or separations; sedimentation methodologies (e.g., centrifugation); immunoprecipitation; two-hybrid assays, such as mammalian two-hybrid assays and yeast two-hybrid assays; fluorescence resonance energy transfer (FRET) assays; affinity chromatography; and the like. In certain embodiments detecting such an interaction comprises employing magnetic-activated cell sorting (MAGS); fluorescence assisted cell sorting (FACS); and/or combinations of magnetic-activated cell sorting (MAGS) and fluorescence assisted cell sorting (FACS).

[0131] A “developability score” also known as a “developability profile”, refers to an index that may be assigned to the inventive CD3 binding domains and/or antibodies comprising them upon assessing developability as described herein and in, e.g., WO 2014/179363 and Xu et al., *Protein Eng Des Sol*, Vol. 26, pages 663-670 (2013). The developability score is thus a measure or metric by which developability of CD3 binders and/or antibodies comprising them may be assessed, compared, and/or ranked. Such developability scores serve as a measure of the degree of interaction of CD3 binders and antibodies comprising them. The degree of interaction may be assessed by any number of means available in the art that provides an output value that correlates with a strength or affinity of a polypeptide for a moiety to which it is bound. Exemplary such means include flow cytometry means, such as FACS; ELISA; quantitative immunoaffinity assays or immunoprecipitation assays; mammalian two-hybrid or yeast two-hybrid assays, and the like. In the context of FACS, as demonstrated in the Examples, a degree of interaction between polypeptides in the plurality and the PSR may be ascertained by generating a mean fluorescence intensity (MFI) for each polypeptide-PSR interaction that is detected, and then ordering the MFI in either ascending or descending order, thereby ranking the polypeptides in the plurality according to the relative degree of interaction between each detected polypeptide and the PSR. Such a ranking provides for a ranking of polypeptides of the plurality such that those polypeptides possessing enhanced developability are readily ascertained, as are those polypeptides possessing decreased developability. In certain embodiments, an MFI of 500 or less is demonstrative of a polypeptide possessing enhanced developability. In certain embodiments, an MFI of 400 or less is demonstrative of a polypeptide possessing enhanced developability. In certain embodiments, an MFI of 300 or less is demonstrative of a polypeptide possessing enhanced developability. In certain embodiments, an MFI of 200 or less is demonstrative of a polypeptide possessing enhanced developability. In certain embodiments, an MFI of 100 or less is demonstrative of a polypeptide possessing enhanced developability. In certain embodiments, an MFI of 1000 or more is demonstrative of polypeptide possessing decreased developability. In certain embodiments, an MFI of 900 or more is demonstrative of polypeptide possessing decreased developability. In certain embodiments, an MFI of 800 or more is demonstrative of polypeptide possessing decreased developability. In certain embodiments, an MFI of 700 or more is demonstrative of polypeptide possessing decreased developability. In certain embodiments, an MFI of 600 or less is demonstrative of a polypeptide possessing decreased developability.

[0132] A developability score may also take the form of a normalized score, for example, on a scale of 0.0 to 1.0, in which the score of one or more test CD3 binders and/or antibodies comprising them are normalized to the developability score determined by performing the assay with a standard, or control, polypeptide or antibody. An exemplary such standard or control antibody may comprise, e.g., a hen egg lysozyme-binding (HEL) antibody, such as ADI-03847.

[0133] The terms “cytokine release syndrome”, “cytokine release crisis”, or “cytokine storm” refers to a pro-inflammatory, positive feedback loop between cytokines and immune cells leading to excessive or uncontrolled release of pro-inflammatory cytokines by cells within immune system (e.g., T cells) (see, e.g., Lee et al., Blood, Vol. 124, pages 188-195 (2014) and Tisoncik et al., Microbiol Mol Biol Rev, Vol. 76, pages 16-32 (2012). Without wishing to be bound by any theory, it is believed that upon stimulation and activation, the immune cells (e.g., T cells) release a series of cytokines to a level and degree that generates untoward biological/physiological effects or varying degree and severity, including acute inflammation characterized by, e.g., rubor (redness), swelling or edema, calor (heat), dolor (pain), and “functio laesa” (loss of function); when localized in skin or other tissue: increase blood flow, enabling vascular leukocytes and plasma proteins to reach extravascular sites of injury, increasing local temperatures and generation of pain, tissue edema and extravascular pressure and a reduction in tissue perfusion; organ and system dysfunction, such as cardiac dysfunction, adult respiratory distress syndrome, neurologic toxicity, renal and/or hepatic failure, and disseminated intravascular coagulation. Although numerous cytokines appear to associate with onset of CRS, elevated levels of IFNγ, IL-6, TNFα, TGFbeta, IL-2, granulocyte macrophage–colony-stimulating factor (GM-CSF), IL-10, IL-8, IL-5, and/or fractalkine are implicated as predictive and/or causative of CRS or the propensity to elicit CRS upon T-cell stimulation. In certain embodiments of the invention, elevated levels of Interleukin 6 (IL-6); Interleukin 12 (IL-12); tumor necrosis factor alpha (TNFa); (TGFb); Interleukin-2 (IL-2); and/or interferon gamma (IFNg) production by T-cells incubated with the CD3 binding domains and antibodies comprising them are predictive of the propensity to elicit CRS. In certain embodiments of the invention, elevated levels interferon gamma (IFNg) production by T-cells incubated with the CD3 binding domains and antibodies comprising them are predictive of the propensity to elicit CRS.

[0134] A “cytokine release syndrome risk score”, also known as a “cytokine release syndrome risk profile”, “CRS risk score”, or “CRS risk profile”, refers to an index that may be assigned to the inventive CD3 binding domains and/or antibodies comprising them upon assessing the propensity to elicit cytokine production levels from T cells incubated or contacted with the inventive CD3 binding domains (and/or antibodies comprising them) to levels that would be predicted or expected, and/or in fact demonstrated, to be sufficient to induce cytokine release syndrome in subjects. The developability score is thus a measure or metric by which CRS risk of CD3 binders and/or antibodies comprising them may be assessed, compared, and/or ranked. Such CRS risk scores serve as a measure of the propensity, either predictive or demonstrative, of CD3 binders and antibodies comprising them to elicit cytokine release when assessed in either an in vitro (e.g., cell-based) or an in vivo (e.g., in a test subject or patient) cytokine release assay. Such assays are available to the artisan and include, in certain embodiments of the invention e.g., the use of PBMCs, either as cultured cell lines or as primary cells obtained from living donors, to assess the ability of immunomodulatory agents, such as CD3 binding domains and antibodies comprising them, to induce cytokine production/secretion in cell-based cytokine release assays performed in immobilized or, preferably soluble antibody formats (see, e.g., Vessillier et al., J Immunol Methods, Vol. 424, pages 43-52 (2015). Generally, production levels of cytokines that are measured as indicators or predictive of CRS risk, as understood by the artisan and/or as disclosed therein and throughout, that are lower for test molecules than that determined for known (i.e., “positive control”) inducers of cytokine release syndrome or cytokine storm are indicative of diminished risk of inducing CRS by the test inducers.

[0135] The term “recombinant” generally refers to any protein, polypeptide, or cell expressing a gene of interest that is produced by genetic engineering methods. The term “recombinant” as used with respect to a protein or polypeptide, means a polypeptide produced by expression of a recombinant polynucleotide. The proteins used in the immunogenic compositions of the invention may be isolated from a natural source or produced by genetic engineering methods.

[0136] The antibodies of the invention may, in some embodiments, be recombinant human antibodies. The term “recombinant human antibody”, as used herein, is intended to include all antibodies, including human or humanized antibodies, that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described further below), antibodies isolated from a recombinant, combinatorial human antibody library (described further below), antibodies isolated from an animal (e.g., a mouse) that is transgenic for human immunoglobulin genes (see e.g., Taylor et al. (1992) Nucl. Acids Res. 20:6287-6295) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies are subjected to in vitro mutagenesis (or, when an animal transgenic for human Ig sequences is used, in vivo somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire in vivo.

[0137] The term “specifically binds,” or “binds specifically to”, or the like, means that an antibody or antigen-binding fragment thereof forms a complex with an antigen that is relatively stable under physiologic conditions. Specific binding can be characterized by an equilibrium dissociation constant of at least about 1×10^{-6} M or less (e.g., a smaller K_D denotes a tighter binding). Methods for determining whether two molecules specifically bind are well known in the art and include, for example, equilibrium dialysis, surface plasmon resonance, and the like. As described herein, antibodies have been identified by surface plasmon resonance, e.g., BIACORE™, biolayer interferometry measurements using, e.g., a FORTEBIO Octet HTX instrument (Pall Life Sciences), which bind specifically to CD3. Moreover, multi-specific antibodies that bind to CD3 and one or more additional antigens, or a bi-specific that binds to two different regions of CD3 and/or different regions of an additional antigen are nonetheless considered antibodies that "specifically bind", as used herein. In certain embodiments, the antibodies disclosed herein display equilibrium dissociation constants (and hence specificities) of about 1 x 10^{-6} M; about 1 x 10^{-7} M; about 1 x 10^{-8} M; about 1 x 10^{-9} M; about 1 x 10^{-10} M; between about 1 x 10^{-6} M and about 1 x 10^{-7} M; between about 1 x 10^{-7} M and about 1 x 10^{-8} M; between about 1 x 10^{-8} M and about 1 x 10^{-9} M; or between about 1 x 10^{-9} M and about 1 x 10^{-10} M.

[0138] The term "high affinity" antibody refers to those mAbs having a binding affinity to CD3, expressed as K_D, of at least 10^{-9} M; more preferably 10^{-10} M, more preferably 10^{-11} M, more preferably 10^{-12} M as measured by surface plasmon resonance, e.g., BIACOR, biolayer interferometry measurements using, e.g., a FORTEBIO Octet HTX instrument (Pall Life Sciences), or solution-affinity ELISA.

[0139] By the term "slow off rate", is meant an antibody that dissociates from CD3, with a rate constant (K_{off} or $K_{D)}$ of 1 x 10^{-3} s^{-1} or less, preferably 1 x 10^{-4} s^{-1} or less, as determined by surface plasmon resonance, e.g., BIACORE™ or a FORTEBIO Octet HTX instrument (Pall Life Sciences).

[0140] Further with regard to antibody fragments such antibody fragments may include a Fab fragment, a $F(ab')_2$ fragment, a Fv fragment, a dAb fragment, a fragment containing a CDR, or an isolated CDR. Antigen-binding fragments of an antibody may be derived, e.g., from full antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and (optionally) constant domains. Such DNA is known and/or is readily available from, e.g., commercial sources, DNA libraries (including, e.g., phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, etc.

[0141] Non-limiting examples of antigen-binding fragments include: (i) Fab fragments; (ii) $F(ab')_2$ fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single-chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units consisting of the amino acid residues that mimic the hypervariable region of an antibody (e.g., an isolated complementarity determining region (CDR) such as a CDR3 peptide), or a constrained FR3-CDR3-FR4 peptide. Other engineered molecules, such as domain-specific antibodies, single domain antibodies, domain- deleted antibodies, chimeric antibodies, CDR-grafted antibodies, diabodies, triabodies, tetrabodies, minibodies, nanobodies (e.g., monovalent nanobodies, bivalent nanobodies, etc.), small modular immunopharmaceuticals (SMIPs), and shark variable IgNAR domains, are also encompassed within the expression "antigen-binding fragment," as used herein.

[0142] An antigen-binding fragment of an antibody will typically comprise at least one variable domain. The variable domain may be of any size or amino acid composition and will generally comprise at least one CDR, which is adjacent to or in frame with one or more framework sequences. In antigen-binding fragments having a V_H domain associated with a V_L domain, the V_H and V_L domains may be situated relative to one another in any suitable arrangement. For example, the variable region may be dimeric and contain V_H - V_H, V_H - V_L or V_L - V_L dimers. Alternatively, the antigen-binding fragment of an antibody may contain a monomeric V_H or V_L domain.

[0143] In certain embodiments, an antigen-binding fragment of an antibody may contain at least one variable domain covalently linked to at least one constant domain. Non-limiting, exemplary configurations of variable and constant domains that may be found within an antigen-binding fragment of an antibody of the present invention include: (i) V_H -C_H1 ; (ii) V_H -C_H2; (iii) V_H -C_H3; (iv) V_H -C_h1 -C_h2; (V) V_H -C_h1-C_h2-C_h3; (vi) V_H -C_H2-C_H3; (vii) V_H -C_L; (viii) V_L - C_H1 ; (ix) V_L - C_H2; (x) V_L -C_H3; (xi) V_L -C_H1-C_H2; (xii) V_L -C_H1-C_H2-C_H3; (xiii) V_L -C_H2-C_H3; and (xiv) V_L -C_L. In any configuration of variable and constant domains, including any of the exemplary configurations listed above, the variable and constant domains may be either directly linked to one another or may be linked by a full or partial hinge or linker region. A hinge region may consist of at least 2 (e.g., 5, 10, 15, 20, 40, 60 or more) amino acids, which result in a flexible or semi-flexible linkage between adjacent variable and/or constant domains in a single polypeptide molecule. Moreover, an antigen-binding fragment of an antibody of the present invention may comprise a homo-dimer or hetero-dimer (or other multimer) of any of the variable and constant domain configurations listed above in non-covalent association with one another and/or with one or more monomeric V_H or V_L domain (e.g., by disulfide bond(s)).

[0144] As with full antibody molecules, antigen-binding fragments may be mono-specific or multi-specific (e.g., bi-specific). A multi-specific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multi-specific antibody format, including the exemplary bi-specific antibody formats disclosed herein, may be adapted for use in the context of an antigen-binding fragment of an antibody of the present invention using routine techniques available in the art. Non-limiting examples of multispecific and bispecific formats that re amenable to incorporation of the inventive anti-CD3 binding domains include, e.g., Fab-Fc-scFv ("bottle-opener") (XENCOR), Mab-scFv (XENCOR), Mab-Fv (XENCOR), Dual scFv (XENCOR),central Fv (XENCOR), central scFv(XENCOR), one-arm central scFv (XENCOR), Fab-Fab (XENCOR), Fab-Fv (XENCOR), mAb-Fv (XENCOR), mAb-Fab (XENCOR), DART (MACROGENICS), BiTE (AMGEN/MICROMET), KiTE, common light chain-IgG (Genentech), TandAb (SFFIMED) Cross-Mab (ROCHE), SEED (EMD SERONO), BEAT (GLENMARK), TrioMab (TRION PHARMA/FRESENIUS BIOTECH), DuetMab (MEDIMMUNE), and others, as dislosed, e.g., in (WO 95/09917; WO 2008/119566; WO 2008/119567; WO2011/121110; WO 2010/037835; WO 2007/042261; WO 2007/110205; WO 2011/121110; WO 2012/055961; WO 2012/16067; WO 2016/086189; WO 2016/182751; WO 2015/006749; WO 2014/049003; WO 2013/177101; WO 2015/128509; US 7,951,917; US 2009/0252729; US 2014/0348839; US 7,183,076; Mazor et al., *Mabs*, Vol. 7, pages 377-389 (2015); Muda et al., *Protein Engineering, Designe, & Selection*, Vol. 24, pages 447-454 (2011); and Del Bano et al., *Antibodies*, Vol. 5, pages 1-23 (2016).

[0145] The specific embodiments, antibody or antibody fragments of the invention may be conjugated to a therapeutic moiety ("immunoconjugate"), such as an antibiotic, a second anti-CD3 antibody, a vaccine, or a toxoid, or any other useful therapeutic moiety.

[0146] An “isolated antibody”, as used herein, is intended to refer to an antibody that is substantially free of other antibodies (Abs) having different antigenic specificities (e.g., an isolated antibody that specifically binds CD3, or a fragment thereof, is substantially free of Abs that specifically bind antigens other than CD3.

[0147] A “blocking antibody” or a “neutralizing antibody”, as used herein (or an “antibody that neutralizes CD3 activity”), is intended to refer to an antibody whose binding to CD3, as the case may be as disclosed herein, results in inhibition of at least one biological activity of CD3.

[0148] The term “surface plasmon resonance”, as used herein, refers to an optical phenomenon that allows for the analysis of real-time biomolecular interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIACORE™ system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, N.J.).

[0149] The term “K_D“, as used herein, is intended to refer to the equilibrium dissociation constant of a particular antibody-antigen interaction.

[0150] The term “epitope” refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. The term “epitope” also refers to a site on an antigen to which B and/or T cells respond. It also refers to a region of an antigen that is bound by an antibody. Epitopes may be defined as structural or functional. Functional epitopes are generally a subset of the structural epitopes and have those residues that directly contribute to the affinity of the interaction. Epitopes may also be conformational, that is, composed of non-linear amino acids. In certain embodiments, epitopes may include determinants that are chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl groups, or sulfonyl groups, and, in certain embodiments, may have specific three-dimensional structural characteristics, and/or specific charge characteristics.

[0151] The term “substantial identity”, or “substantially identical,” when referring to a nucleic acid or fragment thereof, or an amino acid sequence or a fragment thereof, indicates that, when optimally aligned with appropriate insertions or deletions with another nucleic acid sequence or amino acid sequence, as the case may be, (or its complementary strand), there is sequence identity in at least about 100%, at least about 99%, at least about 98%, at least about 97%, at least about 96%, at least about 95%, at least about 94%, at least about 93%, at least about 92%, at least about 91%, at least about 90%, at least about 89%, at least about 88%, at least about 87%, at least about 86%, at about 85%, at least about 84%, at least about 83%, at least about 82%, at least about 80%, and optionally so on, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or GAP, as discussed below. Accordingly, sequences that display a certain percentage "identity" share that percentage identity, and/or are that percentage "identical" to one another.

[0152] In certain embodiments, the disclosed CD3 binding domains, and/or the individual heavy chain (HC) sequence, light chain (LC) sequence, CDRH3 sequence, CDRH2 sequence, CHRH1 sequence, CDRL3 sequence, CDRL2 sequence, CDRL1 sequence, and/or framework sequences are independently at least about 100%, at least about 99%, at least about 98%, at least about 97%, at least about 96%, at least about 95%, at least about 94%, at least about 93%, at least about 92%, at least about 91%, at least about 90%, at least about 89%, at least about 88%, at least about 87%, at least about 86%, at about 85%, at least about 84%, at least about 83%, at least about 82%, at least about 80%; and/or all percentages of identity in between; to other sequences and/or share such percentage identities with one another (or with certain subsets of the herein-disclosed antibody sequences).

[0153] In certain embodiments, the disclosed antibody amino acid sequences are, e.g.,: at least 70% identical; at least 75% identical; 80% identical; at least 85% identical; at least 90% identical; at least 95% identical; at least 96% identical; at least 97% identical; at least 98% identical; at least 99%; and/or all percentages of identity in between; to other sequences and/or share such percentage identities with one another (or with certain subsets of the herein-disclosed antibody sequences).

[0154] Preferably, residue positions, which are not identical, differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well known to those of skill in the art. (See, e.g., Pearson (1994) Methods Mol. Biol. 24: 307- 331). Examples of groups of amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; 2) aliphatic- hydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; 6) acidic side chains: aspartate and glutamate, and 7) sulfur-containing side chains: cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al. (1992) Science 256: 1443 45. A “moderately conservative” replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0155] Sequence similarity for polypeptides is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as GAP and BESTFIT which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA with default or recommended parameters; a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) supra). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially BLASTP or TBLASTN, using default parameters. (See, e.g., Altschul et al. (1990) J. Mol. Biol. 215: 403 410 and (1997) Nucleic Acids Res. 25:3389 402).

[0156] In certain embodiments, the antibody or antibody fragment for use in the method of the invention may be mono-specific, bi-specific, or multi-specific. Multi-specific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for epitopes of more than one target polypeptide. An exemplary bi-specific antibody format that can be used in the context of the present invention involves the use of a first immunoglobulin (Ig) C_H3 domain and a second Ig C_H3 domain, wherein the first and second Ig C_H3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces binding of the bi-specific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference. In one embodiment, the first Ig C_H3 domain binds Protein A and the second Ig C_H3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R modification (by IMGT exon numbering; H435R by EU numbering). The second C_H3 may further comprise an Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second C_H3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 mAbs; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 mAbs; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of IgG4 mAbs. Variations on the bi-specific antibody format described above are contemplated within the scope of the present invention.

[0157] *Exemplary Anti-CD3 binding domains and antibodies comprising them*

[0158] As mentioned above, in certain embodiments of the invention a large series of CD3 binding domains and antibodies comprising them, and methods of preparing and using them are provided. Surprisingly, species of this large series of CD3 binding domains collectively display desirable properties, including, e.g., a broad range of affinities for CD3 epsilon; cross-reactivity towards both human CD3 (“Hu CD3”) and cynomolgus CD3 (“Cy CD3”); as well as desirable developability profiles and/or cytokine release syndrome (CRS) risk profiles. In certain embodiments, the inventive CD3 binding domains, and antibodies comprising them, display developability profiles and/or CRS risk profiles that are superior to the developability profiles and/or CRS risk profiles of other anti-CD3 antibodies. In certain embodiments, the inventive CD3 binding domains, and antibodies comprising them, display developability profiles and/or

CRS risk profiles that are superior to the developability profiles and/or CRS risk profiles of, e.g., I2C; SP34; 38E4; CAB21609_A01, CAB21609_B01, CAB21609_C01, and/or CAB21609_D01 as disclosed herein as well as in Yang et al., J Immunol, Vol 137, pages 1097-1100 (August 4, 1986); US 2014/008295; and WO 2015/095392.

[0159] In certain embodiments, the invention provides CD3 binding domains and antibodies comprising them that bind to CD3 (e.g., CD3ε and/or CD3γ).

[0160] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them are provided which display an enhanced developability profile relative to other CD3 binding domains (or antibodies comprising them). In certain embodiments, the inventive CD3 binding domains and antibodies comprising them are provided which display an enhanced developability profile relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab 366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0161] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them display a developability score of: between about 0 MFI and about 500 MFI; between about 0 MFI and about 450 MFI; between about 0 MFI and about 400 MFI; between about 0 MFI and about 350 MFI; between about 0 MFI and about 300 MFI; between about 0 MFI and about 250 MFI; between about 0 MFI and about 200 MFI; between about 0 MFI and about 150 MFI; between about 0 MFI and about 100 MFI; between about 0 MFI and about 50 MFI; between about 200 MFI and 500 MFI; ; between about 200 MFI and about 450 MFI; between about 200 MFI and about 400 MFI; between about 200 MFI and about 350 MFI; between about 200 MFI and about 300 MFI; between about 200 MFI and about 250 MFI; between about 100 MFI and about 450 MFI; between about 100 MFI and about 400 MFI; between about 100 MFI and about 350 MFI; between about 100 MFI and about 300 MFI; between about 100 MFI and about 250 MFI; between about 100 MFI and about 200 MFI; or between about 100 MFI and about 150 MFI.

[0162] In other embodiments, the inventive CD3 binders and antibodies comprising them display a normalized developability score of between about 0.0 and about 0.6; between about 0.0 and about 0.57; between about 0.0 and about 0.55; between about 0.0 and about 0.53; between about 0.0 and about 0.51; between about 0.0 and about 0.49; between about 0.0 and about 0.47;

between about 0.0 and about 0.45; between about 0.0 and about 0.43; between about 0.0 and about 0.41; between about 0.0 and about 0.39; between about 0.0 and about 0.37; between about 0.0 and about 0.35; between about 0.0 and about 0.33; between about 0.0 and about 0.31; between about 0.0 and about 0.29; between about 0.0 and about 0.27; between about 0.0 and about 0.25; between about 0.0 and about 0.23; between about 0.0 and about 0.21; between about 0.0 and about 0.19; between about 0.0 and about 0.17; between about 0.0 and about 0.15; between about 0.0 and about 0.13; between about 0.0 and about 0.11; between about 0.0 and about 0.09; between about 0.0 and about 0.07; or between about 0.0 and about 0.05.

[0163] In certain embodiments, the developability profile and/or developability score for the inventive CD3 binders and antibodies comprising them is obtained by performing a PSR assay; an SCP assay; AS-CINS; a BVP assay; an ELISA; a DSF assay; a Tm assay; a HIC assay; a CIC assay; or combinations thereof.

[0164] In other embodiments, the inventive CD3 binding domains and antibodies comprising them elicit potent T cell activation or T cell killing while displaying a decreased propensity to elicit cytokine production to levels capable of inducing cytokine release syndrome. In certain embodiments, at least one cytokine for which cytokine production levels are measured in order to assess the propensity to elicit cytokine production levels capable of inducing cytokine release syndrome is selected from the group consisting of: Interleukin 6 (IL-6); Interleukin 12 (IL-12); tumor necrosis factor alpha (TNFa); (TGFb); Interleukin-2 (IL-2); and Interferon gamma (IFNg).

[0165] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them elicit T cell activation or T cell killing while displaying a decreased propensity to elicit cytokine production to levels capable of inducing cytokine release relative to that observed one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2. In certain embodiments, at least one cytokine for which cytokine production levels are measured in order to assess the propensity to elicit cytokine production levels capable of inducing cytokine release syndrome is selected from the group consisting of: Interleukin 6 (IL-6); Interleukin 12 (IL-12); tumor necrosis factor alpha (TNFa); (TGFb); Interleukin-2 (IL-2); and Interferon gamma (IFNg).

[0166] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them display a cytokine release syndrome risk profile that is indicative of decreased risk of eliciting cytokine release syndrome (CRS). In other embodiments, the inventive CD3 binding domains and antibodies comprising them display a cytokine release syndrome risk profile that is indicative of decreased risk of eliciting cytokine release syndrome (CRS) when compared to the cytokine release syndrome risk profile assessed for one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0167] In certain embodiments, the invention provides an antibody comprising a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH3 is not 100% identical to the CDRH3 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0168] In certain embodiments, the invention provides an antibody comprising a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH2 is not 100% identical to the CDRH2 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0169] In certain embodiments, the invention provides an antibody comprising a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97%

identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH1 is not 100% identical to the CDRH1 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0170] In certain embodiments, the invention provides an antibody comprising a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL3 is not 100% identical to the CDRL3 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0171] In certain embodiments, the invention provides an antibody comprising a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL2 is not 100% identical to the CDRL2 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0172] In certain embodiments, the invention provides an antibody comprising a CDRL1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97%

identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL1 is not 100% identical to the CDRL1 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0173] In certain embodiments, the invention provides an antibody comprising a heavy chain (HC) variable region that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; an HC variable region selected from the group consisting of the HC variable regions of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the HC variable region is not 100% identical to the HC variable region of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0174] In certain embodiments, the invention provides an antibody comprising a light chain (LC) variable region that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a LC variable region selected from the group consisting of the LC variable regions of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the LC variable region is not 100% identical to the LC variable region of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0175] In certain embodiments, the invention provides an antibody comprising a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the neither the CDRH3, CDRH2, nor the CHRH1 is 100% identical to the CHRH3, CDRH2, or CDRH1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0176] In certain embodiments, the invention provides an antibody comprising a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and a CDRL1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical; to a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the neither the CDRL3, CDRL2, nor the CHRL1 is 100% identical to the CHRL3, CDRL2, or CDRL1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0177] In certain embodiments, the invention provides an antibody comprising a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least

94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and a CDRL1 that is:100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87%

identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the neither the CDRH3, CDRH2, CDRH1, CDRL3, CDHL2, nor the CHRL1 is 100% identical to the CHRH3, CDRH2, CDRH1, CDRL3, CDHL2, or the CDRL1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

[0178] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-15512; ADI-15516; and ADI-16513; as provided in Table 2.

[0179] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-18562; ADI-18564; ADI-18565; ADI-18566; ADI-18567; ADI-18568; ADI-18570; ADI-18571; ADI-18572; ADI-18573; ADI-18563; ADI-18569; ADI-18574; ADI-18575; ADI-18576; ADI-18578; ADI-18579; ADI-18580; ADI-18581; ADI-18582; ADI-18584; ADI-18585; ADI-18577; ADI-18583; ADI-18588; ADI-18589; ADI-18590; ADI-18591; ADI-18593; ADI-18594; ADI-18595; ADI-18596; ADI-18597; ADI-18592; ADI-18587; ADI-18586; and; ADI-16606; as provided in Table 2.

[0180] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-18576; ADI-20820; ADI-20578; ADI-20571; ADI-21097; ADI-20577; ADI-20576; ADI-20568; ADI-20582; ADI-20575; ADI-20567; ADI-20574; ADI-20573; ADI-20579; ADI-18565; ADI-20818; ADI-20587; ADI-20588; ADI-20589; ADI-20590; ADI-20594; ADI-20596; ADI-20599; ADI-20605; ADI-20607; ADI-20608; and ADI-20609; as provided in Table 2.

[0181] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-16606; ADI-20587; ADI-20607; ADI-20590; ADI-28708; ADI-28709; ADI-28710; ADI-21943; ADI-28711; ADI-28712; ADI-28713; ADI-28714; ADI-28715; ADI-21944; ADI-28716; ADI-21945; ADI-21946; ADI-28717; ADI-21947; ADI-28718; ADI-28719; ADI-28720; ADI-28721; ADI-28722; ADI-28723; ADI-28724; ADI-28725; ADI-28726; ADI-28727; ADI-28728; ADI-28729;

ADI-28730; ADI-28731; ADI-28732; ADI-28733; ADI-28734; ADI-28735; ADI-28736; ADI-28737; ADI-28738; ADI-28739; ADI-28740; ADI-28741; ADI-28742; ADI-28743; ADI-21948; ADI-21949; ADI-28744; ADI-21950; ADI-28745; ADI-28746; ADI-28747; ADI-28748; ADI-21951; ADI-21952; ADI-28749; ADI-28750; ADI-28751; ADI-21953; ADI-28752; ADI-21954; ADI-28753; ADI-28754; ADI-28755; ADI-28756; ADI-28757; ADI-28758; ADI-28759; ADI-28760; ADI-28761; ADI-28762; ADI-28763; ADI-28764; ADI-28765; ADI-28766; ADI-28767; ADI-28768; ADI-21955; ADI-28769; ADI-28770; ADI-21956; ADI-28771; ADI-28772; ADI-28773; ADI-28774; and ADI-28775; as provided in Table 2.

[0182] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-21959; ADI-21963; ADI-21965; ADI-21967; ADI-21970; ADI-21971; ADI-21972; ADI-21973; ADI-21974; ADI-21975; ADI-21976; ADI-21977; ADI-21978; ADI-21979; ADI-21943; ADI-21944; ADI-21945; ADI-21946; ADI-21947; ADI-21948; ADI-21949; ADI-21950; ADI-21951; ADI-21952; ADI-21953; ADI-21954; ADI-21955; and ADI-21956; as provided in Table 2.

[0183] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-21952; ADI-22523; ADI-24403; ADI-24404; ADI-24405; ADI-24407; ADI-24408; ADI-24409; ADI-24410; ADI-24411; ADI-24412; ADI-24413; ADI-24414; ADI-24415; ADI-24416; ADI-24417; ADI-24418; ADI-24434; ADI-24435; ADI-24436; ADI-24437; ADI-24438; ADI-24439; ADI-24440; ADI-24441; ADI-24442; ADI-24443; ADI-24444; ADI-24445; ADI-24446; ADI-24449; ADI-24388; ADI-24389; ADI-24390; ADI-24391; ADI-24392; ADI-24393; ADI-24394; ADI-24395; ADI-24396; ADI-24397; ADI-24398; ADI-24399; ADI-24400; ADI-24401; ADI-24402; ADI-24419; ADI-24420; ADI-24421; ADI-24422; ADI-24423; ADI-24424; ADI-24425; ADI-24426; ADI-24427; ADI-24428; ADI-24429; ADI-24430; ADI-24431; ADI-24432; ADI-24433; ADI-24447; and ADI-24448; as provided in Table 2.

[0184] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-23652; ADI-23653; ADI-23654; ADI-23655; ADI-23656; ADI-23657; ADI-23658; ADI-23651; ADI-23644; ADI-23645; ADI-23646; ADI-23647; ADI-23648; ADI-23649; ADI-23650; ADI-23667; ADI-23668; ADI-23669; ADI-23670; ADI-23671; ADI-23672; ADI-23673; ADI-

23659; ADI-23660; ADI-23661; ADI-23663; ADI-23664; ADI-23639; ADI-23641; ADI-23642; ADI-23640; ADI-23643; ADI-21952; ADI-23633; ADI-23634; ADI-23635; ADI-23636; ADI-23637; ADI-23638; ADI-23632; and ADI-23629; as provided in Table 2.

[0185] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26909; ADI-26910; ADI-26912; ADI-26913; ADI-26915; ADI-26916; ADI-26917; ADI-26918; ADI-26919; ADI-26920; ADI-26921; ADI-26924; ADI-26925; ADI-26927; ADI-26928; ADI-26929; ADI-26930; ADI-26932; ADI-26933; ADI-26938; ADI-26939; ADI-26940; ADI-26941; ADI-26942; ADI-26943; ADI-26944; ADI-26945; ADI-26950; ADI-26954; ADI-23672; ADI-23673; ADI-23664; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26968; ADI-26969; ADI-26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; ADI-26994; and ADI-26995; as provided in Table 2.

[0186] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26910; ADI-26913; ADI-26915; ADI-26919; ADI-26920; ADI-26921; ADI-26943; ADI-26954; ADI-21952; ADI-26955; ADI-26956; ADI-26962; ADI-26978; ADI-26983; and ADI-26994; as provided in Table 2.

[0187] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: ADI-15512; ADI-16513; ADI-15516; ADI-18565; ADI-18589; ADI-18585; ADI-18590; ADI-18576; ADI-20568; ADI-20580; ADI-21978; ADI-22523; ADI-25133; and ADI-26906.

[0188] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: ADI-16606; ADI-29601; ADI-29602; ADI-29603; ADI-20587; ADI-20607; ADI-20590; ADI-21952; ADI-23633; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26961; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26967; ADI-26968; ADI-26969; ADI-26970; ADI-

26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; and ADI-26994.

[0189] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of:ADI-32238, ADI-32241, ADI-32244, ADI-32247, ADI-32250, ADI-32253, ADI-32256, ADI-32259, ADI-32239, ADI-32242, ADI-32245, ADI-32248, ADI-32251, ADI-32254, ADI-32257, ADI-32260, ADI-32240, ADI-32243, ADI-32246, ADI-32249, ADI-32252, ADI-32255, ADI-32258, and ADI-32261.

[0190] In certain embodiments, the invention provides an antibody comprising a CD3 binding domain selected from the group consisting of: ADI-29295, ADI-32249, ADI-29298, ADI-29300, and ADI-26915.

[0191] In certain embodiments either alone or in combination with other embodiments of the invention, the inventive CD3 binding domains and antibodies comprising them display a decreased propensity for degradation relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0192] In certain embodiments either alone or in combination with other embodiments of the invention, the inventive CD3 binding domains and antibodies comprising them display a decreased CRS risk profile relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

[0193] In certain embodiments and/or in combination with any of the embodiments disclosed herein and throughout, provided are CD3 binding domains and antibodies comprising them that are humanized. In certain embodiments, such CD3 binding domains comprise CDRs of such other embodiments, and further comprise an acceptor human framework, e.g., a human immunoglobulin framework or a human consensus framework.

[0194] In certain embodiments and/or in combination with any of the embodiments disclosed herein and throughout provided are CD3 binding domains and antibodies comprising them comprising a VH as in any of the embodiments provided herein and throughout, and a VL as in any of the embodiments provided herein and throughout, wherein one or both of the variable domain sequences include post-translational modifications.

[0195] In a further aspect of the invention, provided are CD3 binding domains and antibodies comprising them that bind to the same epitope as a CD3 binding domain provided in the other embodiments disclosed therein and throughout.

[0196] In certain embodiments, CD3 binding domains and/or antibodies comprising them have a CD3 dissociation constant (Kd) of ≤ 1 μM, ≤ 100 nM, ≤ 10 nM, ≤ 1 nM, ≤ 0.1 nM, ≤ 0.01 nM, or ≤ 0.001 nM (e.g., 10^{-8} M or less, e.g., from 10^{-8} M to 10^{-13} M, e.g., from 10^{-9} M to 10^{-13} M).

[0197] In certain embodiments, Kd is measured by: biolayer interferometry (BLI), surface plasmon resonance (SPR), solution equilibrium based kinetic exclusion assays, KinExA direct association, assays using FORTEBIO instruments and reagents, such as Octet RED 384 and HTX BLI-based instruments, enzyme-linked immunosorbent assays (ELISA), or radioimmunoassay (RIA). In certain embodiments, the Kd measurement is performed with the Fab version of an inventive CD3 binding domain or antibody comprising it. For example, solution binding affinity of Fabs for antigen is measured by equilibrating Fab with a minimal concentration of (125I)-labeled antigen in the presence of a titration series of unlabeled antigen, then capturing bound antigen with an anti-Fab antibody-coated plate (see, e.g., Chen et al., J. Mol. Biol. 293:865-881 (1999)). To establish conditions for the assay, MICROTITER® multi-well plates (Thermo Scientific) are coated overnight with 5 μg/ml of a capturing anti-Fab antibody (Cappel Labs) in 50 mM sodium carbonate (pH 9.6), and subsequently blocked with 2% (w/v) bovine serum albumin in PBS for two to five hours at room temperature (approximately 23° C). In a non-adsorbent plate (Nunc #269620), 100 pM or 26 pM [125I]-antigen are mixed with serial dilutions of a Fab of interest (e.g., consistent with assessment of the anti-VEGF antibody, Fab-12, in Presta et al., Cancer Res. 57:4593-4599 (1997)). The Fab of interest is then incubated overnight; however, the incubation may continue for a longer period (e.g., about 65 hours) to ensure that equilibrium is reached. Thereafter, the mixtures are transferred to the capture plate for incubation at room temperature (e.g., for one hour). The solution is then removed and the plate washed eight times with 0.1% polysorbate 20 (TWEEN-

20®) in PBS. When the plates have dried, 150 μl/well of scintillant (MICROSCINT-20™; Packard) is added, and the plates are counted on a TOPCOUNT™ gamma counter (Packard) for ten minutes. Concentrations of each Fab that give less than or equal to 20% of maximal binding are chosen for use in competitive binding assays.

[0198] In other embodiments, Kd is measured using a BIACORE® surface plasmon resonance assay. For example, an assay using a BIACORE®-2000 or a BIACORE®-3000 (BIACORE, Inc., Piscataway, N.J.) is performed at 25° C. with immobilized antigen CM5 chips at ˜10 response units (RU). In one embodiment, carboxymethylated dextran biosensor chips (CM5, BIACORE, Inc.) are activated with N-ethyl-N'-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and N-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, pH 4.8, to 5 μg/ml (˜0.2 μM) before injection at a flow rate of 5 μl/minute to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (0.78 nM to 500 nM) are injected in PBS with 0.05% polysorbate 20 (TWEEN-20™) surfactant (PBST) at 25° C. at a flow rate of approximately 25 μl/min. Association rates (k_{on}) and dissociation rates (KO are calculated using a simple one-to-one Langmuir binding model (BIACORE® Evaluation Software version 3.2) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant (Kd) is calculated as the ratio kon/koff. See, for example, Chen et al., J. Mol. Biol. 293:865-881 (1999). If the on-rate exceeds 106 M−1s−1 by the surface plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission intensity (excitation=295 nm; emission=340 nm, 16 nm band-pass) at 25° C of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer, such as a stop-flow equipped spectrophotometer (Aviv Instruments) or a 8000-series SLM-AMINC spectrophotometer (THERMOSPECTRONIC) with a stirred cuvette.

[0199] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise an antibody fragment. Antibody fragments include, but are not limited to, Fab, Fab', Fab'-SH, $F(ab')_2$, Fv, and scFv fragments, and other fragments described herein and throughout. For a review of certain antibody fragments, see, e.g., Hudson et al. Nat.

Med. 9:129-134 (2003). For a review of scFv fragments, see, e.g., Pluckthün, in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., (Springer-Verlag, New York), pp. 269-315 (1994); see also WO 93/16185; and U.S. Pat. Nos. 5,571,894 and 5,587,458. For discussion of Fab and F(ab')2 fragments comprising salvage receptor binding epitope residues and having increased in vivo half-life, see U.S. Pat. No. 5,869,046.

[0200] Diabodies are antibody fragments with two antigen-binding sites that may be bivalent or bispecific. See, for example, EP 404,097; WO 1993/01161; Hudson et al. Nat. Med. 9:129-134 (2003); and Hollinger et al. Proc. Natl. Acad. Sci. USA 90: 6444-6448 (1993). Triabodies and tetrabodies are also described in Hudson et al. Nat. Med. 9:129-134 (2003).

[0201] Single-domain antibodies are antibody fragments comprising all or a portion of the heavy chain variable domain or all or a portion of the light chain variable domain of an antibody. In certain embodiments, a single-domain antibody is a human single-domain antibody (Domantis, Inc., Waltham, Mass.; see, e.g., U.S. Pat. No. 6,248,516 B1).

[0202] Antibody fragments can be made by various techniques, including but not limited to proteolytic digestion of an intact antibody as well as production by recombinant host cells (e.g. E. coli or phage), as described herein.

[0203] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a chimeric antibody. Certain chimeric antibodies are described, e.g., in U.S. Pat. No. 4,816,567; and Morrison et al. Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). In one example, a chimeric antibody comprises a non-human variable region (e.g., a variable region derived from a mouse, rat, hamster, rabbit, or non-human primate, such as a monkey) and a human constant region. In a further example, a chimeric antibody is a "class switched" antibody in which the class or subclass has been changed from that of the parent antibody. Chimeric antibodies include antigen-binding fragments thereof.

[0204] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a chimeric antibody that is a humanized antibody. Typically, a non-human antibody is humanized to reduce immunogenicity to humans, while retaining the specificity and affinity of the parental non-human antibody. Generally, a humanized antibody comprises one or more variable domains in which CDRs (or portions thereof) are derived from a non-human antibody, and FRs (or portions thereof) are derived from human antibody sequences. A humanized antibody optionally will also comprise at least a portion of a human constant region. In some embodiments, some FR residues in a humanized antibody are substituted with corresponding residues from a non-human antibody (e.g., the antibody from which the CDR residues are derived), e.g., to restore or improve antibody specificity, affinity, lack or immunogenicity, stability, developability profile, CRS risk, and the like.

[0205] Humanized antibodies and methods of making them are reviewed, e.g., in Almagro and Fransson, Front. Biosci. 13:1619-1633 (2008), and are further described, e.g., in Riechmann et al., Nature 332:323-329 (1988); Queen et al., Proc. Nat'l Acad. Sci. USA 86:10029-10033 (1989); U.S. Pat. Nos. 5,821,337, 7,527,791, 6,982,321, and 7,087,409; Kashmiri et al., Methods 36:25-34 (2005) (describing specificity determining region (SDR) grafting); Padlan, Mol. Immunol. 28:489-498 (1991) (describing “resurfacing”); Dall'Acqua et al., Methods 36:43-60 (2005) (describing “FR shuffling”); and Osbourn et al., Methods 36:61-68 (2005) and Klimka et al., Br. J. Cancer, 83:252-260 (2000) (describing the “guided selection” approach to FR shuffling).

[0206] Human framework regions that may be used for humanization include but are not limited to: framework regions selected using the “best-fit” method (see, e.g., Sims et al. J. Immunol. 151:2296 (1993)); framework regions derived from the consensus sequence of human antibodies of a particular subgroup of light or heavy chain variable regions (see, e.g., Carter et al. Proc. Natl. Acad. Sci. USA, 89:4285 (1992); and Presta et al. J. Immunol., 151:2623 (1993)); human mature (somatically mutated) framework regions or human germline framework regions (see, e.g., Almagro and Fransson, Front. Biosci. 13:1619-1633 (2008)); and framework regions derived from screening FR libraries (see, e.g., Baca et al., J. Biol. Chem. 272:10678-10684 (1997) and Rosok et al., J. Biol. Chem. 271:22611-22618 (1996)).

[0207] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a human antibody. Human antibodies can be produced using various techniques known in the art. Human antibodies are described generally in van Dijk and van de Winkel, Curr. Opin. Pharmacol. 5: 368-74 (2001) and Lonberg, Curr. Opin. Immunol. 20:450-459 (2008).

[0208] Human antibodies may be prepared by administering an immunogen to a transgenic animal that has been modified to produce intact human antibodies or intact antibodies with human variable regions in response to antigenic challenge. Such animals typically contain all or a portion of the human immunoglobulin loci, which replace the endogenous immunoglobulin loci, or which are present extrachromosomally or integrated randomly into the animal's chromosomes. In such transgenic mice, the endogenous immunoglobulin loci have generally been inactivated. For review of methods for obtaining human antibodies from transgenic animals, see Lonberg, Nat. Biotech. 23:1117-1125 (2005). See also, e.g., U.S. Pat. Nos. 6,075,181 and 6,150,584 describing XENOMOUSE technology; U.S. Pat. No. 5,770,429 describing HUMAB® technology; U.S. Pat. No. 7,041,870 describing K-M MOUSE® technology, and U.S. Patent Application Publication No. US 2007/0061900, describing VELOCIMOUSE® technology). Human variable regions from intact antibodies generated by such animals may be further modified, e.g., by combining with a different human constant region.

[0209] Human antibodies can also be made by hybridoma-based methods. Human myeloma and mouse-human heteromyeloma cell lines for the production of human monoclonal antibodies have been described. (See, e.g., Kozbor J. Immunol., 133: 3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987); and Boerner et al., J. Immunol., 147: 86 (1991).) Human antibodies generated via human B-cell hybridoma technology are also described in Li et al., Proc. Natl. Acad. Sci. LISA. 103; 3557-3562 (2006). Additional methods include those described, for example, in U.S. Pat. No. 7,189,826 (describing production of monoclonal human IgM antibodies from hybridoma cell lines) and Ni, Xiandai Mianyixue, 26(4):265-268 (2006) (describing human-human hybridomas). Human hybridoma technology (Trioma technology) is also described in Vollmers and Brandlein, Histology and Histopathology, 20(3):927-937 (2005) and Vollmers and Brandlein, Methods and Findings in Experimental and Clinical Pharmacology, 27(3):185-91 (2005).

[0210] Human antibodies may also be generated by isolating Fv clone variable domain sequences selected from human-derived phage display libraries. Such variable domain sequences may then be combined with a desired human constant domain. Techniques for selecting human antibodies from antibody libraries are described herein and throughout.

[0211] Antibodies of the invention may be isolated by screening combinatorial libraries for antibodies with the desired activity or activities. For example, a variety of methods are known in the art for generating phage display libraries and screening such libraries for antibodies possessing the desired binding characteristics. Such methods are reviewed, e.g., in Hoogenboom et al. in Methods in Molecular Biology 178:1-37 (O'Brien et al., ed., Human Press, Totowa, N.J., 2001) and further described, e.g., in the McCafferty et al., Nature 348:552-554; Clackson et al., Nature 352: 624-628 (1991); Marks et al., J. Mol. Biol. 222: 581-597 (1992); Marks and Bradbury, in Methods in Molecular Biology 248:161-175 (Lo, ed., Human Press, Totowa, N.J., 2003); Sidhu et al., J. Mol. Biol. 338(2): 299-310 (2004); Lee et al., J. Mol. Biol. 340(5): 1073-1093 (2004); Fellouse, Proc. Natl. Acad. Sci. USA 101(34): 12467-12472 (2004); and Lee et al., J. Immunol. Methods 284(1-2): 119-132(2004).

[0212] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be selected from yeast-based antibody libraries, such as those disclosed in, e.g., WO 2009/0363379; WO 2010/105256; and WO 2012/009568. In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be optimized (also known as “affinity matured) as disclosed herein and throughout as well as in WO 2009/0363379; WO 2010/105256; and WO 2012/009568 and via other techniques available in the art.

[0213] In certain phage display methods, repertoires of VH and VL genes are separately cloned by polymerase chain reaction (PCR) and recombined randomly in phage libraries, which can then be screened for antigen-binding phage as described in Winter et al., Ann. Rev. Immunol., 12: 433-455 (1994). Phage typically display antibody fragments, either as single-chain Fv (scFv) fragments or as Fab fragments. Libraries from immunized sources provide high-affinity antibodies to the immunogen without the requirement of constructing hybridomas. Alternatively, the naive repertoire can be cloned (e.g., from human) to provide a single source of antibodies to a wide range of non-self and also self antigens without any immunization as described by Griffiths et al., EMBO J, 12: 725-734 (1993). Finally, naive libraries can also be made synthetically by cloning unrearranged V-gene segments from stem cells and using PCR primers containing random sequence to encode the highly variable CDR3 regions and to accomplish rearrangement in vitro, as described by Hoogenboom and Winter, J. Mol. Biol., 227: 381-388 (1992). Patent publications describing human antibody phage libraries include, for example: U.S. Pat. No. 5,750,373, and US Patent Publication Nos. 2005/0079574, 2005/0119455, 2005/0266000, 2007/0117126, 2007/0160598, 2007/0237764, 2007/0292936, and 2009/0002360.

[0214] Antibodies or antibody fragments isolated from human antibody libraries are considered human antibodies or human antibody fragments herein.

[0215] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody. Multispecific antibodies are monoclonal antibodies that have binding specificities for at least two different antigens, or at least two different epitopes present on the same antigen. In certain embodiments, bispecific antibodies may bind to two different epitopes of CD3 (e.g., CD3ε or CD3γ). In certain embodiments, one of the binding specificities is for CD3 (e.g., CD3ε or CD3γ) and the other is for any other antigen (e.g., a second biological molecule, e.g., a cell surface antigen, e.g., a tumor antigen). Accordingly, a bispecific anti-CD3 antibody may have binding specificities for CD3 and a second biological molecule, such as a second biological molecule (e.g., a tumor antigen) listed in Table 1 and described in U.S. Pub. No. 2010/0111856.In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody wherein the multispecific antibody comprises a second binding domain having specificity for a second antigen, such as: a human leukocyte antigen (HLA)-peptide complex presented on the cell surface by MHC.

[0216] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody wherein the multispecific antibody comprises a second binding domain having specificity for a second antigen selected from the group consisting of: 0772P (CA125, MUC16; Genbank accession no. AF36148); adipophilin (perilipin-2, Adipose differentiation-related protein, ADRP, ADFP, MGC10598; NCBI Reference Sequence: NP—001113.2); AIM-2 (Absent In Melanoma 2, PYHIN4, Interferon-Inducible Protein AIM2; NCBI Reference Sequence: NP—004824.1); ALDH1 A1 (Aldehyde Dehydrogenase 1 Family, Member A1, ALDH1, PUMB1, Retinaldehyde Dehydrogenase 1, ALDC, ALDH-E1, ALHDII, RALDH 1, EC 1.2.1.36, ALDH11, HEL-9, HEL-S-53e, HEL12, RALDH1, Acetaldehyde Dehydrogenase 1, Aldehyde Dehydrogenase 1, Soluble, Aldehyde Dehydrogenase, Liver Cytosolic, ALDH Class 1, Epididymis Luminal Protein 12, Epididymis Luminal Protein 9, Epididymis Secretory Sperm Binding Protein Li 53e, Retinal Dehydrogenase 1, RaIDH1, Aldehyde Dehydrogenase Family 1 Member A1, Aldehyde Dehydrogenase, Cytosolic, EC 1.2.1; NCBI Reference Sequence: NP—000680.2); alpha-actinin-4 (ACTN4, Actinin, Alpha 4, FSGS1, Focal Segmental Glomerulosclerosis 1, Non-Muscle Alpha-Actinin 4, F-Actin Cross-Linking Protein, FSGS, ACTININ-4, Actinin Alpha4 Isoform, alpha-actinin-4; NCBI Reference Sequence: NP—004915.2); alpha-fetoprotein (AFP, HPAFP, FETA, alpha-1-fetoprotein, alpha-fetoglobulin, Alpha-1-fetoprotein, Alpha-fetoglobulin, HP; GenBank: AAB58754.1); Amphiregulin (AREG, SDGF, Schwannoma-Derived Growth Factor, Colorectum Cell-Derived Growth Factor, AR, CRDGF; GenBank: AAA51781.1); ARTC1 (ART1, ADP-Ribosyltransferase 1, Mono(ADP-Ribosyl)Transferase 1, ADP-Ribosyltransferase C2 And C3 Toxin-Like 1, ART2, CD296, RT6, ADP-Ribosyltransferase 2, GPI-Linked NAD(P)(+)-Arginine ADP-Ribosyltransferase 1, EC 2.4.2.31, CD296 Antigen; NP); ASLG659; ASPHD1 (Aspartate Beta-Hydroxylase Domain Containing 1, Aspartate Beta-Hydroxylase Domain-Containing Protein 1, EC 1.14.11.-, EC 1.14.11; GenBank: AAI44153.1); B7-H4 (VTCN1, V-Set Domain Containing T Cell Activation Inhibitor 1, B7H4, B7 Superfamily Member 1, Immune Costimulatory Protein B7-H4, B7h.5, T-Cell Costimulatory Molecule B7x, B7S1, B7X, VCTN1, H4, B7 Family Member, PRO1291, B7 Family Member, H4, T Cell Costimulatory Molecule B7x, V-Set Domain-Containing T-Cell Activation Inhibitor 1, Protein B7S1; GenBank: AAZ17406.1); BAFF-R (TNFRSF13C, Tumor Necrosis Factor Receptor Superfamily, Member 13C, BAFFR, B-Cell-Activating Factor Receptor, BAFF Receptor, BLyS Receptor 3, CVID4, BROMIX, CD268, B Cell-Activating Factor Receptor, prolixin, Tumor Necrosis Factor Receptor Superfamily Member 13C, BR3, CD268 Antigen; NCBI Reference Sequence: NP—443177.1); BAGE-1; BCLX (L); BCR-ABL fusion protein (b3a2); beta-catenin (CTNNB1, Catenin (Cadherin-Associated Protein), Beta 1, 88 kDa, CTNNB, MRD19, Catenin (Cadherin-Associated Protein), Beta 1 (88kD), armadillo, Catenin Beta-1; GenBank: CAA61107.1); BING-4 (WDR46, WD Repeat Domain 46, C6orf11, BING4, WD Repeat-Containing Protein BING4, Chromosome 6 Open Reading Frame 11, FP221, UTP7, WD Repeat-Containing Protein 46; NP); BMPR1 B (bone morphogenetic protein receptor-type IB, Genbank accession no. NM—00120; NP); B-RAF (Brevican (BCAN, BEHAB, Genbank accession no.

AF22905); Brevican (BCAN, Chondroitin Sulfate Proteoglycan 7, Brain-Enriched Hyaluronan-Binding Protein, BEHAB, CSPG7, Brevican Proteoglycan, Brevican Core Protein, Chondroitin Sulfate Proteoglycan BEHAB; GenBank: AAH27971.1); CALCA (Calcitonin-Related Polypeptide Alpha, CALC1, Calcitonin 1, calcitonin, Alpha-Type CGRP, Calcitonin Gene-Related Peptide I, CGRP-I, CGRP, CGRP1, CT, KC, Calcitonin/Calcitonin-Related Polypeptide, Alpha, katacalcin; NP); CASP-5 (CASP5, Caspase 5, Apoptosis-Related Cysteine Peptidase, Caspase 5, Apoptosis-Related Cysteine Protease, Protease ICH-3, Protease TY, ICE(rel)-111, ICE(rel)III, ICEREL-III, ICH-3, caspase-5, TY Protease, EC 3.4.22.58, ICH3, EC 3.4.22; NP); CASP-8; CD19 (CD19-B-lymphocyte antigen CD19 isoform 2 precursor, B4, CVID3 [Homo sapiens], NCBI Reference Sequence: NP—001761.3); CD20 (CD20-B-lymphocyte antigen CD20, membrane-spanning 4-domains, subfamily A, member 1, B1,Bp35,CD20,CVID5,LEU-16,MS4A2,S7; NCBI Reference Sequence: NP—690605.1); CD21 (CD21 (CR2 (Complement receptor or C3DR (C3d/Epstein Barr virus receptor) or Hs.73792 Genbank accession no. M2600); (CD22 (B-cell receptor CD22-B isoform, BL-CAM, Lyb-8, LybB, SIGLEC-2, FLJ22814, Genbank accession No. AK02646); CD22; CD33 (CD33 Molecule, CD33 Antigen (Gp67), Sialic Acid Binding Ig-Like Lectin 3, Sialic Acid-Binding Ig-Like Lectin 3, SIGLEC3, gp67, SIGLEC-3, Myeloid Cell Surface Antigen CD33, p67, Siglec-3, CD33 Antigen; GenBank: AAH28152.1); CD45; CD70 (CD70-tumor necrosis factor (ligand) superfamily, member 7; surface antigen CD70; Ki-24 antigen; CD27 ligand; CD27-L; tumor necrosis factor ligand superfamily member 7; NCBI Reference Sequence for species homo sapiens: NP—001243.1); CD72 (CD72 (B-cell differentiation antigen CD72, Lyb-; 359 aa, µl: 8.66, MW: 40225, TM: 1 [P] Gene Chromosome: 9p13.3, Genbank accession No. NP—001773.); CD79a (CD79a (CD79A, CD79a, immunoglobulin-associated alpha, a B cell-specific protein that covalently interacts with Ig beta (CD79B) and forms a complex on the surface with Ig M molecules, transduces a signal involved in B-cell differentiation), µl: 4.84, MW: 25028 TM: 2 [P] Gene Chromosome: 19q13.2, Genbank accession No. NP—001774.1); CD79b (CD79b (CD79B, CD79b, IGb (immunoglobulin-associated beta), B29, Genbank accession no. NM—000626 or 1103867); Cdc27 (Cell Division Cycle 27, D0S1430E, D17S978E, Anaphase Promoting Complex Subunit 3, Anaphase-Promoting Complex Subunit 3, ANAPC3, APC3, CDC27Hs, H-NUC, CDC27 Homolog, Cell Division Cycle 27 Homolog (S. Cerevisiae), HNUC, NUC2, Anaphase-Promoting Complex, Protein 3, Cell Division Cycle 27 Homolog, Cell Division Cycle

Protein 27 Homolog, Nuc2 Homolog; GenBank: AAH11656.1); CDK4 (Cyclin-Dependent Kinase 4, Cell Division Protein Kinase 4, PSK-J3, EC 2.7.11.22, CMM3, EC 2.7.11; NCBI Reference Sequence: NP—000066.1); CDKN2A (Cyclin-Dependent Kinase Inhibitor 2A, MLM, CDKN2, MTS1, Cyclin-Dependent Kinase Inhibitor 2A (Melanoma, P16, Inhibits CDK4), Cyclin-Dependent Kinase 4 Inhibitor A, Multiple Tumor Suppressor 1, CDK4I, MTS-1, CMM2, P16, ARF, INK4, INK4A, P14, P14ARF, P16-INK4A, P16INK4, P16INK4A, P19, P19ARF, TP16, CDK4 Inhibitor P16-INK4, Cell Cycle Negative Regulator Beta, p14ARF, p16-INK4, p16-INK4a, p16INK4A, p19ARF; NP); CEA; CLL1 (CLL-1 (CLEC12A, MICL, and DCAL, encodes a member of the C-type lectin/C-type lectin-like domain (CTL/CTLD) superfamily. Members of this family share a common protein fold and have diverse functions, such as cell adhesion, cell-cell signaling, glycoprotein turnover, and roles in inflammation and immune response. The protein encoded by this gene is a negative regulator of granulocyte and monocyte function. Several alternatively spliced transcript variants of this gene have been described, but the full-length nature of some of these variants has not been determined. This gene is closely linked to other CTL/CTLD superfamily members in the natural killer gene complex region on chromosome 12p13 (Drickamer K Curr. Opin. Struct. Biol. 9):585-90; van Rhenen A, et al., Blood 110):2659-66; Chen C H, et al. Blood 107):1459-67; Marshall A S, et al. Eur. J. Immunol. 36):2159-69; Bakker A B, et al Cancer Res. 64:8443-50; Marshall A S, et al J. Biol. Chem. 279:14792-80. CLL-1 has been shown to be a type II transmembrane receptor comprising a single C-type lectin-like domain (which is not predicted to bind either calcium or sugar), a stalk region, a transmembrane domain and a short cytoplasmic tail containing an ITIM motif.); CLPP (Caseinolytic Mitochondrial Matrix Peptidase Proteolytic Subunit, Endopeptidase Clp, EC 3.4.21.92, PRLTS3, ATP-Dependent Protease ClpAP (E. Coli), ClpP (Caseinolytic Protease, ATP-Dependent, Proteolytic Subunit, E. Coli) Homolog, ClpP Caseinolytic Peptidase, ATP-Dependent, Proteolytic Subunit Homolog (E. Coli), ClpP Caseinolytic Protease, ATP-Dependent, Proteolytic Subunit Homolog (E. Coli), human, Proteolytic Subunit, ATP-Dependent Protease ClpAP, Proteolytic Subunit, Human, ClpP Caseinolytic Peptidase ATP-Dependent, Proteolytic Subunit, ClpP Caseinolytic Peptidase, ATP-Dependent, Proteolytic Subunit Homolog, ClpP Caseinolytic Protease, ATP-Dependent, Proteolytic Subunit Homolog, Putative ATP-Dependent Clp Protease Proteolytic Subunit, Mitochondrial; NP); COA-1; CPSF; CRIPTO (CRIPTO (CR, CR1, CRGF, CRIPTO, TDGF1, teratocarcinoma-derived growth factor, Genbank accession no. NP—003203 or NM—00321); Cw6; CXCR5 CXCR5 (Burkitt's lymphoma receptor 1, a G protein-coupled receptor that is activated by the CXCL13 chemokine, functions in lymphocyte migration and humoral defense, plays a role in HIV-2 infection and perhaps development of AIDS, lymphoma, myeloma, and leukemia); 372 aa, µl: 8.54 MW: 41959 TM: 7 [P] Gene Chromosome: 11q23.3, Genbank accession No. NP—001707.); CXORF61 CXORF61—chromosome X open reading frame 61[Homo sapiens], NCBI Reference Sequence: NP—001017978.1); cyclin D1 (CCND1, BCL1, PRAD1, D11S287E, B-Cell CLL/Lymphoma 1, B-Cell Lymphoma 1 Protein, BCL-1 Oncogene, PRAD1 Oncogene, Cyclin D1 (PRAD1: Parathyroid Adenomatosis 1), G1/S-Specific Cyclin D1, Parathyroid Adenomatosis 1, U21B31, G1/S-Specific Cyclin-D1, BCL-1; NCBI Reference Sequence: NP—444284.1); Cyclin-A1 (CCNA1, CT146, Cyclin A1; GenBank: AAH36346.1); dek-can fusion protein; DKK1 (Dickkopf WNT Signaling Pathway Inhibitor 1, SK, hDkk-1, Dickkopf (Xenopus Laevis) Homolog 1, Dickkopf 1 Homolog (Xenopus Laevis), DKK-1, Dickkopf 1 Homolog, Dickkopf Related Protein-1, Dickkopf-1 Like, Dickkopf-Like Protein 1, Dickkopf-Related Protein 1, Dickkopf-1, Dkk-1; GenBank: AAQ89364.1); DR1 (Down-Regulator Of Transcription 1, TBP-Binding (Negative Cofactor 2), Negative Cofactor 2-Beta, TATA-Binding Protein-Associated Phosphoprotein, NC2, NC2-BETA, Protein Dr1, NC2-beta, Down-Regulator Of Transcription 1; NCBI Reference Sequence: NP—001929.1); DR13 (Major Histocompatibility Complex, Class II, DR Beta 1, HLA-DR1B, DRw10, DW2.2/DR2.2, SS1, DRB1, HLA-DRB, HLA Class II Histocompatibility Antigen, DR-1 Beta Chain, Human Leucocyte Antigen DRB1, Lymphocyte Antigen DRB1, MHC Class II Antigen, MHC Class II HLA-DR Beta 1 Chain, MHC Class II HLA-DR-Beta Cell Surface Glycoprotein, MHC Class II HLA-DRw10-Beta, DR-1, DR-12, DR-13, DR-14, DR-16, DR-4, DR-5, DR-7, DR-8, DR-9, DR1, DR12, DR13, DR14, DR16, DR4, DR5, DR7, DRB, DR9, DRw11, DRw8, HLA-DRB2, Clone P2-Beta-3, MHC Class II Antigen DRB1*1, MHC Class II Antigen DRB1*10, MHC Class II Antigen DRB1*11, MHC Class II Antigen DRB1*12, MHC Class II Antigen DRB1*13, MHC Class II Antigen DRB1*14, MHC Class II Antigen DRB1*15, MHC Class II Antigen DRB1*16, MHC Class II Antigen DRB1*3, MHC Class II Antigen DRB1*4, MHC Class II Antigen DRB1*7, MHC Class II Antigen DRB1*8, MHC Class II Antigen DRB1*9; NP); E16 (E16 (LAT1, SLC7A5, Genbank accession no. NM—00348); EDAR (EDAR— tumor necrosis factor receptor superfamily member EDAR precursor, EDA-A1 receptor; downless homolog; ectodysplasin-A receptor; ectodermal dysplasia receptor; anhidrotic ectodysplasin receptor 1, DL; ECTD10A; ECTD10B; ED1R; ED3; ED5; EDA-A1R; EDA1R; EDA3; HRM1 [Homo sapiens]; NCBI Reference Sequence: NP—071731.1); EFTUD2 (Elongation Factor Tu GTP Binding Domain Containing 2, Elongation Factor Tu GTP-Binding Domain-Containing Protein 2, hSNU114, SNU114 Homolog, U5 SnRNP-Specific Protein, 116 KDa, MFDGA, KIAA0031, 116 KD, U5 SnRNP Specific Protein, 116 KDa U5 Small Nuclear Ribonucleoprotein Component, MFDM, SNRNP116, Snrp116, Snu114, U5-116KD, SNRP116, U5-116 KDa; GenBank: AAH02360.1); EGFR (Epidermal Growth Factor Receptor, ERBB, Proto-Oncogene C-ErbB-1, Receptor Tyrosine-Protein Kinase ErbB-1, ERBB1, HER1, EC 2.7.10.1, Epidermal Growth Factor Receptor (Avian Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog), Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog (Avian), PIG61, Avian Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog, Cell Growth Inhibiting Protein 40, Cell Proliferation-Inducing Protein 61, mENA, EC 2.7.10; GenBank: AAH94761.1); EGFR-G719A; EGFR-G719C; EGFR-G719S; EGFR-L858R; EGFR-L861 Q; EGFR-57681; EGFR-T790M; Elongation factor 2 (EEF2, Eukaryotic Translation Elongation Factor 2, EF2, Polypeptidyl-TRNA Translocase, EF-2, SCA26, EEF-2; NCBI Reference Sequence: NP—001952.1); ENAH (hMena) (Enabled Homolog (Drosophila), MENA, Mammalian Enabled, ENA, NDPP1, Protein Enabled Homolog; GenBank: AAH95481.1)—results for just “ENAH” not “ENAH (hMena)”; EpCAM (Epithelial Cell Adhesion Molecule, M4S1, MIC18, Tumor-Associated Calcium Signal Transducer 1, TACSTD1, TROP1, Adenocarcinoma-Associated Antigen, Cell Surface Glycoprotein Trop-1, Epithelial Glycoprotein 314, Major Gastrointestinal Tumor-Associated Protein GA733-2, EGP314, KSA, DIAR5, HNPCC8, Antigen Identified By Monoclonal Antibody AUA1, EGP-2, EGP40, ESA, KS1/4, MK-1, Human Epithelial Glycoprotein-2, Membrane Component, Chromosome 4, Surface Marker (35kD Glycoprotein), EGP, Ep-CAM, GA733-2, M1S2, CD326 Antigen, Epithelial Cell Surface Antigen, hEGP314, KS 1/4 Antigen, ACSTD1; GenBank: AAH14785.1); EphA3 (EPH Receptor A3, ETK1, ETK, TYRO4, HEK, Eph-Like Tyrosine Kinase 1, Tyrosine-Protein Kinase Receptor ETK1, EK4, EPH-Like Kinase 4, EC 2.7.10.1, EPHA3, HEK4, Ephrin Type-A Receptor 3, Human Embryo Kinase 1, TYRO4 Protein Tyrosine Kinase, hEK4, Human Embryo Kinase, Tyrosine-Protein Kinase TYRO4, EC 2.7.10; GenBank: AAH63282.1); EphB2R; Epiregulin (EREG, ER, proepiregulin; GenBank: AAI36405.1); ETBR (EDNRB, Endothelin Receptor Type B, HSCR2, HSCR, Endothelin Receptor Non-Selective

Type, ET-B, ET-BR, ETRB, ABCDS, WS4A, ETB, Endothelin B Receptor; NP); ETV6-AML1 fusion protein; EZH2 (Enhancer Of Zeste Homolog 2 (Drosophila), Lysine N-Methyltransferase 6, ENX-1, KMT6 EC 2.1.1.43, EZH1, WVS, Enhancer Of Zeste (Drosophila) Homolog 2, ENX1, EZH2b, KMT6A, WVS2, Histone-Lysine N-Methyltransferase EZH2, Enhancer Of Zeste Homolog 2, EC 2.1.1; GenBank: AAH10858.1); FcRH1 (FCRL1, Fc Receptor-Like 1, FCRH1, Fc Receptor Homolog 1, FcR-Like Protein 1, Immune Receptor Translocation-Associated Protein 5, IFGP1, IRTA5, hIFGP1, IFGP Family Protein 1, CD307a, Fc Receptor-Like Protein 1, Immunoglobulin Superfamily Fc Receptor, Gp42, FcRL1, CD307a Antigen; GenBank: AAH33690.1); FcRH2 (FCRL2, Fc Receptor-Like 2, SPAP1, SH2 Domain-Containing Phosphatase Anchor Protein 1, Fc Receptor Homolog 2, FcR-Like Protein 2, Immunoglobulin Receptor Translocation-Associated Protein 4, FCRH2, IFGP4, IRTA4, IFGP Family Protein 4, SPAP1A, SPAP1 B, SPAP1C, CD307b, Fc Receptor-Like Protein 2, Immune Receptor Translocation-Associated Protein 4, Immunoglobulin Superfamily Fc Receptor, Gp42, SH2 Domain Containing Phosphatase Anchor Protein 1, FcRL2, CD307b Antigen; GenBank: AAQ88497.1); FcRH5 (FCRL5, Fc Receptor-Like 5, IRTA2, Fc Receptor Homolog 5, FcR-Like Protein 5, Immune Receptor Translocation-Associated Protein 2, BXMAS1, FCRH5, CD307, CD307e, PRO820, Fc Receptor-Like Protein 5, Immunoglobulin Superfamily Receptor Translocation Associated 2 (IRTA2), FCRL5, CD307e Antigen; GenBank: AAI01070.1); FLT3-ITD; FN1(Fibronectin 1, Cold-Insoluble Globulin, FN, Migration-Stimulating Factor, CIG, FNZ, GFND2, LETS, ED-B, FINC, GFND, MSF, fibronectin; GenBank: AAI43764.1); G250 (MN, CAIX, Carbonic Anhydrase IX, Carbonic Dehydratase, RCC-Associated Protein G250, Carbonate Dehydratase IX, Membrane Antigen MN, Renal Cell Carcinoma-Associated Antigen G250, CA-IX, P54/58N, pMW1, RCC-Associated Antigen G250, Carbonic Anhydrase 9; NP);—alias results for “G250” not “G250/MN/CAIX”; GAGE-1,2,8; GAGE-3,4,5,6,7; GDNF-Ra1 (GDNF family receptor alpha 1; GFRA1; GDNFR; GDNFRA; RETL1; TRNR1; RET1 L; GDNFR-alpha1; GFR-ALPHA-; U95847; BC014962; NM—145793 NM—005264); GEDA (Genbank accession No. AY26076); GFRA1—GDNF family receptor alpha-1; GDNF receptor alpha-1; GDNFR-alpha-1; GFR-alpha-1; RET ligand 1; TGF-beta-related neurotrophic factor receptor 1 [Homo sapiens]; ProtKB/Swiss-Prot: P56159.2; glypican-3 (GPC3, Glypican 3, SDYS, Glypican Proteoglycan 3, Intestinal Protein OCI-5, GTR2-2, MXR7, SGBS1, DGSX, OCI-5. SGB, SGBS, Heparan Sulphate Proteoglycan, Secreted Glypican-3, OCI5; GenBank:

AAH35972.1); GnTVf; gp100 (PMEL, Premelanosome Protein, SILV, D12S53E, PMEL17, SIL, Melanocyte Protein Pmel 17, Melanocytes Lineage-Specific Antigen GP100, Melanoma-Associated ME20 Antigen, Silver Locus Protein Homolog, ME20-M, ME20M, P1, P100, Silver (Mouse Homolog) Like, Silver Homolog (Mouse), ME20, SI, Melanocyte Protein Mel 17, Melanocyte Protein PMEL, Melanosomal Matrix Protein17, Silver, Mouse, Homolog Of; GenBank: AAC60634.1); GPC; GPNMB (Glycoprotein (Transmembrane) Nmb, Glycoprotein NMB, Glycoprotein Nmb-Like Protein, osteoactivin, Transmembrane Glycoprotein HGFIN, HGFIN, NMB, Transmembrane Glycoprotein, Transmembrane Glycoprotein NMB; GenBank: AAH32783.1); GPR172A (G protein-coupled receptor 172A; GPCR41; FLJ11856; D15Ertd747e); NP—078807.1; NM—024531.3); GPR19 (G protein-coupled receptor 19; Mm.478; NP—006134.1; NM—006143.2); GPR54 (KISS1 receptor; KISS1R; GPR54; HOT7T175; AXOR1; NP—115940.2; NM—032551.4); HAVCR1 (Hepatitis A Virus Cellular Receptor 1, T-Cell Immunoglobulin Mucin Family Member 1, Kidney Injury Molecule 1, KIM-1, KIM1, TIM, TIM-1, TIM1, TIMD-1, TIMD1, T-Cell Immunoglobulin Mucin Receptor 1, T-Cell Membrane Protein 1, HAVCR, HAVCR-1, T Cell Immunoglobin Domain And Mucin Domain Protein 1, HAVcr-1, T-Cell Immunoglobulin And Mucin Domain-Containing Protein 1; GenBank: AAH13325.1); HER2 (ERBB2, V-Erb-B2 Avian Erythroblastic Leukemia Viral Oncogene Homolog 2, NGL, NEU, Neuro/Glioblastoma Derived Oncogene Homolog, Metastatic Lymph Node Gene 19 Protein, Proto-Oncogene C-ErbB-2, Proto-Oncogene Neu, Tyrosine Kinase-Type Cell Surface Receptor HER2, MLN 19, p185erbB2, EC 2.7.10.1, V-Erb-B2 Avian Erythroblastic Leukemia Viral Oncogene Homolog 2 (Neuro/Glioblastoma Derived Oncogene Homolog), CD340, HER-2, HER-2/neu, TKR1, C-Erb B2/Neu Protein, herstatin, Neuroblastoma/Glioblastoma Derived Oncogene Homolog, Receptor Tyrosine-Protein Kinase ErbB-2, V-Erb-B2 Erythroblastic Leukemia Viral Oncogene Homolog 2, Neuro/Glioblastoma Derived Oncogene Homolog, MLN19, CD340 Antigen, EC 2.7.10; NP); HER-2/neu—alias of above; HERV-K-MEL; HLA-DOB (Beta subunit of MHC class II molecule (la antigen) that binds peptides and presents them to CD4+ T lymphocytes); 273 aa, μl: 6.56, MW: 30820.TM: 1 [P] Gene Chromosome: 6p21.3, Genbank accession No. NP—002111); hsp70-2 (HSPA2, Heat Shock 70 kDa Protein 2, Heat Shock 70kD Protein 2, HSP70-3, Heat Shock-Related 70 KDa Protein 2, Heat Shock 70 KDa Protein 2; GenBank: AAD21815.1); IDO1 (Indoleamine 2,3-Dioxygenase 1, IDO, INDO, Indoleamine-Pyrrole 2,3-Dioxygenase, ID0-1, Indoleamine-Pyrrole

2,3 Dioxygenase, Indolamine 2,3 Dioxygenase, Indole 2,3 Dioxygenase, EC 1.13.11.52; NCBI Reference Sequence: NP—002155.1); IGF2B3; IL13Ralpha2 (IL13RA2, Interleukin 13 Receptor, Alpha 2, Cancer/Testis Antigen 19, Interleukin-13-Binding Protein, IL-13R-alpha-2, IL-13RA2, IL-13 Receptor Subunit Alpha-2, IL-13R Subunit Alpha-2, CD213A2, CT19, IL-13R, IL13BP, Interleukin 13 Binding Protein, Interleukin 13 Receptor Alpha 2 Chain, Interleukin-13 Receptor Subunit Alpha-2, IL13R, CD213a2 Antigen; NP); IL20Rα; Intestinal carboxyl esterase; IRTA2 (alias of FcRH5); Kallikrein 4 (KLK4, Kallikrein-Related Peptidase 4, PRSS17, EMSP1, Enamel Matrix Serine Proteinase 1, Kallikrein-Like Protein 1, Serine Protease 17, KLK-L1, PSTS, AI2A1, Kallikrein 4 (Prostase, Enamel Matrix, Prostate), ARM1, EMSP, Androgen-Regulated Message 1, Enamel Matrix Serine Protease 1, kallikrein, kallikrein-4, prostase, EC 3.4.21.-, Prostase, EC 3.4.21; GenBank: AAX30051.1); KIF20A (Kinesin Family Member 20A, RAB6KIFL, RAB6 Interacting, Kinesin-Like (Rabkinesin6), Mitotic a; LAGE-1; LDLR-fucosyltransferaseASfusion protein; Lengsin (LGSN, Lengsin, Lens Protein With Glutamine Synthetase Domain, GLULD1, Glutamate-Ammonia Ligase Domain-Containing Protein 1, LGS, Glutamate-Ammonia Ligase (Glutamine Synthetase) Domain Containing 1, Glutamate-Ammonia Ligase (Glutamine Synthase) Domain Containing 1, Lens Glutamine Synthase-Like; GenBank: AAF61255.1); LGR5 (leucine-rich repeat-containing G protein-coupled receptor 5; GPR49, GPR6; NP—003658.1; NM—003667.2; LY64 (Lymphocyte antigen 64 (RP10, type I membrane protein of the leucine rich repeat (LRR) family, regulates B-cell activation and apoptosis, loss of function is associated with increased disease activity in patients with systemic lupus erythematosis); 661 aa, μl: 6.20, MW: 74147 TM: 1 [P] Gene Chromosome: 5q12, Genbank accession No. NP—005573.; Ly6E (lymphocyte antigen 6 complex, locus E; Ly67, RIG-E,SCA-2, TSA-; NP—002337.1; NM—002346.2); Ly6G6D (lymphocyte antigen 6 complex, locus G6D; Ly6-D, MEGT; NP—067079.2; NM—021246.2); LY6K (lymphocyte antigen 6 complex, locus K; LY6K; HSJ001348; FLJ3522; NP—059997.3; NM—017527.3); LyPD1-LY6/PLAUR domain containing 1, PHTS [Homo sapiens], GenBank: AAH17318.1); MAGE-A1 (Melanoma Antigen Family A, 1 (Directs Expression Of Antigen MZ2-E, MAGE1, Melanoma Antigen Family A 1, MAGEA1, Melanoma Antigen MAGE-1, Melanoma-Associated Antigen 1, Melanoma-Associated Antigen MZ2-E, Antigen MZ2-E, Cancer/Testis Antigen 1.1, CT1.1, MAGE-1 Antigen, Cancer/Testis Antigen Family 1, Member 1, Cancer/Testis Antigen Family 1, Member 1, MAGE1A; NCBI Reference Sequence: NP—004979.3); MAGE-A10

(MAGEA10, Melanoma Antigen Family A, 10, MAGE10, MAGE-10 Antigen, Melanoma-Associated Antigen 10, Cancer/Testis Antigen 1.10, CT1.10, Cancer/Testis Antigen Family 1, Member 10, Cancer/Testis Antigen Family 1, Member 10; NCBI Reference Sequence: NP—001238757.1); MAGE-A12 (MAGEA12, Melanoma Antigen Family A, 12, MAGE12, Cancer/Testis Antigen 1.12, CT1.12, MAGE12F Antigen, Cancer/Testis Antigen Family 1, Member 12, Cancer/Testis Antigen Family 1, Member 12, Melanoma-Associated Antigen 12, MAGE-12 Antigen; NCBI Reference Sequence: NP—001159859.1); MAGE-A2 (MAGEA2, Melanoma Antigen Family A, 2, MAGE2, Cancer/Testis Antigen 1.2, CT1.2, MAGEA2A, MAGE-2 Antigen, Cancer/Testis Antigen Family 1, Member 2, Cancer/Testis Antigen Family 1, Member 2, Melanoma Antigen 2, Melanoma-Associated Antigen 2; NCBI Reference Sequence: NP—001269434.1); MAGE-A3 (MAGEA3, Melanoma Antigen Family A, 3, MAGE3, MAGE-3 Antigen, Antigen MZ2-D, Melanoma-Associated Antigen 3, Cancer/Testis Antigen 1.3, CT1.3, Cancer/Testis Antigen Family 1, Member 3, HIPS, HYPD, MAGEA6, Cancer/Testis Antigen Family 1, Member 3; NCBI Reference Sequence: NP—005353.1); MAGE-A4 (MAGEA4, Melanoma Antigen Family A, 4, MAGE4, Melanoma-Associated Antigen 4, Cancer/Testis Antigen 1.4, CT1.4, MAGE-4 Antigen, MAGE-41 Antigen, MAGE-X2 Antigen, MAGE4A, MAGE4B, Cancer/Testis Antigen Family 1, Member 4, MAGE-41, MAGE-X2, Cancer/Testis Antigen Family 1, Member 4; NCBI Reference Sequence: NP—001011550.1); MAGE-A6 (MAGEA6, Melanoma Antigen Family A, 6, MAGE6, MAGE-6 Antigen, Melanoma-Associated Antigen 6, Cancer/Testis Antigen 1.6, CT1.6, MAGE3B Antigen, Cancer/Testis Antigen Family 1, Melanoma Antigen Family A 6, Member 6, MAGE-3b, MAGE3B, Cancer/Testis Antigen Family 1, Member 6; NCBI Reference Sequence: NP—787064.1); MAGE-A9 (MAGEA9, Melanoma Antigen Family A, 9, MAGE9, MAGE-9 Antigen, Melanoma-Associated Antigen 9, Cancer/Testis Antigen 1.9, CT1.9, Cancer/Testis Antigen Family 1, Member 9, Cancer/Testis Antigen Family 1, Member 9, MAGEA9A; NCBI Reference Sequence: NP—005356.1); MAGE-C1 (MAGEC1, Melanoma Antigen Family C, 1, Cancer/Testis Antigen 7.1, CT7.1, MAGE-C1 Antigen, Cancer/Testis Antigen Family 7, Member 1, CT7, Cancer/Testis Antigen Family 7, Member 1, Melanoma-Associated Antigen C1; NCBI Reference Sequence: NP—005453.2); MAGE-C2 (MAGEC2, Melanoma Antigen Family C, 2, MAGEE1, Cancer/Testis Antigen 10, CT10, HCA587, Melanoma Antigen, Family E, 1, Cancer/Testis Specific, Hepatocellular Carcinoma-Associated Antigen 587, MAGE-C2 Antigen, MAGE-E1 Antigen, Hepatocellular Cancer Antigen 587, Melanoma-Associated Antigen C2; NCBI Reference Sequence: NP—057333.1); mammaglobin-A (SCGB2A2, Secretoglobin, Family 2A, Member 2, MGB1, Mammaglobin 1, UGB2, Mammaglobin A, mammaglobin-A, Mammaglobin-1, Secretoglobin Family 2A Member 2; NP); MART2 (H HAT, Hedgehog Acyltransferase, SKI1, Melanoma Antigen Recognized By T-Cells 2, Skinny Hedgehog Protein 1, Skn, Melanoma Antigen Recognized By T Cells 2, Protein-Cysteine N-Palmitoyltransferase HHAT, EC 2.3.1.-; GenBank: AAH39071.1); M-CSF (CSF1, Colony Stimulating Factor 1 (Macrophage), MCSF, CSF-1, lanimostim, Macrophage Colony-Stimulating Factor 1, Lanimostim; GenBank: AAH21117.1); MCSP (SMCP, Sperm Mitochondria-Associated Cysteine-Rich Protein, MCS, Mitochondrial Capsule Selenoprotein, HSMCSGEN1, Sperm Mitochondrial-Associated Cysteine-Rich Protein; NCBI Reference Sequence: NP—109588.2); XAGE-1b/GAGED2a; WT1 (Wilms Tumor 1, WAGR, GUD, WIT-2, WT33, Amino-Terminal Domain Of EWS, NPHS4, Last Three Zinc Fingers Of The DNA-Binding Domain Of WT1, AWT1, Wilms Tumor Protein, EWS-WT1; GenBank: AAB33443.1); VEGF; Tyrosinase (TYR; OCAIA; OCA1A; tyrosinase; SHEP; NP—000363.1; NM—000372.4; GenBank: AAB60319.1); TrpM4 (BR22450, FLJ20041, TRPM4, TRPM4B, transient receptor potential cation channel, subfamily M, member 4, Genbank accession no. NM—01763); TRP2-INT2; TRP-2; TRP-1/gp75 (Tyrosinase-Related Protein 1, 5,6-Dihydroxyindole-2-Carboxylic Acid Oxidase, CAS2, CATB, TYRP, OCAS, Catalase B, b-PROTEIN, Glycoprotein 75, EC 1.14.18., Melanoma Antigen Gp75, TYRP1, TRP, TYRRP, TRP1, SHEP11, DHICA Oxidase, EC 1.14.18, GP75, EC 1.14.18.1; Triosephosphate isomerase (Triosephosphate isomerase 1, TPID, Triose-Phosphate Isomerase, HEL-S-49, TIM, Epididymis Secretory Protein Li 49, TPI, Triosephosphate Isomerase, EC 5.3.1.1; TRAG-3 (CSAG Family Member 2, Cancer/Testis Antigen Family 24, CSAG3B, Member 2, CSAG Family Member 3B, Cancer/Testis Antigen Family 24 Member 2, Cancer/Testis Antigen 24.2, Chondrosarcoma-Associated Gene 2/3 Protein, Taxol-Resistant-Associated Gene 3 Protein, Chondrosarcoma-Associated Gene 2/3 Protein-Like, CT24.2, Taxol Resistance Associated Gene 3, TRAG-3, CSAG3A, TRAG3;); TMEM46 (shisa homolog 2 (Xenopus laevis); SHISA; NP—001007539.1; NM—001007538.1; TMEM118 (ring finger protein, transmembrane2; RNFT2; FLJ1462; NP—001103373.1; NM—001109903.1; TMEFF1 (transmembrane protein with EGF-like and two follistatin-like domains 1; Tomoregulin-; H7365; C9orf2; C9ORF2; U19878; X83961; NM—080655; NM—003692; TGF-betaRII (TGFBR2, Transforming Growth Factor, Beta Receptor II (70/80 kDa), TGFbeta-RII, MFS2, tbetaR-II, TGFR-2, TGF-Beta Receptor Type IIB, TGF-Beta Type II Receptor, TGF-Beta Receptor Type-2, EC 2.7.11.30, Transforming Growth Factor Beta Receptor Type IIC, AAT3, TbetaR-II, Transforming Growth Factor, Beta Receptor II (70-80kD), TGF-Beta Receptor Type II, FAA3, Transforming Growth Factor-Beta Receptor Type II, LDS1 B, HNPCC6, LDS2B, LDS2, RITC, EC 2.7.11, TAAD2; TENB2 (TMEFF2, tomoregulin, TPEF, HPP1, TR, putative transmembrane proteoglycan, related to the EGF/heregulin family of growth factors and follistatin); 374 aa, NCBI Accession: AAD55776, AAF91397, AAG49451, NCBI RefSeq: NP—057276; NCBI Gene: 23671; OMIM: 605734; SwissProt Q9UIK5; Genbank accession No. AF179274; AY358907, CAF85723, CQ782436; TAG-2; TAG-1 (Contactin 2 (Axonal), TAG-1, AXT, Axonin-1 Cell Adhesion Molecule, TAX, Contactin 2 (transiently Expressed), TAXI, Contactin-2, Axonal Glycoprotein TAG-1, Transiently-Expressed Axonal Glycoprotein, Transient Axonal Glycoprotein, Axonin-1, TAX-1, TAG1, FAMES; PRF: 444868); SYT-SSX1 or -SSX2 fusion protein; survivin; STEAP2 (HGNC 8639, IPCA-1, PCANAP1, STAMP1, STEAP2, STMP, prostate cancer associated gene 1, prostate cancer associated protein 1, six transmembrane epithelial antigen of prostate 2, six transmembrane prostate protein, Genbank accession no. AF45513; STEAP1 (six transmembrane epithelial antigen of prostate, Genbank accession no. NM—01244; SSX-4; SSX-2 (SSX2, Synovial Sarcoma, X Breakpoint2, X Breakpoint 2, SSX, X Breakpoint 2B, Cancer/Testis Antigen 5.2, X-Chromosome-Related 2, Tumor Antigen HOM-MEL-40, CT5.2, HD21, Cancer/Testis Antigen Family 5, HOM-MEL-40, Isoform B, Cancer/Testis Antigen Family 5 member 2a, member 2a, Protein SSX2, Sarcoma, Sarcoma, Synovial, X-Chromosome-Related 2, synovial, Synovial Sarcoma, X Breakpoint 2B, Synovial Sarcomam, SSX2A; Sp17; SOX10 (SRY (Sex Determining Region Y)-Box 10, mouse, PCWH, DOM, WS4, WS2E, WS4C, Dominant Megacolon, mouse, Human Homolog Of, Dominant Megacolon, SRY-Related HMG-Box Gene 10, Human Homolog Of, transcription Factor SOX-10; GenBank: CAG30470.1); SNRPD1 (Small Nuclear Ribonucleoprotein D1, Small Nuclear Ribonucleoprotein D1, Polypeptide 16 kDa, Polypeptide (16kD), SNRPD, HsT2456, Sm-D1, SMD1, Sm-D Autoantigen, Small Nuclear Ribonucleoprotein D1 Polypeptide 16 kDa Pseudogene, SnRNP Core Protein D1, Small Nuclear Ribonucleoprotein Sm D1; SLC35D3 (Solute Carrier Family 35, Member D3, FRCL1, Fringe Connection-Like Protein 1, bA55K22.3, Frc, Fringe-Like 1, Solute Carrier Family 35 Member D3; NCBI GenBank: NC—000006.11

NC—018917.2 NT—025741.16); SIRT2 (Sirtuin 2, NAD-Dependent Deacetylase Sirtuin-2, SIRL2, Silent Information Regulator 2, Regulatory Protein SIR2 Homolog 2, Sir2-Related Protein Type 2, SIR2-Like Protein 2, Sirtuin Type 2, Sirtuin (Silent Mating Type Information Regulation 2 Homolog) 2 (S. cerevisiae), Sirtuin-2, Sirtuin (Silent Mating Type Information Regulation 2, S. cerevisiae, Homolog) 2, EC 3.5.1., SIR2; GenBank: AAK51133.1); Sema 5b (FLJ10372, KIAA1445, Mm.42015, SEMA5B, SEMAG, Semaphorin 5b Hlog, sema domain, seven thrombospondin repeats (type 1 and type 1-like), Transmembrane Domain™ and short cytoplasmic domain, (semaphorin) 5B, Genbank accession no. AB04087; secernin 1 (SCRN1, SES1, KIAA0193, secerin-1; GenBank: EAL24458.1); SAGE (SAGE1, Sarcoma Antigen 1, Cancer/Testis Antigen 14, CT14, Putative Tumor Antigen; NCBI Reference Sequence: NP—061136.2); RU2AS (KAAG1, Kidney Associated Antigen 1, RU2AS, RU2 Antisense Gene Protein, Kidney-Associated Antigen 1; GenBank: AAF23613.1); RNF43-E3 ubiquitin-protein ligase RNF43 precursor [Homo sapiens], RNF124; URCC; NCBI Reference Sequence: NP—060233.3; RhoC (RGS5 (Regulator Of G-Protein Signaling 5, MSTP032, Regulator Of G-Protein Signalling 5, MSTP092, MST092, MSTP106, MST106, MSTP129, MST129; GenBank: AAB84001.1); RET (ret proto-oncogene; MEN2A; HSCR1; MEN2B; MTC1; PTC; CDHF12; Hs.168114; RET51; RET-ELE; NP—066124.1; NM—020975.4); RBAF600 (UBR4, Ubiquitin Protein Ligase E3 Component N-Recognin 4, Zinc Finger, UBR1 Type 1, ZUBR1, E3 Ubiquitin-Protein Ligase UBR4, RBAF600, 600 KDa Retinoblastoma Protein-Associated Factor, Zinc Finger UBR1-Type Protein 1, EC 6.3.2., N-recognin-4, KIAA0462, p600, EC 6.3.2, KIAA1307; GenBank: AAL83880.1); RAGE-1 (MOK, MOK Protein Kinase, Renal Tumor Antigen, RAGE, MAPK/MAK/MRK Overlapping Kinase, Renal Tumor Antigen 1, Renal Cell Carcinoma Antigen, RAGE-1, EC 2.7.11.22, RAGE1; UniProtKB/Swiss-Prot: Q9UQ07.1); RAB38/NY-MEL-1 (RAB38, NY-MEL-1, RAB38, Member RAS Oncogene Family, Melanoma Antigen NY-MEL-1, Rab-Related GTP-Binding Protein, Ras-Related Protein Rab-38, rrGTPbp; GenBank: AAH15808.1); PTPRK (DJ480J14.2.1 (Protein Tyrosine Phosphatase, Receptor Type, K R-PTP-KAPPA, Protein Tyrosine Phosphatase Kappa, Protein Tyrosine Phosphatase Kappa), Protein Tyrosine Phosphatase, Receptor Type, K, Protein-Tyrosine Phosphatase Kappa, Protein-Tyrosine Phosphatase, Receptor Type, Kappa, R-PTP-kappa, Receptor-Type Tyrosine-Protein Phosphatase Kappa, EC 3.1.3.48, PTPK; GenBank: AAI44514.1); PSMA; PSCA hIg(2700050C12Rik, C530008016Rik, RIKEN cDNA 2700050C12, RIKEN cDNA

2700050C12 gene, Genbank accession no. AY358628); PSCA (Prostate stem cell antigen precursor, Genbank accession no. AJ29743; PRDX5 (Peroxiredoxin 5, EC 1.11.1.15, TPx Type VI, B166, Antioxidant Enzyme B166, HEL-S-55, Liver Tissue 2D-Page Spot 71 B, PMP20, Peroxisomal Antioxidant Enzyme, PRDX6, Thioredoxin Peroxidase PMP20, PRXV, AOEB166, Epididymis Secretory Protein Li 55, Alu Co-Repressor 1, Peroxiredoxin-5, Mitochondrial, Peroxiredoxin V, prx-V, Thioredoxin Reductase, Prx-V, ACR1, Alu Corepressor, PLP; GenBank: CAG33484.1); PRAME (Preferentially Expressed Antigen In Melanoma, Preferentially Expressed Antigen Of Melanoma, MAPE, 01P-4, OIPA, CT130, Cancer/Testis Antigen 130, Melanoma Antigen Preferentially Expressed In Tumors, Opa-Interacting Protein 4, Opa-Interacting Protein 01P4; GenBank: CAG30435.1); pml-RARalpha fusion protein; PMEL17 (silver homolog; SILV; D12S53E; PMEL17; SI; SIL); ME20; gp10 BC001414; BT007202; M32295; M77348; NM—006928; PBF (ZNF395, Zinc Finger Protein 395, PRF-1, Huntington disease regulatory, HD Gene Regulatory Region-Binding Protein, Region-Binding Protein 2, Protein 2, Papillomavirus Regulatory Factor 1, HD-Regulating Factor 2, Papillomavirus-Regulatory Factor, PRF1, HDBP-2, Si-1-8-14, HDBP2, Huntington'S Disease Gene Regulatory Region-Binding Protein 2, HDRF-2, Papillomavirus Regulatory Factor PRF-1, PBF; GenBank: AAH01237.1); PAX5 (Paired Box 5, Paired Box Homeotic Gene 5, BSAP, Paired Box Protein Pax-5, B-Cell Lineage Specific Activator, Paired Domain Gene 5, Paired Box Gene 5 (B-Cell Lineage Specific Activator Protein), B-Cell-Specific Transcription Factor, Paired Box Gene 5 (B-Cell Lineage Specific Activator); PAP (REG3A, Regenerating Islet-Derived 3 Alpha, INGAP, PAP-H, Hepatointestinal Pancreatic Protein, PBBCGF, Human Proislet Peptide, REG-Ill, Pancreatitis-Associated Protein 1, Regi, Reg III-Alpha, hepatocarcinoma-intestine-pancreas, Regenerating Islet-Derived Protein III-Alpha, Pancreatic Beta Cell Growth Factor, HIP, PAP Homologous Protein, HIP/PAP, Proliferation-Inducing Protein 34, PAP1, Proliferation-Inducing Protein 42, REG-3-alpha, Regenerating Islet-Derived Protein 3-Alpha, Pancreatitis-Associated Protein; GenBank: AAH36776.1); p53 (TP53, Tumor Protein P53, TPR53, P53, Cellular Tumor Antigen P53, Antigen NY-CO-13, Mutant Tumor Protein 53, Phosphoprotein P53, P53 Tumor Suppressor, BCC7, Transformation-Related Protein 53, LFS1, tumor Protein 53, Li-Fraumeni Syndrome, Tumor Suppressor P53; P2X5 (Purinergic receptor P2X ligand-gated ion channel 5, an ion channel gated by extracellular ATP, may be involved in synaptic transmission and neurogenesis, deficiency may contribute to the pathophysiology of idiopathic detrusor instability); 422 aa), μl: 7.63, MW: 47206 TM: 1 [P] Gene Chromosome: 17p13.3, Genbank accession No. NP—002552.; OGT (0-Linked N-Acetylglucosamine (GlcNAc) Transferase, O-GlcNAc Transferase P110 Subunit, 0-Linked N-Acetylglucosamine (GlcNAc) Transferase (UDP-N-Acetylglucosamine:Polypeptide-N-Acetylglucosaminyl Transferase, UDP-N-Acetylglucosamine-Peptide N-Acetylglucosaminyltransferase 110 KDa Subunit, UDP-N-Acetylglucosamine:Polypeptide-N-Acetylglucosaminyl Transferase, Uridinediphospho-N-Acetylglucosamine:Polypeptide Beta-N-Acetylglucosaminyl Transferase, O-GlcNAc Transferase Subunit P110, EC 2.4.1.255, 0-Linked N-Acetylglucosamine Transferase 110 KDa Subunit, EC 2.4.1, HRNT1, EC 2.4.1.186, 0-GLCNAC; GenBank: AAH38180.1); 0A1 (Osteoarthritis QTL 1, OASD; GenBank: CAA88742.1); NY-ESO-1/LAGE-2 (Cancer/Testis Antigen 1 B, CTAG1 B, NY-ESO-1, LAGE-2, ESO1, CTAG1, CTAG, LAGE2B, Cancer/Testis Antigen 1, Autoimmunogenic Cancer/Testis Antigen NY-ESO-1, Ancer Antigen 3, Cancer/Testis Antigen 6.1, New York Esophageal Squamous Cell Carcinoma 1, L Antigen Family Member 2, LAGE2, CT6.1, LAGE2A; GenBank: AAI30365.1); NY-BR-1 (ANKRD30A, Ankyrin Repeat Domain 30A, Breast Cancer Antigen NY-BR-1, Serologically Defined Breast Cancer Antigen NY-BR-1, Ankyrin Repeat Domain-Containing Protein 30A; NCBI Reference Sequence: NP—443723.2); N-ras (NRAS, Neuroblastoma RAS Viral (V-Ras) Oncogene Homolog, NRAS1, Transforming Protein N-Ras, GTPase NRas, ALPS4, N-Ras Protein Part 4, NS6, Oncogene Homolog, HRAS1; GenBank: AAH05219.1); NFYC (Nuclear Transcription Factor Y, Gamma, HAP5, HSM, Nuclear Transcription Factor Y Subunit C, Transactivator HSM-1/2, CCAAT Binding Factor Subunit C, NF-YC, CCAAT Transcription Binding Factor Subunit Gamma, CAAT Box DNA-Binding Protein Subunit C, Histone H1 Transcription Factor Large Subunit 2A, CBFC, Nuclear Transcription Factor Y Subunit Gamma, CBF-C, Transactivator HSM-1, H1TF2A, Transcription Factor NF-Y, C Subunit; neo-PAP (PAPOLG, Poly(A) Polymerase Gamma, Neo-Poly(A) Polymerase, Nuclear Poly(A) Polymerase Gamma, Polynucleotide Adenylyltransferase Gamma, SRP RNA 3′ Adenylating Enzyme/Pap2, PAP-gamma, Neo-PAP, SRP RNA 3′-Adenylating Enzyme, PAP2, EC 2.7.7.19, PAPG; NCBI Reference Sequence: NP—075045.2); NCA (CEACAM6, Genbank accession no. M1872); Napi3b (NAPI-3B, NPTIIb, SLC34A2, solute carrier family 34 (sodium phosphate), member 2, type II sodium-dependent phosphate transporter 3b, Genbank accession no. NM—00642); Myosin class I; MUM-3; MUM-2 (TRAPPC1, Trafficking Protein Particle Complex 1, BETS, BETS Homolog, MUM2, Melanoma

Ubiquitous Mutated 2, Multiple Myeloma Protein 2, Trafficking Protein Particle Complex Subunit 1; MUM-1f; Mucin (MUC1, Mucin 1, Cell Surface Associated, PEMT, PUM, CA 15-3, MCKD1, ADMCKD, Medullary Cystic Kidney Disease 1 (Autosomal Dominant), ADMCKD1, Mucin 1, Transmembrane, CD227, Breast Carcinoma-Associated Antigen DF3, MAM6, Cancer Antigen 15-3, MCD, Carcinoma-Associated Mucin, MCKD, Krebs Von Den Lungen-6, MUC-1/SEC, Peanut-Reactive Urinary Mucin, MUC1/ZD, Tumor-Associated Epithelial Membrane Antigen, DF3 Antigen, Tumor-Associated Mucin, episialin, EMA, H23 Antigen, H23AG, Mucin-1, KL-6, Tumor Associated Epithelial Mucin, MUC-1, Episialin, PEM, CD227 Antigen; UniProtKB/Swiss-Prot: P15941.3); MUCSAC (Mucin SAC, Oligomeric Mucus/Gel-Forming, Tracheobronchial Mucin' MUC5, TBM, Mucin 5, Subtypes A And C, Tracheobronchial/Gastric, leB, Gastric Mucin, Mucin SAC, Oligomeric Mucus/Gel-Forming Pseudogene, Lewis B Blood Group Antigen, LeB, Major Airway Glycoprotein, MUC-SAC, Mucin-5 Subtype AC, Tracheobronchial; MUC1 (Mucin 1, Cell Surface Associated, PEMT, PUM, CA 15-3, MCKD1, ADMCKD, Medullary Cystic Kidney Disease 1 (Autosomal Dominant), ADMCKD1, Mucin 1, Transmembrane, CD227, Breast Carcinoma-Associated Antigen DF3, MAM6, Cancer Antigen 15-3, MCD, Carcinoma-Associated Mucin, MCKD, Krebs Von Den Lungen-6, MUC-1/SEC, Peanut-Reactive Urinary Mucin, MUC-1/X, Polymorphic Epithelial Mucin, MUC1/ZD, Tumor-Associated Epithelial Membrane Antigen, DF3 Antigen, Tumor-Associated Mucin, episialin, EMA, h23 Antigen, H23AG, mucin-1, KL-6, Tumor Associated Epithelial Mucin, MUC-1, Episialin, PEM, CD227 Antigen; MSG783 (RNF124, hypothetical protein FLJ20315, Genbank accession no. NM-01776; MRP4-multidrug resistance-associated protein 4 isoform 3, MOAT-B; MOATB [Homo sapiens]; NCBI Reference Sequence: NP—001288758.1; MPF (MPF, MSLN, SMR, megakaryocyte potentiating factor, mesothelin, Genbank accession no. NM—00582; MMP-7 (MMP7, matrilysin, MPSL1, matrin, Matrix Metalloproteinase 7 (Matrilysin, Uterine), Uterine Matrilysin, Matrix Metalloproteinase-7, EC 3.4.24.23, Pump-1 Protease, Matrin, Uterine Metalloproteinase, PUMP1, MMP-7, EC 3.4.24, PUMP-1; GenBank: AAC37543.1); MMP-2 (MMP2, Matrix Metallopeptidase 2 (Gelatinase A, 72 kDa Gelatinase, 72 kDa Type IV Collagenase), MONA, CLG4A, Matrix Metalloproteinase 2 (Gelatinase A, 72kD Gelatinase, 72kD Type IV Collagenase), CLG4, 72 kDa Gelatinase, 72 kDa Type IV Collagenase), Matrix Metalloproteinase-2, MMP-II, 72 KDa Gelatinase, Collagenase Type IV-A, MMP-2, Matrix

Metalloproteinase-II, TBE-1, Neutrophil Gelatinase, EC 3.4.24.24, EC 3.4.24; GenBank: AAH02576.1); and Meloe.

[0217] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody wherein the multispecific antibody comprises a second binding domain having specificity for a second antigen selected from the group consisting of: 17-IA, 4-1BB, 4Dc, 6- keto-PGFla, 8-iso-PGF2a, 8-oxo-dG, Al Adenosine Receptor, A33, ACE, ACE-2, Activin, Activin A, Activin AB, Activin B, Activin C, Activin RIA, Activin RIA ALK-2, Activin RIB ALK-4, Activin RIIA, Activin RUB, ADAM, ADAM10, ADAM12, ADAM15, ADAM17/TACE, ADAM8, ADAM9, ADAMTS, ADAMTS4, ADAMTS5, Addressins, aFGF, ALCAM, ALK, ALK-1, ALK-7, alpha-l-antitrypsin, alpha-V/beta-1 antagonist, ANG, Ang, APAF-1, APE, APJ, APP, APRIL, AR, ARC, ART, Artemin, anti-Id, ASPARTIC, Atrial natriuretic factor, av/b3 integrin, Axl, b2M, B7-1, B7-2, B7-H, B-lymphocyte Stimulator (BlyS), BACE, BACE-1, Bad, BAFF, BAFF-R, Bag-1, BAK, Bax, BCA-1, BCAM, Bel, BCMA, BDNF, b-ECGF, bFGF, BID, Bik, BIM, BLC, BL-CAM, BLK, BMP, BMP-2 BMP-2a, BMP-3 Osteogenin, BMP-4 BMP-2b, BMP-5, BMP-6 Vgr-1, BMP-7 (OP-1), BMP-8 (BMP-8a, OP-2), BMPR, BMPR-IA (ALK-3), BMPR-IB (ALK-6), BRK-2, RPK-1, BMPR-II (BRK-3), BMPs, b- NGF, BOK, Bombesin, Bone-derived neurotrophic factor, BPDE, BPDE-DNA, BTC, complement factor 3 (C3), C3a, C4, C5, C5a, CIO, CA125, CAD-8, Calcitonin, cAMP, carcinoembryonic antigen (CEA), carcinoma-associated antigen, Cathepsin A, Cathepsin B, Cathepsin C/DPPI, Cathepsin D, Cathepsin E, Cathepsin H, Cathepsin L, Cathepsin O, Cathepsin S, Cathepsin V, Cathepsin X/Z/P, CBL, CCI, CCK2, CCL, CCLl, CCLl1, CCL12, CCL13, CCL 14, CCL15, CCL16, CCLl 7, CCL18, CCL19, CCL2, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CCL3, CCL4, CCL5, CCL6, CCL7, CCL8, CCL9/10, CCR, CCR1, CCR10, CCR10, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CD1, CD2, CD4, CD5, CD6, CD7, CD8, CD10, CDlla, CDllb, CDllc, CD13, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD27L, CD28, CD29, CD30, CD30L, CD32, CD33 (p67 proteins), CD34, CD38, CD40, CD40L, CD44, CD45, CD46, CD49a, CD52, CD54, CD55, CD56, CD61, CD64, CD66e, CD74, CD80 (B7-1), CD89, CD95, CD123, CD137, CD138, CD140a, CD146, CD147, CD148, CD152, CD164, CEACAM5, CFTR, cGMP, CINC, Clostridium botulinum toxin, Clostridium perfringens toxin, CKb8-l, CLC, CMV, CMV UL, CNTF, CNTN-1, COX, C-Ret, CRG-2, CT-1,

CTACK, CTGF, CTLA-4, CX3CL1, CX3CR1, CXCL, CXCLl, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9, CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CXCR, CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, cytokeratin tumor-associated antigen, DAN, DCC, DcR3, DC-SIGN, Decay accelerating factor, des(l-3)-IGF-I (brain IGF-1), Dhh, digoxin, DNAM-1, Dnase, Dpp, DPPIV/CD26, Dtk, ECAD, EDA, EDA-A1, EDA-A2, EDAR, EGF, EGFR (ErbB-1), EMA, EMMPRIN, EN A, endothelin receptor, Enkephalinase, eNOS, Eot, eotaxinl, EpCAM, Ephrin B2/ EphB4, EPO, ERCC, E-selectin, ET-1, Factor Ila, Factor VII, Factor VIIIc, Factor IX, fibroblast activation protein (FAP), Fas, FcRl, FEN-1, Ferritin, FGF, FGF-19, FGF-2, FGF3, FGF-8, FGFR, FGFR-3, Fibrin, FL, FLIP, Flt-3, Flt-4, Follicle stimulating hormone, Fractalkine, FZD1, FZD2, FZD3, FZD4, FZD5, FZD6, FZD7, FZD8, FZD9, FZD10, G250, Gas 6, GCP-2, GCSF, GD2, GD3, GDF, GDF-1, GDF-3 (Vgr-2), GDF-5 (BMP-14, CDMP- 1), GDF-6 (BMP-13, CDMP-2), GDF-7 (BMP-12, CDMP-3), GDF-8 (Myostatin), GDF-9, GDF- 15 (MIC-1), GDNF, GDNF, GFAP, GFRa-1, GFR-alphal, GFR-alpha2, GFR-alpha3, GITR, Glucagon, Glut 4, glycoprotein Ilb/IIIa (GP Ilb/IIIa), GM-CSF, gpl30, gp72, GRO, Growth hormone releasing factor, Hapten (NP-cap or NIP-cap), HB-EGF, HCC, HCMV gB envelope glycoprotein, HCMV) gH envelope glycoprotein, HCMV UL, Hemopoietic growth factor (HGF), Hep B gpl20, heparanase, Her2, Her2/neu (ErbB-2), Her3 (ErbB-3), Her4 (ErbB-4), herpes simplex virus (HSV) gB glycoprotein, HSV gD glycoprotein, HGFA, High molecular weight melanoma-associated antigen (HMW-MAA), HIV gpl20, HIV IIIB gp 120 V3 loop, HLA, HLA-DR, HM1.24, HMFG PEM, HRG, Hrk, human cardiac myosin, human cytomegalovirus (HCMV), human growth hormone (HGH), HVEM, 1-309, IAP, ICAM, ICAM-1, ICAM-3, ICE, ICOS, IFNg, Ig, IgA receptor, IgE, IGF, IGF binding proteins, IGF-1R, IGFBP, IGF-I, IGF-II, IL, IL-1, IL-1R, IL-2, IL-2R, IL-4, IL-4R, IL-5, IL-5R, IL-6, IL-6R, IL-8, IL- 9, IL-10, IL-12, IL-13, IL-15, IL-18, IL-18R, IL-23, interferon (INF)-alpha, INF-beta, INF- gamma, Inhibin, iNOS, Insulin A-chain, Insulin B-chain, Insulin-like growth factor 1, integrin alpha2, integrin alpha3, integrin alpha4, integrin alpha4/betal, integrin, alpha4/beta7, integrin alpha5 (alphaV), integrin alpha5/betal, integrin alpha5/beta3, integrin alpha6, integrin betal, integrin beta2, interferon gamma, IP-10, 1-TAC, JE, Kallikrein 2, Kallikrein 5, Kallikrein 6, , Kallikrein 11, Kallikrein 12, Kallikrein 14, Kallikrein 15, Kallikrein LI, Kallikrein L2, Kallikrein L3, Kallikrein L4, KC, KDR, Keratinocyte Growth Factor (KGF), laminin 5, LAMP, LAP, LAP (TGF- 1), Latent TGF-1, Latent TGF-1 bpl, LBP, LDGF, LECT2, Lefty, Lewis-Y antigen, Lewis-Y related antigen, LFA-1, LFA-3, Lfo, LIF, LIGHT, lipoproteins, LIX, LKN, Lptn, L-Selectin, LT-a, LT-b, LTB4, LTBP-1, Lung surfactant, Luteinizing hormone, Lymphotoxin Beta Receptor, Mac-1, MAdCAM, MAG, MAP2, MARC, MCAM, MCAM, MCK-2, MCP, M-CSF, MDC, Mer, METALLOPROTEASES, MGDF receptor, MGMT, MHC (HLA-DR), MIF, MIG, MIP, MIP-1-alpha, MK, MMAC1, MMP, MMP-1, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-2, MMP-24, MMP- 3, MMP-7, MMP-8, MMP-9, MPIF, Mpo, MSK, MSP, mucin (Mucl), MUC18, Muellerian- inhibitin substance, Mug, MuSK, NAIP, NAP, NCAD, N-Cadherin, NCA 90, NCAM, NCAM, Neprilysin, Neurotrophin-3,-4, or -6, Neurturin, Neuronal growth factor (NGF), NGFR, NGF-beta, nNOS, NO, NOS, Npn, NRG-3, NT, NTN, OB, OGG1, OPG, OPN, OSM, OX40L, OX40R, pl50, p95, PADPr, Parathyroid hormone, PARC, PARP, PBR, PBSF, PCAD, P-Cadherin, PCNA, PDGF, PDGF, PDK-1, PECAM, PEM, PF4, PGE, PGF, PGI2, PGJ2, PIN, PLA2, placental alkaline phosphatase (PLAP), P1GF, PLP, PP14, Proinsulin, Prorelaxin, Protein C, PS, PSA, PSCA, prostate specific membrane antigen (PSMA), PTEN, PTHrp, Ptk, PTN, R51, RANK, RANKL, RANTES, RANTES, Relaxin A-chain, Relaxin B-chain, renin, respiratory syncytial virus (RSV) F, RSV Fgp, Ret, Rheumatoid factors, RLIP76, RPA2, RSK, S100, SCF/KL, SDF-1, SERINE, Serum albumin, sFRP-3, Shh, SIGIRR, SK-1, SLAM, SLPI, SMAC, SMDF, SMOH, SOD, SPARC, Stat, STEAP, STEAP-II, TACE, TACI, TAG-72 (tumor-associated glycoprotein-72), TARC, TCA-3, T-cell receptors (e.g., T-cell receptor alpha/beta), TdT, TECK, TEM1, TEM5, TEM7, TEM8, TERT, testicular PLAP-like alkaline phosphatase, TfR, TGF, TGF-alpha, TGF-beta, TGF-beta Pan Specific, TGF-beta RI (ALK-5), TGF-beta RII, TGF-beta Rllb, TGF-beta RIII, TGF-betal, TGF-beta2, TGF-beta3, TGF-beta4, TGF-beta5, Thrombin, Thymus Ck-1, Thyroid stimulating hormone, Tie, TIMP, TIQ, Tissue Factor, TMEFF2, Tmpo, TMPRSS2, TNF, TNF-alpha, TNF-alpha beta, TNF-beta2, TNFc, TNF-RI, TNF-RII, TNFRSF10A (TRAIL Rl Apo-2, DR4), TNFRSFIOB (TRAIL R2 DR5, KILLER, TRICK-2A, TRICK-B), TNFRSF10C (TRAIL R3 DcRl, LIT, TRID), TNFRSF10D (TRAIL R4 DcR2, TRUNDD), TNFRSF11A (RANK ODF R, TRANCE R), TNFRSFllB (OPG OCIF, TR1), TNFRSF12 (TWEAK R FN14), TNFRSF13B (TACI), TNFRSF13C (BAFF R), TNFRSF14 (HVEM ATAR, HveA, LIGHT R, TR2), TNFRSF16 (NGFR p75NTR), TNFRSF17 (BCMA), TNFRSF18 (GITR AITR), TNFRSF19 (TROY TAJ, TRADE), TNFRSF19L (RELT), TNFRSFIA (TNF RI CD120a, p55-60), TNFRSFIB (TNF RII CD120b, p75-80), TNFRSF26

(TNFRH3), TNFRSF3 (LTbR TNF RIII, TNFC R), TNFRSF4 (OX40 ACT35, TXGP1 R), TNFRSF5 (CD40 p50), TNFRSF6 (Fas Apo-1, APT1, CD95), TNFRSF6B (DcR3 M68, TR6), TNFRSF7 (CD27), TNFRSF8 (CD30), TNFRSF9 (4-lBB CD137, ILA), TNFRSF21 (DR6), TNFRSF22 (DcTRAIL R2 TNFRH2), TNFRST23 (DcTRAIL Rl TNFRH1), TNFRSF25 (DR3 Apo-3, LARD, TR-3, TRAMP, WSL-1), TNFSF10 (TRAIL Apo-2 Ligand, TL2), TNFSF11 (TRANCE/RANK Ligand ODF, OPG Ligand), TNFSF12 (TWEAK Apo-3 Ligand, DR3 Ligand), TNFSF13 (APRIL TALL2), TNFSF13B (BAFF BLYS, TALL1, THANK, TNFSF20), TNFSF14 (LIGHT HVEM Ligand, LTg), TNFSF15 (TL1A/VEGI), TNFSF18 (GITR Ligand AITR Ligand, TL6), TNFSFIA (TNF-a Conectin, DIF, TNFSF2), TNFSF1B (TNF-b LTa, TNFSF1), TNFSF3 (LTb TNFC, p33), TNFSF4 (OX40 Ligand gp34, TXGP1), TNFSF5 (CD40 Ligand CD154, gp39, HIGM1, IMD3, TRAP), TNFSF6 (Fas Ligand Apo-1 Ligand, APT1 Ligand), TNFSF7 (CD27 Ligand CD70), TNFSF8 (CD30 Ligand CD153), TNFSF9 (4-lBB Ligand CD137 Ligand), TP-1, t-PA, Tpo, TRAIL, TRAIL R, TRAIL-R1, TRAIL-R2, TRANCE, transferring receptor, TRF, Trk, TROP-2, TSG, TSLP, tumor-associated antigen CA 125, tumor-associated antigen expressing Lewis Y related carbohydrate, TWEAK, TXB2, Ung, uPAR, uPAR-1, Urokinase, VCAM, VCAM-1, VECAD, VE-Cadherin, VE-cadherin-2, VEFGR-1 (flt-1), VEGF, VEGFR, VEGFR-3 (flt-4), VEGI, VIM, Viral antigens, VLA, VLA-1, VLA-4, VNR integrin, von Willebrands factor, WIF- 1, WNT1, WNT2, WNT2B/13, WNT3, WNT3A, WNT4, WNT5A, WNT5B, WNT6, WNT7A, WNT7B, WNT8A, WNT8B, WNT9A, WNT9A, WNT9B, WNT10A, WNT10B, WNT11, WNT16, XCL1, XCL2, XCR1, XCR1, XEDAR, XIAP, XPD, CTLA4 (cytotoxic T lymphocyte antigen-4), PD1 (programmed cell death protein 1), PD-L1 (programmed cell death ligand 1), LAG-3 (lymphocyte activation gene-3), TIM-3 (T cell immunoglobulin and mucin protein-3), receptors for hormones, and growth factors.

[0218] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them comprise a multispecific antibody, for example, a bispecific antibody wherein the multispecific antibody comprises a second binding domain having specificity for a second antigen selected from the group consisting of: BCMA, CTLA4 (cytotoxic T lymphocyte antigen-4), PD1 (programmed cell death protein 1), PD-L1 (programmed cell death ligand 1), LAG-3 (lymphocyte activation gene-3), TIM-3, CD20, CD2, CD19, Her2, EGFR, EpCAM, FcyRIIIa (CD16), FcyRIIa (CD32a), FcyRIIb (CD32b), FcyRI (CD64), Toll-like receptors (TLRs), TLR4, TLR9, cytokines, IL-2, IL-5, IL-13, IL-6, IL-17, IL-12, IL-23, TNFa, TGFb, cytokine receptors, IL-2R, chemokines, chemokine receptors, growth factors, VEGF, and HGF.

[0219] In some embodiments, the invention provides bispecific antibodies having affinity to CD3 and HER2. In some embodiments, the invention provides bispecific antibodies comprising an antibody fragment (e.g., an Fab) of trastuzumab. Exemplary bispecific CD3 antibodies include ADI-29291, ADI-29292, ADI-29293, ADI-29294, ADI-29295, ADI-29297, ADI-29298, ADI-29300, ADI-29301, ADI-29302, ADI-29303, ADI-29304, ADI-29305, and ADI-29306.

[0220] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be prepared according to a variety of techniques available to the artisan and include, but are not limited to, recombinant co-expression of two immunoglobulin heavy chain-light chain pairs having different specificities (see Milstein and Cuello, Nature 305: 537 (1983)), WO 93/08829, and Traunecker et al., EMBO J. 10: 3655 (1991)), and "knob-in-hole" engineering (see, e.g., U.S. Pat. No. 5,731,168). "Knob-in-hole" engineering of multispecific antibodies may be utilized to generate a first arm containing a knob and a second arm containing the hole into which the knob of the first arm may bind. The knob of the multispecific antibodies of the invention may be an anti-CD3 arm in one embodiment. Alternatively, the knob of the multispecific antibodies of the invention may be an anti-target/antigen arm in one embodiment. The hole of the multispecific antibodies of the invention may be an anti-CD3 arm in one embodiment. Alternatively, the hole of the multispecific antibodies of the invention may be an anti-target/antigen arm in one embodiment. Multispecific antibodies may also be engineered using immunoglobulin crossover (also known as Fab domain exchange or CrossMab format) technology (see e.g., WO2009/080253; Schaefer et al., Proc. Natl. Acad. Sci. USA, 108:11187-11192 (2011)). Multispecific antibodies may also be made by engineering electrostatic steering effects for making antibody Fc-heterodimeric molecules (WO 2009/089004A1); cross-linking two or more antibodies or fragments (see, e.g., U.S. Pat. No. 4,676,980, and Brennan et al., Science, 229: 81 (1985)); using leucine zippers to produce bi-specific antibodies (see, e.g., Kostelny et al., J. Immunol, 148(5):1547-1553 (1992)); using "diabody" technology for making bispecific antibody fragments (see, e.g., Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993)); and using single-chain Fv (sFv) dimers (see, e.g. Gruber et al., J. ImmunoL, 152:5368 (1994)); and preparing trispecific antibodies as described, e.g., in Tutt et al. J. ImmunoL 147: 60 (1991). Additional non-limiting examples of multispecific and bispecific formats that are amenable to incorporation of the inventive anti-CD3 binding domains include, e.g., Fab-Fc-scFv ("bottle-opener") (XENCOR), Mab-scFv (XENCOR), Mab-Fv (XENCOR), Dual scFv (XENCOR),central Fv (XENCOR), central scFv(XENCOR), one-arm central scFv (XENCOR), Fab-Fab (XENCOR), Fab-Fv (XENCOR), mAb-Fv (XENCOR), mAb-Fab (XENCOR), DART (MacroGenics), BiTE (Amgen/Micromet), KiTE, common light chain-IgG (Genentech), TandAb (Affimed) Cross-Mab (Roche), SEED (EMD Serono), BEAT (Glenmark), TrioMab (Trion Pharma/Fresnius Biotech), DuetMab (MedImmune), and others. Methods for preparing such multispecific antibodies are disclosed in, for example: WO 95/09917; WO 2008/119566; WO 2008/119567; WO2011/121110; WO 2010/037835; WO 2007/042261; WO 2007/110205; WO 2011/121110; WO 2012/055961; WO 2012/16067; WO 2016/086189; WO 2016/182751; WO 2015/006749; WO 2014/049003; WO 2013/177101; WO 2015/128509; US 7,951,917; US 2009/0252729; US 2014/0348839; US 7,183,076; Mazor et al., *Mabs*, Vol. 7, pages 377-389 (2015); Muda et al., *Protein Engineering, Designe, & Selection*, Vol. 24, pages 447-454 (2011); and Del Bano et al., *Antibodies*, Vol. 5, pages 1-23 (2016).

[0221] Still further exemplary bispecific antibody format that can be used in the context of the present invention involves the use of a first immunoglobulin (Ig) CH3 domain and a second Ig CH3 domain, wherein the first and second Ig CH3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces binding of the bi-specific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference. In one embodiment, the first Ig CH3 domain binds Protein A and the second Ig CH3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R modification (by IMGT exon numbering; H435R by EU numbering). The second CH3 may further comprise a Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second CH3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of lgG1 antibodies; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of lgG2 antibodies; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of lgG4 antibodies.

[0222] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be prepared according as engineered antibodies with three or more functional antigen binding sites, including “Octopus antibodies,” as disclosed in, e.g. US 2006/0025576A1.

[0223] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be prepared as a “Dual Acting FAb” or “DAF” comprising an antigen binding site that binds to CD3 as well as another, different antigen as disclosed in e.g., US 2008/0069820.

[0224] As disclosed herein and throughout, the inventive CD3 binding domains and antibodies comprising them may comprise monospecific, bispecific, or multispecific antibodies. Multispecific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for more than one target polypeptide. See, e.g., Tutt et al., 1991, J. Immunol. 147:60-69; Kufer et al., 2004, Trends Biotechnol. 22:238-244. The antibodies of the present invention can be linked to or co- expressed with another functional molecule, e.g., another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment to produce a bi-specific or a multi-specific antibody with a second binding specificity.

[0225] In certain embodiments, amino acid sequence variants of the inventive CD3 binding domains and antibodies comprising them are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of an antibody may be prepared by introducing appropriate modifications into the nucleotide sequence encoding the antibody, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of residues within the amino acid sequences of the antibody. Any combination of deletion, insertion, and substitution can be made to arrive at the final construct, provided that the final construct possesses the desired characteristics, for example, antigen-binding. In certain embodiments, such variants having one or more amino acid substitutions are provided. Sites of interest for substitutional mutagenesis include the CDRs and FRs. Amino acid substitutions may be introduced into an antibody of interest and the products screened for a desired activity, for example, retained/improved antigen binding, decreased immunogenicity, or improved ADCC or CDC.

[0226] One type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e.g., a humanized or human antibody). Generally, the resulting variant(s) selected for further study will have modifications (e.g., improvements) in certain biological properties (e.g., increased affinity, reduced immunogenicity) relative to the parent antibody and/or will have substantially retained certain biological properties of the parent antibody. An exemplary substitutional variant is an affinity matured antibody, which may be conveniently generated, e.g., using phage display-based affinity maturation techniques. Briefly, one or more CDR residues are mutated and the variant antibodies displayed on phage and screened for a particular biological activity (e.g., binding affinity).

[0227] Alterations (e.g., substitutions) may be made in CDRs, e.g., to improve antibody affinity. Such alterations may be made in CDR “hotspots,” i.e., residues encoded by codons that undergo mutation at high frequency during the somatic maturation process (see, e.g., Chowdhury, Methods Mol. Biol. 207:179-196 (2008)), and/or residues that contact antigen, with the resulting variant VH or VL being tested for binding affinity. Affinity maturation by constructing and reselecting from secondary libraries has been described, e.g., in Hoogenboom et al. in Methods in Molecular Biology 178:1-37 (O'Brien et al., ed., Human Press, Totowa, N.J., (2001).) In some embodiments of affinity maturation, diversity is introduced into the variable genes chosen for maturation by any of a variety of methods (e.g., error-prone PCR, chain shuffling, or oligonucleotide-directed mutagenesis). A secondary library is then created. The library is then screened to identify any antibody variants with the desired affinity. Another method to introduce diversity involves CDR-directed approaches, in which several CDR residues (e.g., 4-6 residues at a time) are randomized. CDR residues involved in antigen binding may be specifically identified, e.g., using alanine scanning mutagenesis or modeling. CDR-H3 and CDR-L3 in particular are often targeted.

[0228] In certain embodiments, substitutions, insertions, or deletions may occur within one or more CDRs of the inventive CD3 binding domains and antibodies comprising them, so long as such alterations do not substantially reduce the ability of the antibody to bind antigen. For example, conservative alterations (e.g., conservative substitutions as provided herein) that do not substantially reduce binding affinity may be made in CDRs. Such alterations may, for example, be outside of antigen contacting residues in the CDRs. In certain embodiments of the variant VH and VL sequences provided above, each CDR either is unaltered, or contains no more than one, two or three amino acid substitutions.

[0229] A useful method for identification of residues or regions of an antibody that may be targeted for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells (1989) Science, 244:1081-1085. In this method, a residue or group of target residues (e.g., charged residues such as arg, asp, his, lys, and glu) are identified and replaced by a neutral or negatively charged amino acid (e.g., alanine or polyalanine) to determine whether the interaction of the antibody with antigen is affected. Further substitutions may be introduced at the amino acid locations demonstrating functional sensitivity to the initial substitutions. Alternatively, or additionally, a crystal structure of an antigen-antibody complex to identify contact points between the antibody and antigen. Such contact residues and neighboring residues may be targeted or eliminated as candidates for substitution. Variants may be screened to determine whether they contain the desired properties.

[0230] Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include an antibody with an N-terminal methionyl residue. Other insertional variants of the antibody molecule include the fusion to the N- or C-terminus of the antibody to an enzyme (e.g. for ADEPT) or a polypeptide which increases the serum half-life of the antibody.

[0231] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them can be altered to increase or decrease the extent to which the antibody is glycosylated. Addition or deletion of glycosylation sites to anti-CD3 antibody of the invention may be conveniently accomplished by altering the amino acid sequence such that one or more glycosylation sites is created or removed.

[0232] Where the antibody comprises an Fc region, the carbohydrate attached thereto may be altered. Antibodies produced by mammalian cells typically comprise a branched, biantennary oligosaccharide that is generally attached by an N-linkage to Asn297 of the CH2 domain of the Fc region. See, e.g., Wright et al. TIBTECH 15:26-32 (1997). The oligosaccharide may include various carbohydrates, e.g., mannose, N-acetyl glucosamine (GlcNAc), galactose, and sialic acid, as well as a fucose attached to a GlcNAc in the "stem" of the biantennary oligosaccharide structure. In some embodiments, modifications of the oligosaccharide in an antibody of the invention may be made in order to create antibody variants with certain improved properties.

[0233] In certain embodiments, variants of the inventive CD3 binding domains and antibodies comprising them are provided having a carbohydrate structure that lacks fucose attached (directly or indirectly) to an Fc region. For example, the amount of fucose in such antibody may be from 1% to 80%, from 1% to 65%, from 5% to 65% or from 20% to 40%. The amount of fucose is determined by calculating the average amount of fucose within the sugar chain at Asn297, relative to the sum of all glycostructures attached to Asn 297 (e.g. complex, hybrid and high mannose structures) as measured by MALDI-TOF mass spectrometry, as described in WO 2008/077546, for example. Asn297 refers to the asparagine residue located at about position 297 in the Fc region (EU numbering of Fc region residues); however, Asn297 may also be located about ±3 amino acids upstream or downstream of position 297, i.e., between positions 294 and 300, due to minor sequence variations in antibodies. Such fucosylation variants may have improved ADCC function. See, e.g., US Patent Publication Nos. US 2003/0157108 (Presta, L.); US 2004/0093621 (Kyowa Hakko Kogyo Co., Ltd). Examples of publications related to "defucosylated" or "fucose-deficient" antibody variants include: US 2003/0157108; WO 2000/61739; WO 2001/29246; US 2003/0115614; US 2002/0164328; US 2004/0093621; US 2004/0132140; US 2004/0110704; US 2004/0110282; US 2004/0109865; WO 2003/085119; WO 2003/084570; WO 2005/035586; WO 2005/035778; WO2005/053742; WO2002/031140; Okazaki et al. J. Mol. Biol. 336:1239-1249 (2004); Yamane-Ohnuki et al. Biotech. Bioeng. 87: 614 (2004). Examples of cell lines capable of producing defucosylated antibodies include Lec13 CHO cells deficient in protein fucosylation (Ripka et al. Arch. Biochem. Biophys. 249:533-545 (1986); US Pat Pub No 2003/0157108 A1, Presta, L; and WO 2004/056312 A1, Adams et al., especially at Example 11), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene, FUT8, knockout CHO cells (see, e.g., Yamane-Ohnuki et al. Biotech. Bioeng. 87: 614 (2004); Kanda, Y. et al., Biotechnol. Bioeng., 94(4):680-688 (2006); and WO2003/085107).

[0234] Anti-CD3 antibodies variants are further provided with bisected oligosaccharides, for example, in which a biantennary oligosaccharide attached to the Fc region of the antibody is bisected by GlcNAc. Such antibody variants may have reduced fucosylation and/or improved ADCC function. Examples of such antibody variants are described, e.g., in WO 2003/011878 (Jean-Mairet et al.); U.S. Pat. No. 6,602,684 (Umana et al.); and US 2005/0123546 (Umana et al.). Antibody variants with at least one galactose residue in the oligosaccharide attached to the Fc region are also provided. Such antibody variants may have improved CDC function. Such antibody variants are described, e.g., in WO 1997/30087 (Patel et al.); WO 1998/58964 (Raju, S.); and WO 1999/22764 (Raju, S.).

[0235] In certain embodiments, one or more amino acid modifications may be introduced into the Fc region of an anti-CD3 antibody of the invention, thereby generating an Fc region variant (see e.g., US 2012/0251531). The Fc region variant may comprise a human Fc region sequence (e.g., a human IgG1, IgG2, IgG3 or IgG4 Fc region) comprising an amino acid modification (e.g., a substitution) at one or more amino acid positions.

[0236] In certain embodiments, the invention contemplates an anti-CD3 antibody variant that possesses some but not all effector functions, which make it a desirable candidate for applications in which the half life of the antibody in vivo is important yet certain effector functions (such as complement and ADCC) are unnecessary or deleterious. In vitro and/or in vivo cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks FcγR binding (hence likely lacking ADCC activity) but retains FcRn binding ability. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991). Non-limiting examples of in vitro assays to assess ADCC activity of a molecule of interest is described in U.S. Pat. No. 5,500,362 (see, e.g. Hellstrom, I. et al. Proc. Nat'l Acad. Sci. USA 83:7059-7063 (1986)) and Hellstrom, I et al., Proc. Nat'l Acad. Sci. USA 82:1499-1502 (1985); U.S. Pat. No. 5,821,337 (see Bruggemann, M. et al., J. Exp. Med. 166:1351-1361 (1987)). Alternatively, non-radioactive assays methods may be employed (see, for example, ACTI™ non-radioactive cytotoxicity assay for flow cytometry (Cell Technology, Inc. Mountain

View, Calif.; and CytoTox 96® non-radioactive cytotoxicity assay (Promega, Madison, Wis.). Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed in vivo, e.g., in an animal model such as that disclosed in Clynes et al. Proc. Nat'l Acad. Sci. USA 95:652-656 (1998). C1q binding assays may also be carried out to confirm that the antibody is unable to bind C1q and hence lacks CDC activity. See, e.g., C1q and C3c binding ELISA in WO 2006/029879 and WO 2005/100402. To assess complement activation, a CDC assay may be performed (see, for example, Gazzano-Santoro et al. J. ImmunoL Methods 202:163 (1996); Cragg, M. S. et al. Blood. 101:1045-1052 (2003); and Cragg, M. S. and M. J. Glennie Blood. 103:2738-2743 (2004)). FcRn binding and in vivo clearance/half life determinations can also be performed using methods known in the art (see, e.g., Petkova, S. B. et al. Int'l. ImmunoL 18(12):1759-1769 (2006)).

[0237] Antibodies with reduced effector function include those with substitution of one or more of Fc region residues 238, 265, 269, 270, 297, 327 and 329 (U.S. Pat. Nos. 6,737,056 and 8,219,149). Such Fc mutants include Fc mutants with substitutions at two or more of amino acid positions 265, 269, 270, 297 and 327, including the so-called “DANA” Fc mutant with substitution of residues 265 and 297 to alanine (U.S. Pat. Nos. 7,332,581 and 8,219,149).

[0238] In certain embodiments, the proline at position 329 of a wild-type human Fc region in the antibody is substituted with glycine or arginine or an amino acid residue large enough to destroy the proline sandwich within the Fc/Fc gamma receptor interface that is formed between the proline 329 of the Fc and tryptophan residues Trp 87 and Trp 110 of FcgRIII (Sondermann et al.: Nature 406, 267-273 (20 Jul. 2000)). In certain embodiments, the antibody comprises at least one further amino acid substitution. In one embodiment, the further amino acid substitution is S228P, E233P, L234A, L235A, L235E, N297A, N297D, or P331S, and still in another embodiment the at least one further amino acid substitution is L234A and L235A of the human IgG1 Fc region or S228P and L235E of the human IgG4 Fc region (see e.g., US 2012/0251531), and still in another embodiment the at least one further amino acid substitution is L234A and L235A and P329G of the human IgG1 Fc region.

[0239] Certain antibody variants with improved or diminished binding to FcRs are described. (See, e.g., U.S. Pat. No. 6,737,056; WO 2004/056312, and Shields et al., J. Biol. Chem. 9(2): 6591-6604 (2001).)

[0240] In certain embodiments, an antibody variant comprises an Fc region with one or more amino acid substitutions which improve ADCC, e.g., substitutions at positions 298, 333, and/or 334 of the Fc region (EU numbering of residues).

[0241] In some embodiments, alterations are made in the Fc region that result in altered (i.e., either improved or diminished) C1q binding and/or Complement Dependent Cytotoxicity (CDC), e.g., as described in U.S. Pat. No. 6,194,551, WO 99/51642, and Idusogie et al. J. Immunol. 164: 4178-4184 (2000).

[0242] Antibodies with increased half lives and improved binding to the neonatal Fc receptor (FcRn), which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)), are described in US2005/0014934A1 (Hinton et al.). Those antibodies comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn. Such Fc variants include those with substitutions at one or more of Fc region residues: 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424 or 434, e.g., substitution of Fc region residue 434 (U.S. Pat. No. 7,371,826). See also Duncan & Winter, Nature 322:738-40 (1988); U.S. Pat. No. 5,648,260; U.S. Pat. No. 5,624,821; and WO 94/29351 concerning other examples of Fc region variants.

[0243] In some embodiments, the anti-CD3 antibody (e.g., bispecific anti-CD3 antibody) comprises an Fc region comprising an N297G mutation.

[0244] In some embodiments, the anti-CD3 antibody comprising the N297G mutation comprises one or more heavy chain constant domains, wherein the one or more heavy chain constant domains are selected from a first CH1 (CH11) domain, a first CH2 (CH21) domain, a first CH3 (CH31) domain, a second CH1 (CH12) domain, second CH2 (CH22) domain, and a second CH3 (CH32) domain. In some instances, at least one of the one or more heavy chain constant domains is paired with another heavy chain constant domain. In some instances, the CH31 and CH32 domains each comprise a protuberance or cavity, and wherein the protuberance or cavity in the CH31 domain is positionable in the cavity or protuberance, respectively, in the CH32 domain. In some instances, the CH31 and CH32 domains meet at an interface between said protuberance and cavity. In some instances, the CH21 and CH22 domains each comprise a protuberance or cavity, and wherein the protuberance or cavity in the CH21 domain is positionable in the cavity or protuberance, respectively, in the CH22 domain. In other instances, the CH21 and CH22 domains meet at an interface between said protuberance and cavity. In some instances, the anti-CD3 antibody is an IgG1 antibody.

[0245] In certain embodiments, it may be desirable to create cysteine engineered antibodies, e.g., “thioMAbs,” in which one or more residues of an antibody are substituted with cysteine residues. In particular embodiments, the substituted residues occur at accessible sites of the antibody. By substituting those residues with cysteine, reactive thiol groups are thereby positioned at accessible sites of the antibody and may be used to conjugate the antibody to other moieties, such as drug moieties or linker-drug moieties, to create an immunoconjugate, as described further herein. In certain embodiments, any one or more of the following residues may be substituted with cysteine: V205 (Kabat numbering) of the light chain; A118 (EU numbering) of the heavy chain; and S400 (EU numbering) of the heavy chain Fc region. Cysteine engineered antibodies may be generated as described, for example, in U.S. Pat. No. 7,521,541.

[0246] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be further modified to contain additional nonproteinaceous moieties that are known in the art and readily available. The moieties suitable for derivatization of the antibody include but are not limited to water soluble polymers. Non-limiting examples of water soluble polymers include, but are not limited to, polyethylene glycol (PEG), copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1,3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, polypropylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water. The polymer may be of any molecular weight, and may be branched or unbranched. The number of polymers attached to the antibody may vary, and if more than one polymer are attached, they can be the same or different molecules. In general, the number and/or type of polymers used for derivatization can be determined based on considerations including, but not limited to, the particular properties or functions of the antibody to be improved, whether the antibody derivative will be used in a therapy under defined conditions, etc.

[0247] In another embodiment, conjugates of an antibody and nonproteinaceous moiety that may be selectively heated by exposure to radiation are provided. In one embodiment, the nonproteinaceous moiety is a carbon nanotube (Kam et al., Proc. Natl. Acad. Sci. USA 102: 11600-11605 (2005)). The radiation may be of any wavelength, and includes, but is not limited to, wavelengths that do not harm ordinary cells, but which heat the nonproteinaceous moiety to a temperature at which cells proximal to the antibody-nonproteinaceous moiety are killed.

[0248] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be produced using recombinant methods and compositions, for example, as described in U.S. Pat. No. 4,816,567. In one embodiment, isolated nucleic acid encoding an anti-CD3 antibody described herein is provided. Such nucleic acid may encode an amino acid sequence comprising the VL and/or an amino acid sequence comprising the VH of the antibody (e.g., the light and/or heavy chains of the antibody). In a further embodiment, one or more vectors (e.g., expression vectors) comprising such nucleic acid are provided. In a further embodiment, a host cell comprising such nucleic acid is provided. In one such embodiment, a host cell comprises (e.g., has been transformed with): (1) a vector comprising a nucleic acid that encodes an amino acid sequence comprising the VL of the antibody and an amino acid sequence comprising the VH of the antibody, or (2) a first vector comprising a nucleic acid that encodes an amino acid sequence comprising the VL of the antibody and a second vector comprising a nucleic acid that encodes an amino acid sequence comprising the VH of the antibody. In one embodiment, the host cell is eukaryotic, e.g. a Chinese Hamster Ovary (CHO) cell or lymphoid cell (e.g., Y0, NS0, Sp20 cell). In one embodiment, a method of making an anti-CD3 antibody is provided, wherein the method comprises culturing a host cell comprising a nucleic acid encoding the antibody, as provided above, under conditions suitable for expression of the antibody, and optionally recovering the antibody from the host cell (or host cell culture medium).

[0249] For recombinant production of an anti-CD3 antibody, nucleic acid encoding an antibody, e.g., as described above, is isolated and inserted into one or more vectors for further cloning and/or expression in a host cell. Such nucleic acid may be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the antibody).

[0250] Suitable host cells for cloning or expression of antibody-encoding vectors include prokaryotic or eukaryotic cells described herein. For example, antibodies may be produced in bacteria, in particular when glycosylation and Fc effector function are not needed. For expression of antibody fragments and polypeptides in bacteria, see, e.g., U.S. Pat. Nos. 5,648,237, 5,789,199, and 5,840,523. (See also Charlton, Methods in Molecular Biology, Vol. 248 (B.K.C. Lo, ed., Humana Press, Totowa, N.J., 2003), pp. 245-254, describing expression of antibody fragments in E. coli.) After expression, the antibody may be isolated from the bacterial cell paste in a soluble fraction and can be further purified.

[0251] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for antibody-encoding vectors, including fungi and yeast strains whose glycosylation pathways have been “humanized,” resulting in the production of an antibody with a partially or fully human glycosylation pattern. See, e.g., Gerngross, Nat. Biotech. 22:1409-1414 (2004), and Li et al., Nat. Biotech. 24:210-215 (2006); WO 2009/036379; WO 2010/105256; and WO 2012/009568.

[0252] Suitable host cells for the expression of glycosylated antibody are also derived from multicellular organisms (invertebrates and vertebrates). Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of Spodoptera frugiperda cells.

[0253] Plant cell cultures can also be utilized as hosts. See, e.g., U.S. Pat. Nos. 5,959,177, 6,040,498, 6,420,548, 7,125,978, and 6,417,429 (describing PLANTIBODIES™ technology for producing antibodies in transgenic plants).

[0254] Vertebrate cells may also be used as hosts. For example, mammalian cell lines that are adapted to grow in suspension may be useful. Other examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7); human embryonic kidney line (293 or 293 cells as described, e.g., in Graham et al., J. Gen Virol. 36:59 (1977)); baby hamster kidney cells (BHK); mouse sertoli cells (TM4 cells as described, e.g., in Mather, Biol. Reprod. 23:243-251 (1980)); monkey kidney cells (CV1); African green monkey kidney cells (VERO-76); human cervical carcinoma cells (HELA); canine kidney cells (MDCK; buffalo rat liver cells (BRL 3A); human lung cells (W138); human liver cells (Hep G2); mouse mammary tumor (MMT 060562); TRI cells, as described, e.g., in Mather et al., Annals N.Y. Acad. Sci. 383:44-68 (1982); MRC 5 cells; and FS4 cells. Other useful mammalian host cell lines include Chinese hamster ovary (CHO) cells, including DHFR−CHO cells (Urlaub et al., Proc. Natl. Acad. Sci. USA 77:4216 (1980)); and myeloma cell lines such as Y0, NS0 and Sp2/0. For a review of certain mammalian host cell lines suitable for antibody production, see, e.g., Yazaki and Wu, Methods in Molecular Biology, Vol. 248 (B.K.C. Lo, ed., Humana Press, Totowa, N.J.), pp. 255-268 (2003).

[0255] In certain embodiments, the inventive CD3 binding domains and antibodies comprising them may be identified, screened for, selected for or characterized for their physical/chemical properties and/or biological activities by various assays known in the art.

[0256] In one aspect, an anti-CD3 antibody of the invention is tested for its antigen binding activity, for example, by known methods such as ELISA, Western blot, etc.

[0257] In another aspect, competition assays may be used to identify an antibody that competes with an anti-CD3 antibody of the invention for binding to CD3.

[0258] In an exemplary competition assay, immobilized CD3 is incubated in a solution comprising a first labeled antibody that binds to CD3 and a second unlabeled antibody that is being tested for its ability to compete with the first antibody for binding to CD3. The second antibody may be present in a hybridoma supernatant. As a control, immobilized CD3 is incubated in a solution comprising the first labeled antibody but not the second unlabeled antibody. After incubation under conditions permissive for binding of the first antibody to CD3, excess unbound antibody is removed, and the amount of label associated with immobilized CD3 is measured. If the amount of label associated with immobilized CD3 is substantially reduced in the test sample relative to the control sample, then that indicates that the second antibody is competing with the first antibody for binding to CD3. See, e.g., Harlow and Lane (1988)

Antibodies: A Laboratory Manual. Ch.14 (Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.).

[0259] In one aspect, assays are provided for identifying anti-CD3 antibodies thereof having biological activity. Biological activity may include, for example, binding to CD3 (e.g., CD3 on the surface of a T cell), or a peptide fragment thereof, either in vivo, in vitro, or ex vivo. In the case of a multispecific (e.g., bispecific) anti-CD3 antibody of the invention (e.g., a T-cell Dependent Bispecific Antibody (TDB) having one anti-CD3 arm and one arm that recognizes a second biological molecule, e.g., a cell surface antigen, e.g., a tumor antigen), biological activity may also include, for example, effector cell activation (e.g., T cell (e.g., CD8+ and/or CD4+ T cell) activation), effector cell population expansion (i.e., an increase in T cell count), target cell population reduction (i.e., a decrease in the population of cells expressing the second biological molecule on their cell surfaces), and/or target cell killing. Antibodies having such biological activity in vivo and/or in vitro are provided. In certain embodiments, an antibody of the invention is tested for such biological activity, as described in detail in the Examples herein below.

[0260] In some embodiments, the activity comprises ability to support B cell killing and/or the activation of the cytotoxic T cells. In certain embodiments, an anti-B cell targeting anti-CD3 antibody of the invention is tested for such B cell killing and/or the activation of the cytotoxic effect of T cells biological activity by any of the methods described herein, in particular the Examples. In some embodiments of any of these activity assays, PBMCs may be isolated from whole blood of healthy donors by Ficoll separation. In particular, human blood may be collected in heparinized syringes, and PBMCs isolated using Leucosep and Ficoll Paque Plus. If needed CD4+ T and CD8+ T cells may be separated with Miltenyi kits according to manufacturer's instructions.

[0261] Further, cells may be washed in RPMI medium containing 10% FBS, supplemented with GlutaMax, penicillin & streptomycin, and ˜0.2 million suspended cells added to a 96-well U-bottom plate. Cells may be cultured in RPMI1640 supplemented with 10% FBS at 37° C. in a humidified standard cell culture incubator. For BJAB cell killing assays, 20,000 BJAB cells may be incubated with effector cells, either as huPBMCs or purified T cells, as indicated ratios per assay, in the presence of various concentrations of TDB antibodies for 24 hours. For endogenous B cell killing assays, 200,000 huPBMCs may be incubated with various concentrations of TDB antibodies for 24 hours.

[0262] After culturing, cells may be washed with FACS buffer (0.5% BSA, 0.05% Na Azide in PBS). Cells may then be stained in FACS buffer, washed with FACS buffer and suspended in FACS buffer containing 1 µg/ml Propidium Iodide. Data may be collected on a FACSCalibur flow cytometer and analyzed using FlowJo. Live B cells may be gated out as PI-CD19+ or PI-CD20+B cells by FACS, and absolute cell count may be obtained with FITC beads added to reaction mix as an internal counting control. The percent (%) of cell killing may be calculated based on non-TDB treated controls. Activated T cells may be detected by CD69 and CD25 surface expression using anti-CD69-FITC and anti-CD25-PE.

[0263] The invention also provides immunoconjugates comprising an inventive CD3 binding domain or an antibody comprising it. An anti-CD3 antibody herein conjugated to one or more cytotoxic agents, such as chemotherapeutic agents or drugs, growth inhibitory agents, toxins (e.g., protein toxins, enzymatically active toxins of bacterial, fungal, plant, or animal origin, or fragments thereof), or radioactive isotopes.

[0264] In some embodiments, an immunoconjugate is an antibody-drug conjugate (ADC) in which an antibody is conjugated to one or more drugs, including but not limited to a maytansinoid (see U.S. Pat. Nos. 5,208,020, 5,416,064 and European Patent EP 0 425 235 B1); an auristatin such as monomethylauristatin drug moieties DE and DF (MMAE and MMAF) (see U.S. Pat. Nos. 5,635,483 and 5,780,588, and 7,498,298); a dolastatin; a calicheamicin or derivative thereof (see U.S. Pat. Nos. 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, and 5,877,296; Hinman et al., Cancer Res. 53:3336-3342 (1993); and Lode et al., Cancer Res. 58:2925-2928 (1998)); an anthracycline such as daunomycin or doxorubicin (see Kratz et al., Current Med. Chem. 13:477-523 (2006); Jeffrey et al., Bioorganic & Med. Chem. Letters 16:358-362 (2006); Torgov et al., Bioconj. Chem. 16:717-721 (2005); Nagy et al., Proc. Natl. Acad. Sci. USA 97:829-834 (2000); Dubowchik et al., Bioorg. & Med. Chem. Letters 12:1529-1532 (2002); King et al., J. Med. Chem. 45:4336-4343 (2002); and U.S. Pat. No. 6,630,579); methotrexate; vindesine; a taxane such as docetaxel, paclitaxel, larotaxel, tesetaxel, and ortataxel; a trichothecene; and CC1065.

[0265] In some embodiments, an immunoconjugate comprises an anti-CD3 antibody as described herein conjugated to an enzymatically active toxin or fragment thereof, including but not limited to diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes.

[0266] In some embodiments, an immunoconjugate comprises an anti-CD3 antibody as described herein conjugated to a radioactive atom to form a radioconjugate. A variety of radioactive isotopes are available for the production of radioconjugates. Examples include At211, I131, I125, Y90, Re186, Re188, Sm153, Bi212, P32, Pb212 and radioactive isotopes of Lu. When the radioconjugate is used for detection, it may comprise a radioactive atom for scintigraphic studies, for example tc99m or I123, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, mri), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

[0267] Conjugates of an antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis(p-azidobenzoyl)hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science 238:1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026. The linker may be a “cleavable linker” facilitating release of a cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Res. 52:127-131 (1992); U.S. Pat. No. 5,208,020) may be used.

[0268] The immunuoconjugates or ADCs herein expressly contemplate, but are not limited to such conjugates prepared with cross-linker reagents including, but not limited to, BMPS, EMCS, GMBS, HBVS, LC-SMCC, MBS, MPBH, SBAP, SIA, SIAB, SMCC, SMPB, SMPH, sulfo-EMCS, sulfo-GMBS, sulfo-KMUS, sulfo-MBS, sulfo-SIAB, sulfo-SMCC, and sulfo-SMPB, and SVSB (succinimidyl-(4-vinylsulfone)benzoate) which are commercially available (e.g., from Pierce Biotechnology, Inc., Rockford, Ill., U.S.A).

[0269] In certain embodiments, any of the anti-CD3 antibodies of the invention (e.g., bispecific anti-CD3 antibodies of the invention that bind to CD3 and a second biological molecule, e.g., a cell surface antigen, e.g., a tumor antigen, such as TDB antibodies of the invention or variants thereof) is useful for detecting the presence of CD3 in a biological sample. The term "detecting" as used herein encompasses quantitative or qualitative detection. In certain embodiments, a biological sample comprises a cell or tissue.

[0270] In one embodiment, an anti-CD3 antibody for use in a method of diagnosis or detection is provided. In a further aspect, a method of detecting the presence of CD3 in a biological sample is provided. In certain embodiments, the method comprises contacting the biological sample with an anti-CD3 antibody as described herein under conditions permissive for binding of the anti-CD3 antibody to CD3, and detecting whether a complex is formed between the anti-CD3 antibody and CD3. Such method may be an in vitro or in vivo method.

[0271] In certain embodiments, labeled anti-CD3 antibodies are provided. Labels include, but are not limited to, labels or moieties that are detected directly (such as fluorescent, chromophoric, electron-dense, chemiluminescent, and radioactive labels), as well as moieties, such as enzymes or ligands, that are detected indirectly, e.g., through an enzymatic reaction or molecular interaction. Exemplary labels include, but are not limited to, the radioisotopes 32P, 14C, 125I, 3H, and 131I, fluorophores such as rare earth chelates or fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, luceriferases, e.g., firefly luciferase and bacterial luciferase (U.S. Pat. No. 4,737,456), luciferin, 2,3-dihydrophthalazinediones, horseradish peroxidase (HRP), alkaline phosphatase, β-galactosidase, glucoamylase, lysozyme, saccharide oxidases, e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase, heterocyclic oxidases such as uricase and xanthine oxidase, coupled with an enzyme that employs hydrogen peroxide to oxidize a dye precursor such as HRP, lactoperoxidase, or microperoxidase, biotin/avidin, spin labels, bacteriophage labels, stable free radicals, and the like.

[0272] In certain embodiments, the inventive CD3 binding domains and antibodies comprising may be prepared as pharmaceutical formulations (also known as “pharmaceutical compositions”) by mixing such antibody having the desired degree of purity with one or more optional pharmaceutically acceptable carriers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Pharmaceutically acceptable carriers are generally nontoxic to recipients at the dosages and concentrations employed, and include, but are not limited to: 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 dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as polyethylene glycol (PEG). Exemplary pharmaceutically acceptable carriers herein further include insterstitial 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 Publication Nos. 2005/0260186 and 2006/0104968. In one aspect, a sHASEGP is combined with one or more additional glycosaminoglycanases such as chondroitinases.

[0273] Exemplary lyophilized antibody formulations are described in U.S. Pat. No. 6,267,958. Aqueous antibody formulations include those described in U.S. Pat. No. 6,171,586 and WO2006/044908, the latter formulations including a histidine-acetate buffer.

[0274] The formulation herein may also contain more than one active ingredients as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, it may be desirable to further provide an additional therapeutic agent (e.g., a chemotherapeutic agent, a cytotoxic agent, a growth inhibitory agent, and/or an anti-hormonal agent, such as those recited herein above). Such active ingredients are suitably present in combination in amounts that are effective for the purpose intended.

[0275] Active ingredients may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) 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).

[0276] 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, for example, films, or microcapsules.

[0277] 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.

[0278] In certain embodiments, the inventive CD3 binding domains and antibodies comprising are used in therapeutic methods.

[0279] In one aspect, an anti-CD3 antibody for use as a medicament is provided. In further aspects, an anti-CD3 antibody for use in treating or delaying progression of a cell proliferative disorder (e.g., cancer) or an autoimmune disorder (e.g., arthritis, rheumatoid arthritis, colitis, inflammatory bowel disease, autoimmune type I diabetes, etc.) is provided. In certain embodiments, an anti-CD3 antibody for use in a method of treatment is provided. In certain embodiments, the invention provides an anti-CD3 antibody for use in a method of treating an individual having a cell proliferative disorder or an autoimmune disorder comprising administering to the individual an effective amount of the anti-CD3 antibody. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, for example, as described below. In further embodiments, the invention provides an anti-CD3 antibody for use in enhancing immune function in an individual having a cell proliferative disorder or an autoimmune disorder. In certain embodiments, the invention provides an anti-CD3 antibody for use in a method of enhancing immune function in an individual having a cell proliferative disorder or an autoimmune disorder comprising administering to the individual an effective of the anti-CD3 antibody to activate effector cells (e.g., T cells, e.g., CD8+ and/or CD4+ T cells including Tregs), expand (increase) an effector cell population, reduce a target cell (e.g., a cell expressing a second biological molecule recognized by an anti-CD3 antibody of the invention, such as a bispecific TDB antibody of the invention) population, and/or kill a target cell (e.g., target tumor cell). An “individual” according to any of the above embodiments may be a human.

[0280] In a further aspect, the invention provides for the use of an anti-CD3 antibody in the manufacture or preparation of a medicament. In one embodiment, the medicament is for treatment of a cell proliferative disorder (e.g., cancer) or an autoimmune disorder (e.g., arthritis, rheumatoid arthritis, colitis, inflammatory bowel disease, autoimmune type I diabetes, etc.). In a further embodiment, the medicament is for use in a method of treating a cell proliferative disorder or an autoimmune disorder comprising administering to an individual having a cell proliferative disorder or an autoimmune disorder an effective amount of the medicament. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, for example, as described below. In a further embodiment, the medicament is for activating effector cells (e.g., T cells, e.g., CD8+ and/or CD4+ T cells including Tregs), expanding (increasing) an effector cell population, reducing a target cell (e.g., a cell expressing a second biological molecule recognized by an anti-CD3 antibody of the invention, such as a bispecific TDB antibody of the invention) population, and/or killing target cells (e.g., target tumor cells) in the individual. In a further embodiment, the medicament is for use in a method of enhancing immune function in an individual having a cell proliferative disorder or an autoimmune disorder comprising administering to the individual an amount effective of the medicament to activate effector cells (e.g., T cells, e.g., CD8+ and/or CD4+ T cells), expand (increase) an effector cell population, reduce a target cell (e.g., a cell expressing a second biological molecule recognized by an anti-CD3 antibody of the invention, such as a bispecific TDB antibody of the invention) population, and/or kill a target cell (e.g., target tumor cell). An “individual” according to any of the above embodiments may be a mammal and, in particular, a human.

[0281] In a further aspect, the invention provides a method for treating a disorder comprising a proliferative disorder, an oncological disorder, an immune-oncological disorder, a neurological disorder, a cognitive disorder, a neurodegenerative disorder, an autoimmune disorder. In one embodiment, the method comprises administering to an individual having such disorder an effective amount of an anti-CD3 antibody. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, for example, as described below. An “individual” according to any of the above embodiments may be a mammal and, in particular, a human.

[0282] In a further aspect, the invention provides a method for enhancing immune function in an individual having a disorder in an individual having such disorder. In one embodiment, the method comprises administering to the individual an effective amount of an anti-CD3 antibody to activate effector cells (e.g., T cells, e.g., CD8+ and/or CD4+ T cells), expand (increase) an effector cell population, reduce a target cell population, and/or kill a target cell (e.g., target tumor cell). In one embodiment, an “individual” is a mammal and, in particular, a human.

[0283] In a further aspect, the invention provides a method for treating a hematological cancer, such as a B cell cancer (for example, mature B-cell lymphoma) by administering an effective amount of an anti-CD3 antibody of the invention, such as a bispecific TDB antibody of the invention, such as an anti-B cell targeting TDB, such as a CD20-TDB having an anti-CD3 arm and an anti-CD20 arm. In a further aspect of the embodiment, the mature B-cell lymphoma is a Non-Hodgkin's Lymphoma (NHL). In a further aspect of the embodiment, the NHL is selected from the group comprising: germinal-center B-cell-like (GCB) DLBCL, activated B-cell-like (ABC) DLBCL, follicular lymphoma (FL), mantle cell lymphoma (MCL), acute myeloid leukemia (AML), chronic lymphoid leukemia (CLL), marginal zone lymphoma (MZL), small lymphocytic leukemia (SLL), lymphoplasmacytic lymphoma (LL), Waldenstrom macroglobulinemia (WM), central nervous system lymphoma (CNSL), Burkitt's lymphoma (BL), B-cell prolymphocytic leukemia, Splenic marginal zone lymphoma, Hairy cell leukemia, Splenic lymphoma/leukemia, unclassifiable, Splenic diffuse red pulp small B-cell lymphoma, Hairy cell leukemia variant, Waldenström macroglobulinemia, Heavy chain diseases, α Heavy chain disease, γ Heavy chain disease, μ Heavy chain disease, Plasma cell myeloma, Solitary plasmacytoma of bone, Extraosseous plasmacytoma, Extranodal marginal zone lymphoma of mucosa-associated lymphoid tissue (MALT lymphoma), Nodal marginal zone lymphoma, Pediatric nodal marginal zone lymphoma, Pediatric follicular lymphoma, Primary cutaneous follicle centre lymphoma, T-cell/histiocyte rich large B-cell lymphoma, Primary DLBCL of the CNS, Primary cutaneous DLBCL, leg type, EBV-positive DLBCL of the elderly, DLBCL associated with chronic inflammation, Lymphomatoid granulomatosis, Primary mediastinal (thymic) large B-cell lymphoma, Intravascular large B-cell lymphoma, ALK-positive large B-cell lymphoma, Plasmablastic lymphoma, Large B-cell lymphoma arising in HHV8-associated multicentric Castleman disease, Primary effusion lymphoma: B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma and Burkitt lymphoma, and B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma and classical Hodgkin lymphoma. In a preferred embodiment of the invention, the method comprises treating a cancer comprising germinal-center B-cell-like (GCB) DLBCL, activated B-cell-like (ABC) DLBCL, follicular lymphoma (FL), mantle cell lymphoma (MCL), acute myeloid leukemia (AML), chronic lymphoid leukemia (CLL), marginal zone lymphoma (MZL), small lymphocytic leukemia (SLL), lymphoplasmacytic lymphoma (LL), Waldenstrom macroglobulinemia (WM), central nervous system lymphoma (CNSL), or Burkitt's lymphoma (BL).

[0284] In one embodiment, the method comprises administering to an individual having such a hematological cancer (for example, B cell cancer, for example, B cell lymphoma) an effective amount of an anti-CD3 antibody of the invention, such as a bispecific TDB antibody, such as a CD20 TDB comprising an anti-CD20 targeting arm and an anti-CD3 targeting arm. In other embodiments, a CD20 TDB is co-administered with one or more additional therapeutic agents. In one embodiment, the therapeutic agent is an antibody targeting CD20. In one embodiment, a CD20 TDB is co-administered with one or more antibodies targeting CD20 selected from the chimeric monoclonal CD20 antibody, rituximab (Rituxan®) or the monoclonal CD20 antibody, obinutuzumab (Gazyva®). In one embodiment, a CD20 TDB is co-administered with rituximab. In one embodiment, a CD20 TDB is co-administered with obinutuzumab. In one embodiment, a CD20 TDB is co-administered with obinutuzumab and rituximab.

[0285] In one further embodiment, the anti-CD3 antibody of the invention (for example, the CD20 TDB), with or without a CD20 monoclonal antibody, is administered with a further chemotherapy agent and/or an antibody-drug conjugate (ADC). In one embodiment, a CD20 TDB is co-administered with one or more additional chemotherapy agents selected from cyclophosphamide, doxorubicin, vincristine, and prednisolone (CHOP). In one embodiment, a CD20 TDB is co-administered with an ADC. In one embodiment, a CD20 TDB is co-administered with CHOP, wherein vincristine is replaced with an ADC. In one embodiment, a CD20 TDB is co-administered with an ADC selected from an anti-CD79b antibody drug conjugate (such as anti-CD79b-MC-vc-PAB-MMAE or the anti-CD79b antibody drug conjugate described in any one of U.S. Pat. No. 8,088,378 and/or US 2014/0030280, or polatuzumab vedotin), an anti-CD19 antibody drug conjugate, an anti-CD22 antibody drug conjugate, an anti-CD45 antibody drug conjugate, and an anti-CD32 drug conjugate.

[0286] In one other embodiment the therapeutic agent is a biological modifier. In one embodiment, a CD20 TDB is co-administered with one or more biological modifiers selected from a BCL-2 inhibitor (such as GDC-0199/ABT-199), lenalidomide (Revlimid®), a PI3K-delta inhibitor (such as idelalisib (Zydelig®)), a PD-1 axis binding antagonist, an agonist, e.g., agonist antibody, directed against an activating co-stimulatory molecule, e.g., CD40, CD226, CD28, OX40 (e.g., AgonOX), GITR, CD137 (also known as TNFRSF9, 4-1 BB, or ILA), CD27 (e.g., CDX-1127), HVEM, or CD127, an antagonist, e.g., antagonist antibody, directed against an inhibitory co-stimulatory molecule, e.g., CTLA-4 (also known as CD152), PD-1, TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO (e.g., 1-methyl-D-tryptophan (also known as 1-D-MT)), TIGIT, MICA/B, GITR (e.g., TRX518) or arginase, ipilimumab (also known as MDX-010, MDX-101, or Yervoy®), tremelimumab (also known as ticilimumab or CP-675,206, urelumab (also known as BMS-663513), MGA271, an antagonist directed against a TGF beta, e.g., metelimumab (also known as CAT-192), fresolimumab (also known as GC1008), LY2157299k, and an adoptive transfer of a T cell (e.g., a cytotoxic T cell or CTL) expressing a chimeric antigen receptor (CAR), e.g., adoptive transfer of a T cell comprising a dominant-negative TGF beta receptor, e.g, a dominant-negative TGF beta type II receptor.

[0287] In one embodiment, a CD20 TDB is co-administered with rituximab and one or more chemotherapy agents. In one such embodiment, a CD20 TDB is co-administered with rituximab and CHOP. In one embodiment, a CD20 TDB is co-administered with rituximab and an ADC. In one embodiment, a CD20 TDB is co-administered with rituximab and CHOP, wherein vincristine is replaced with an ADC. In one embodiment, a CD20 TDB is co-administered with an ADC selected from an anti-CD79b antibody drug conjugate (such as anti-CD79b-MC-vc-PAB-MMAE or the anti-CD79b antibody drug conjugate described in any one of U.S. Pat. No. 8,088,378 and/or US 2014/0030280, or polatuzumab vedotin), an anti-CD19 antibody drug conjugate, an anti-CD22 antibody drug conjugate, an anti-CD45 antibody drug conjugate, and an anti-CD32 drug conjugate. In one embodiment, a CD20 TDB is co-administered with rituximab and one or more biological modifiers selected from a BCL-2 inhibitor (such as GDC-0199/ABT-199), lenalidomide (Revlimid®), a PI3K-delta inhibitor (such as idelalisib (Zydelig®)), a PD-1 axis binding antagonist, an agonist, e.g., agonist antibody, directed against an activating co-stimulatory molecule, e.g., CD40, CD226, CD28, OX40 (e.g., AgonOX), GITR, CD137 (also known as TNFRSF9, 4-1 BB, or ILA), CD27 (e.g., CDX-1127), HVEM, or CD127, an antagonist, e.g., antagonist antibody, directed against an inhibitory co-stimulatory molecule, e.g., CTLA-4 (also known as CD152), PD-1, TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO (e.g., 1-methyl-D-tryptophan (also known as 1-D-MT)), TIGIT, MICA/B, GITR (e.g., TRX518) or arginase, ipilimumab (also known as MDX-010, MDX-101, or Yervoy®), tremelimumab (also known as ticilimumab or CP-675,206, urelumab (also known as BMS-663513), MGA271, an antagonist directed against a TGF beta, e.g., metelimumab (also known as CAT-192), fresolimumab (also known as GC1008), LY2157299k, and an adoptive transfer of a T cell (e.g., a cytotoxic T cell or CTL) expressing a chimeric antigen receptor (CAR), e.g., adoptive transfer of a T cell comprising a dominant-negative TGF beta receptor, e.g, a dominant-negative TGF beta type II receptor.

[0288] In one embodiment, a CD20 TDB is co-administered with rituximab, one or more chemotherapy agents, and one or more biological modifiers selected from a BCL-2 inhibitor (such as GDC-0199/ABT-199), lenalidomide (Revlimid®), a PI3K-delta inhibitor (such as idelalisib (Zydelig®)), a PD-1 axis binding antagonist, an agonist, e.g., agonist antibody, directed against an activating co-stimulatory molecule, e.g., CD40, CD226, CD28, OX40 (e.g., AgonOX), GITR, CD137 (also known as TNFRSF9, 4-1 BB, or ILA), CD27 (e.g., CDX-1127), HVEM, or CD127, an antagonist, e.g., antagonist antibody, directed against an inhibitory co-stimulatory molecule, e.g., CTLA-4 (also known as CD152), PD-1, TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO (e.g., 1-methyl-D-tryptophan (also known as 1-D-MT)), TIGIT, MICA/B, GITR (e.g., TRX518) or arginase, ipilimumab (also known as MDX-010, MDX-101, or Yervoy®), tremelimumab (also known as ticilimumab or CP-675,206, urelumab (also known as BMS-663513), MGA271, an antagonist directed against a TGF beta, e.g., metelimumab (also known as CAT-192), fresolimumab (also known as GC1008), LY2157299k, and an adoptive transfer of a T cell (e.g., a cytotoxic T cell or CTL) expressing a chimeric antigen receptor (CAR), e.g., adoptive transfer of a T cell comprising a dominant-negative TGF beta receptor, e.g, a dominant-negative TGF beta type II receptor.

[0289] In one embodiment, a CD20 TDB is co-administered with rituximab, an ADC, and one or more biological modifiers selected from a BCL-2 inhibitor (such as GDC-0199/ABT-199), lenalidomide (Revlimid®), a PI3K-delta inhibitor (such as idelalisib (Zydelig®)), a PD-1 axis binding antagonist, an agonist, e.g., agonist antibody, directed against an activating co-stimulatory molecule, e.g., CD40, CD226, CD28, OX40 (e.g., AgonOX), GITR, CD137 (also known as TNFRSF9, 4-1 BB, or ILA), CD27 (e.g., CDX-1127), HVEM, or CD127, an antagonist, e.g., antagonist antibody, directed against an inhibitory co-stimulatory molecule, e.g., CTLA-4 (also known as CD152), PD-1, TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO (e.g., 1-methyl-D-tryptophan (also known as 1-D-MT)), TIGIT, MICA/B, GITR (e.g., TRX518) or arginase, ipilimumab (also known as MDX-010, MDX-101, or Yervoy®), tremelimumab (also known as ticilimumab or CP-675,206, urelumab (also known as BMS-663513), MGA271, an antagonist directed against a TGF beta, e.g., metelimumab (also known as CAT-192), fresolimumab (also known as GC1008), LY2157299k, and an adoptive transfer of a T cell (e.g., a cytotoxic T cell or CTL) expressing a chimeric antigen receptor (CAR), e.g., adoptive transfer of a T cell comprising a dominant-negative TGF beta receptor, e.g, a dominant-negative TGF beta type II receptor.

[0290] In one embodiment, a CD20 TDB is co-administered with obinutuzumab and one or more chemotherapy agents. In one embodiment, a CD20 TDB is co-administered with obinutuzumab and CHOP. In one embodiment, a CD20 TDB is co-administered with obinutuzumab and an ADC. In one embodiment, a CD20 TDB is co-administered with obinutuzumab and CHOP, wherein vincristine is replaced with an ADC. In one embodiment, a CD20 TDB is co-administered with an ADC selected from an anti-CD79b antibody drug conjugate (such as anti-CD79b-MC-vc-PAB-MMAE or the anti-CD79b antibody drug conjugate described in any one of U.S. Pat. No. 8,088,378 and/or US 2014/0030280, or polatuzumab vedotin), an anti-CD19 antibody drug conjugate, an anti-CD22 antibody drug conjugate, an anti-CD45 antibody drug conjugate, and an anti-CD32 drug conjugate. In one embodiment, a CD20 TDB is co-administered with obinutuzumab and one or more biological modifiers selected from a BCL-2 inhibitor (such as GDC-0199/ABT-199), lenalidomide (Revlimid®), a PI3K-delta inhibitor (such as idelalisib (Zydelig®)), a PD-1 axis binding antagonist, an agonist, e.g., agonist antibody, directed against an activating co-stimulatory molecule, e.g., CD40, CD226, CD28, OX40 (e.g., AgonOX), GITR, CD137 (also known as TNFRSF9, 4-1 BB, or ILA), CD27 (e.g., CDX-1127), HVEM, or CD127, an antagonist, e.g., antagonist antibody, directed against an inhibitory co-stimulatory molecule, e.g., CTLA-4 (also known as CD152), PD-1, TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO (e.g., 1-methyl-D-tryptophan (also known as 1-D-MT)), TIGIT, MICA/B, GITR (e.g., TRX518) or arginase, ipilimumab (also known as MDX-010, MDX-101, or Yervoy®), tremelimumab (also known as ticilimumab or CP-675,206, urelumab (also known as BMS-663513), MGA271, an antagonist directed against a TGF beta, e.g., metelimumab (also known as CAT-192), fresolimumab (also known as GC1008), LY2157299k, and an adoptive transfer of a T cell (e.g., a cytotoxic T cell or CTL) expressing a chimeric antigen receptor (CAR), e.g., adoptive transfer of a T cell comprising a dominant-negative TGF beta receptor, e.g, a dominant-negative TGF beta type II receptor.

[0291] In one embodiment, a CD20 TDB is co-administered with obinutuzumab, an ADC, and one or more biological modifiers selected from a BCL-2 inhibitor (such as GDC-0199/ABT-199), lenalidomide (Revlimid®), a PI3K-delta inhibitor (such as idelalisib (Zydelig®)), a PD-1 axis binding antagonist, an agonist, e.g., agonist antibody, directed against an activating co-stimulatory molecule, e.g., CD40, CD226, CD28, OX40 (e.g., AgonOX), GITR, CD137 (also known as TNFRSF9, 4-1 BB, or ILA), CD27 (e.g., CDX-1127), HVEM, or CD127, an antagonist, e.g., antagonist antibody, directed against an inhibitory co-stimulatory molecule, e.g., CTLA-4 (also known as CD152), PD-1, TIM-3, BTLA, VISTA, LAG-3, B7-H3, B7-H4, IDO (e.g., 1-methyl-D-tryptophan (also known as 1-D-MT)), TIGIT, MICA/B, GITR (e.g., TRX518) or arginase, ipilimumab (also known as MDX-010, MDX-101, or Yervoy®), tremelimumab (also known as ticilimumab or CP-675,206, urelumab (also known as BMS-663513), MGA271, an antagonist directed against a TGF beta, e.g., metelimumab (also known as CAT-192), fresolimumab (also known as GC1008), LY2157299k, and an adoptive transfer of a T cell (e.g., a cytotoxic T cell or CTL) expressing a chimeric antigen receptor (CAR), e.g., adoptive transfer of a T cell comprising a dominant-negative TGF beta receptor, e.g, a dominant-negative TGF beta type II receptor.

[0292] In a further aspect of the invention, the additional therapy comprises an anti-CD20 antibody. In one embodiment, the anti-CD20 antibody is rituximab. In one embodiment, the anti-CD20 antibody is a humanized B-Ly1 antibody. In one embodiment, the humanized B-Ly1 antibody is obinituzumab. In one embodiment, the anti-CD20 antibody is ofatumumab, ublituximab, and/or ibritumomab tiuxetan.

[0293] In a further aspect of the invention, the additional therapy comprises an alkylating agent. In one embodiment, the alkylating agent is 4-[5-[Bis(2-chloroethyl)amino]-1-methylbenzimidazol-2-yl]butanoic acid and salts thereof. In one embodiment, the alkylating agent is bendamustine.

[0294] In a further aspect of the invention, the additional therapy comprises a BCL-2 inhibitor. In one embodiment, the BCL-2 inhibitor is 4-(4-{[2-(4-chlorophenyl)-4,4-dimethylcyclohex-1-en-1-yl]methyl}piperazin-1-yl)-N-({3-nitro-4-[(tetrahydro-2H-pyran-4-ylmethyl)amino]phenyl}sulfonyl)-2-(1H-pyrrolo[2,3-b]pyridin-5-yloxy)benzamide and salts thereof. In one embodiment, the BCL-2 inhibitor is venetoclax (CAS#: 1257044-40-8).

[0295] In a further aspect of the invention, the additional therapy comprises a phosphoinositide 3-kinase (PI3K) inhibitor. In one embodiment, the PI3K inhibitor inhibits delta isoform PI3K (i.e., P1106). In some embodiments, the PI3K inhibitor is 5-Fluoro-3-phenyl-2-[(1S)-1-(7H-purin-6-ylamino)propyl]-4(3H)-quinazolinone and salts thereof. In some embodiments, the PI3K inhibitor is idelalisib (CAS#: 870281-82-6). In one embodiment, the PI3K inhibitor inhibits alpha and delta isoforms of PI3K. In some embodiments, the PI3K inhibitor is 2-{3-[2-(1-Isopropyl-3-methyl-1H-1,2-4-triazol-5-yl)-5,6-dihydrobenzo[f]imidazo[1,2-d][1,4]oxazepin-9-yl]-1H-pyrazol-1-yl}-2-methylpropanamide and salts thereof.

[0296] In a further aspect of the invention, the additional therapy comprises a Bruton's tyrosine kinase (BTK) inhibitor. In one embodiment, the BTK inhibitor is 1-[(3R)-3-[4-Amino-3-(4-phenoxyphenyl)-1H-pyrazolo[3,4-d]pyrimidin-1-yl]piperidin-1-yl]prop-2-en-1-one and salts thereof. In one embodiment, the BTK inhibitor is ibrutinib (CAS#: 936563-96-1).

[0297] In a further aspect of the invention, the additional therapy comprises thalidomide or a derivative thereof. In one embodiment, the thalidomide or a derivative thereof is (RS)-3-(4-Amino-1-oxo 1,3-dihydro-2H-isoindol-2-yl)piperidine-2,6-dione and salts thereof. In one embodiment, the thalidomide or a derivative thereof is lendalidomide (CAS#: 191732-72-6).

[0298] In a further aspect of the invention, the additional therapy comprises one or more of cyclophosphamide, doxorubicin, vincristine, or prednisolone (CHOP). In one embodiment, the additional therapy further comprises an anti-CD20 antibody as described above (e.g., GA-101 and/or Rituxan®). Any of the above methods and therapies may be used, without limitation, for any cancer, including, for example, treatment of a B-cell cancer or breast cancer.

[0299] In a further aspect, the invention provides a method for treating HER2-positive cancers. In one embodiment, the method comprises administering to an individual having such a cancer an effective amount of an anti-HER2 antibody of the invention, such as a bispecific TDB antibody wih an anti-HER2 targeting arm and an anti-CD3 targeting arm. In a preferred embodiment, the HER2-TDB possesses an acceptable toxicity profile when administered in an effective dose in a patient. In one embodiment, the CD3 arm of the HER2-TDB with an acceptable toxicity profile is a low affinity CD3 arm. In one embodiment, the CD3 arm of the HER2-TDB with an acceptable toxicity profile is 40G5c.

[0300] In a preferable embodiment, the HER2-positive cancer is a HER2-positive breast cancer or HER2-positive gastric cancer. In one embodiment, a HER2 TDB is co-administered with one or more additional therapeutic agents that target the HER pathway. In one embodiment, the therapeutic agent that targets the HER pathway is selected from an EGFR inhibitor, a HER2 inhibitor, a HER3 inhibitor, and/or a HER4 inhibitor. In one embodiment, a HER2 TDB is co-administered with one or more additional therapeutic agents selected from trastuzumab (Herceptin®), T-DM1 (Kadcyla®) and pertuzumab (Perjeta®). In one embodiment, a HER2 TDB is co-administered with trastuzumab. In one embodiment, a HER2 TDB is co-administered with T-DM1. In one embodiment, a HER2 TDB is co-administered with pertuzumab. In one embodiment, a HER2 TDB is co-administered with trastuzumab and pertuzumab. In one embodiment, a HER2 TDB is co-administered with T-DM1 and pertuzumab.

[0301] In a further aspect, the invention provides pharmaceutical formulations comprising any of the anti-CD3 antibodies provided herein, e.g., for use in any of the above therapeutic methods. In one embodiment, a pharmaceutical formulation comprises any of the anti-CD3 antibodies provided herein and a pharmaceutically acceptable carrier. In another embodiment, a pharmaceutical formulation comprises any of the anti-CD3 antibodies provided herein and at least one additional therapeutic agent, for example, as described herein.

[0302] Antibodies of the invention can be used either alone or in combination with other agents in a therapy. For instance, an antibody of the invention may be co-administered with at least one additional therapeutic agent. In certain embodiments, an additional therapeutic agent is a chemotherapeutic agent, growth inhibitory agent, cytotoxic agent, agent used in radiation therapy, anti-angiogenesis agent, apoptotic agent, anti-tubulin agent, or other agent, such as a epidermal growth factor receptor (EGFR) antagonist (e.g., a tyrosine kinase inhibitor), HER1/EGFR inhibitor (e.g., erlotinib (Tarceva™)), platelet derived growth factor inhibitor (e.g., Gleevec™ (Imatinib Mesylate)), a COX-2 inhibitor (e.g., celecoxib), interferon, cytokine, antibody other than the anti-CD3 antibody of the invention, such as an antibody that bind to one or more of the following targets ErbB2, ErbB3, ErbB4, PDGFR-beta, BlyS, APRIL, BCMA VEGF, or VEGF receptor(s), TRAIL/Apo2, PD-1, PD-L1, PD-L2, or another bioactive or organic chemical agent.

[0303] In some embodiments, the invention provides a method wherein the additional therapeutic agent is a glucocorticoid. In one embodiment, the glucocorticoid is dexamethasone.

[0304] Such combination therapies noted above encompass combined administration (where two or more therapeutic agents are included in the same or separate formulations), and separate administration, in which case, administration of the antibody of the invention can occur prior to, simultaneously, and/or following, administration of the additional therapeutic agent or agents. In one embodiment, administration of the anti-CD3 antibody and administration of an additional therapeutic agent occur within about one month, or within about one, two or three weeks, or within about one, two, three, four, five, or six days, of each other. Anti-CD3 antibodies of the invention (e.g., bispecific anti-CD3 antibodies of the invention that bind to CD3 and a second biological molecule, e.g., a cell surface antigen, e.g., a tumor antigen, such as a TDB antibody of the invention or variant thereof) can also be used in combination with radiation therapy.

[0305] An antibody of the invention (and/or any additional therapeutic agent) 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. In some embodiments, the antibody is administered by subcutaneous administration. In some embodiments, an anti-CD3 antibody administered by subcutaneous injection exhibits a less toxic response in a patient than the same anti-CD3 antibody administered by intravenous injection. Dosing can be by any suitable route, for example, 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.

[0306] Antibodies of the invention would 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. The antibody need not be, but is optionally formulated with one or more agents currently used to prevent or treat the disorder in question. The effective amount of such other agents depends on the amount of antibody present in the formulation, the type of disorder or treatment, and other factors discussed above. These are generally used in the same dosages and with administration routes as described herein, or about from 1 to 99% of the dosages described herein, or in any dosage and by any route that is empirically/clinically determined to be appropriate.

[0307] For the prevention or treatment of disease, the appropriate dosage of an antibody of the invention (when used alone or in combination with one or more other additional therapeutic agents) will depend on the type of disease to be treated, the type of antibody, the severity and course of the disease, whether the antibody 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 is suitably administered to the patient at one time or over a series of treatments.

[0308] As a general proposition, the therapeutically effective amount of the anti-CD3 antibody administered to human will be in the range of about 0.01 to about 100 mg/kg of patient body weight whether by one or more administrations. In some embodiments, the antibody used is about 0.01 to about 45 mg/kg, about 0.01 to about 40 mg/kg, about 0.01 to about 35 mg/kg, about 0.01 to about 30 mg/kg, about 0.01 to about 25 mg/kg, about 0.01 to about 20 mg/kg, about 0.01 to about 15 mg/kg, about 0.01 to about 10 mg/kg, about 0.01 to about 5 mg/kg, or about 0.01 to about 1 mg/kg administered daily, for example. In one embodiment, an anti-CD3 antibody described herein is administered to a human at a dose of about 100 mg, about 200 mg, about 300 mg, about 400 mg, about 500 mg, about 600 mg, about 700 mg, about 800 mg, about 900 mg, about 1000 mg, about 1100 mg, about 1200 mg, about 1300 mg or about 1400 mg on day 1 of 21-day cycles. The dose may be administered as a single dose or as multiple doses (e.g., 2 or 3 doses), such as infusions. 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 would be in the range from about 0.05 mg/kg to about 10 mg/kg. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 4.0 mg/kg, or 10 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, for example, about six doses of the anti-CD3 antibody). An initial higher loading dose, followed by one or more lower doses may be administered. The progress of this therapy is easily monitored by conventional techniques and assays.

[0309] In some embodiments, the methods may further comprise an additional therapy. The additional therapy may be radiation therapy, surgery, chemotherapy, gene therapy, DNA therapy, viral therapy, RNA therapy, immunotherapy, bone marrow transplantation, nanotherapy, monoclonal antibody therapy, or a combination of the foregoing. The additional therapy may be in the form of adjuvant or neoadjuvant therapy. In some embodiments, the additional therapy is the administration of small molecule enzymatic inhibitor or anti-metastatic agent. In some embodiments, the additional therapy is the administration of side-effect limiting agents (e.g., agents intended to lessen the occurrence and/or severity of side effects of treatment, such as anti-nausea agents, etc.). In some embodiments, the additional therapy is radiation therapy. In some embodiments, the additional therapy is surgery. In some embodiments, the additional therapy is a combination of radiation therapy and surgery. In some embodiments, the additional therapy is gamma irradiation. In some embodiments, the additional therapy may be a separate administration of one or more of the therapeutic agents described above.

[0310] In another aspect of the invention, an article of manufacture containing materials useful for the treatment, prevention and/or diagnosis of the disorders described above is provided. 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). At least one active agent in the composition is an antibody of the invention. The label or package insert indicates that the composition is used for treating the condition of choice. Moreover, the article of manufacture may comprise (a) a first container with a composition contained therein, wherein the composition comprises an antibody of the invention; and (b) a second container with a composition contained therein, wherein the composition comprises a further cytotoxic or otherwise therapeutic agent. The article of manufacture in this embodiment of the invention may further comprise a package insert indicating that the compositions can be used to treat a particular condition. Alternatively, or additionally, the article of manufacture may further comprise a second (or third) 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.

EXAMPLES

[0311] **Example 1: Isolation of anti-CD3 antibodies from immunized mice, and generation and isolation of humanized and optimized variants**

[0312] Immunizations were carried out as in Figure 1. Briefly, balb/c mice were immunized with a primary immunization with 1.0x10^6 human T cells (which express CD3 epsilon) and Sigma® adjuvant in each of ten mice. Twenty-eight days after the primary immunization, a first immunization boost with 1.0x10^6 human T cells (which express CD3 epsilon) and Sigma® adjuvant was performed in each of the ten mice. Twenty-eight days after the first immunization boost, the ten mice were given a second immunization boost with 1.5x10^6 T cells (which express CD3 epsilon) and Sigma® adjuvant; however, for this second boost, five of the mice received human T cells (which express CD3 epsilon) and the other five mice received cynomolgus (cyno) T cells (which express cyno CD3 epsilon). Forty-two days after the second immunization boost, all ten mice received a third immunization boost of fifty micrograms of denatured recombinant cyno CD3epsilon protein mixed with seven micrograms of a peptide-BSA conjugate in which the peptide corresponded to an N-terminal peptide of the native cyno CD3 epsilon protein. Seven days after the third immunization boost, the ten mice were sacrificed and spleens were harvested for B cell sorting.

[0313] Splenic B cells obtained from the harvested spleens were stained with 50 nM recombinant, biotinylated CD3epsilon using routine methods (see, e.g., Tiller *et al, J Immunol Methods*, Vol. **329**, pages 112-124, doi:10.1016/j.jim.2007.09.017 (2008). CD3epsilon-specific B cells were single-cell sorted by flow cytometry using standard methods (see, e.g., Tiller *et al, J Immunol Methods*, Vol. **329**, pages 112-124, doi:10.1016/j.jim.2007.09.017 (2008); WO 2009/036379; WO 2010/105256; and WO 2012/009568). Cognate heavy and light chain pairs were amplified by single-cell PCR using a previously described primer set (see, e.g., Tiller *et al, J Immunol Methods*, Vol. **329**, pages 112-124, doi:10.1016/j.jim.2007.09.017 (2008). An exemplary flow cytometry-based sorting result is depicted in Figure 2, in which 48 cells were isolated and sorted from each of the cyno-boosted (*middle* flow plot of Figure 2) and human-boosted (*right* flow plot of Figure 2) sets of mice. Amplicons were confirmed by agarose gel electrophoresis (Figure 3) and transformed into a highly-engineered strain of *Saccharomyces cerevisiae* (see, e.g., Xu et al., *Protein Eng Des Sel.* Vol. 26(10), pages 663-670 (2013) doi: 10.1093/protein/gzt047; Sivasubramanian et al., *MAbs.* Vol. 9(1), pages 29-42 (2017) doi: 10.1080/19420862.2016.1246096; WO 2009/036379; WO 2010/105256; and WO 2012/009568).

[0314] Antibodies were expressed in *Saccharomyces cerevisiae*, purified using standard procedures, and assayed for binding activity (see, e.g., Xu et al., *Protein Eng Des Sel.* Vol. 26(10), pages 663-670 (2013) doi: 10.1093/protein/gzt047; Sivasubramanian et al., *MAbs.* Vol. 9(1), pages 29-42 (2017) doi: 10.1080/19420862.2016.1246096; WO 2009/036379; WO 2010/105256; and WO 2012/009568. Twenty-one clones bound to recombinant human CD3 epsilon (see, e.g., Figure 4A for relative binding affinities, and Figure 4B for antibody identities and sequence information associated with each of the 21 clones). Of these 21 clones, 14 also bound T cell-surface expressed CD3 epsilon (see, collectively, Figures 5, 6, and Figure 7). Of these 14 clones that bind T cell-surface expressed CD3epsilon, six of these were cyno CD3 epsilon-specific (see Figure 5), while eight of these bound both human- and cyno- CD3 epsilon (see Figures 6 and 7). Competitive binding assays showed that all of the CD3 epsilon-binding clones bound to epitopes overlapping that of I2C and did not compete significantly with OKT3 (Figure 8).

[0315] The three highest affinity CD3 binding clones (ADI-15512, ADH-15516, and ADI-16513; see, e.g., Figure 9) were selected for humanization. In that effort, twelve humanized variants were generated for each clone (36 variants in total) and tested for cell binding activity (see Figure 10A for sequence and germline information for each of these variants vs. the respective parents, ADI-15512, ADI-15516, and ADI-16513). Most of the humanized variants showed similar or improved cell binding profiles compared with the chimeric parents (see, e.g., Figures 10B, 10C, and 10D, for comparison of cell binding profiles of humanized variants and chimeric parents of ADI-15512, ADI-15516, and ADI-16513, respectively).

[0316] Six of the humanized variants, ADI-18565, ADI-18576, ADI-18585, ADI-18589, and ADI-18590, were selected for affinity-based optimization based on their binding (see, e.g., Figures 10B, 10C, 10D, 11A, 11B, 11C, and 13) and polyreactivity profiles (see, e.g., Figures 12A and 12B). Affinity maturation was performed by generating libraries of antibody variants containing mutations in the VH and/or VL of each of the afore-mentioned clones, and selecting for improved binding by flow cytometry (see, e.g., WO 2009/036379; WO 2010/105256; WO 2012/009569; Xu et al., *Protein Eng Des Sel.* Vol. 26(10), pages 663-670 (2013) doi: 10.1093/protein/gzt047; and Sivasubramanian et al., *MAbs.* Vol. 9(1), pages 29-42 (2017) doi: 10.1080/19420862.2016.1246096).

[0317] *Optimization Cycle 1: VH and VK mutagenesis.* For the first optimization cycle ("Cycle 1"), error-prone PCR was performed on both of the antibody VH and VL genes using standard methods and subsequently transformed into yeast using homologous recombination. Briefly, a diversified antibody library was created by introducing stochastic diversity (using standard molecular cloning error-prone PCR techniques) across the heavy and light chain variable domain regions of each antibody. This resulted in a library of roughly 10^8 in size that were ready for selection to enrich for progeny with improved affinity. Selection pressures included human (Hu) and cynomolgus (Cy) CD3εδ heterodimeric Fc fusion monomer (hereafter Hu CD3εδ Fc and Cy CD3εδ Fc, respectively; see Figure 18) antigen titration, biotinylated Hu CD3ε N-terminal peptide (CD3εN27 and CD3εN13 having the sequences described in Materials and Methods) antigen titration, and parental antibody Fab competition. Flow cytometry (FACS) methodology was employed to visualize and select, using standard techniques, the desired population to carry forward into additional selection rounds (see, e.g., Chao *et al.* Nature Protocols, 2006, WO 2009/036379; WO 2010/105256; WO 2012/009569; Xu et al., *Protein Eng Des Sel.* Vol. 26(10), pages 663-670 (2013) doi: 10.1093/protein/gzt047; and Sivasubramanian et al., *MAbs.* Vol. 9(1), pages 29-42 (2017) doi: 10.1080/19420862.2016.1246096). After several rounds of enrichment, yeast were plated to obtain colonies representing monoclonal antibody isolates, which were then sequenced by standard Sanger methodology, produced, and characterized as in the humanization selection described above (see, e.g., Figure 14 for a depiction of an exemplary FACS experiment and the resulting output population). Antibodies identified from the output with improved cell binding affinities were subject to a second cycle of mutagenesis and selection using similar methods as those described above.

[0318] *Optimization Cycle 2; HC x LC chain shuffle.* A second effort was undertaken to affinity-mature human/cyno cross-reactive antibodies derived from the ADI-18589 and 18590 lineages ("Cycle 2"; see, e.g., Figure 15 for exemplary FACS experiment and resulting output population). Briefly, antibody HC and LC were shuffled to create a combinatorial library in yeast for each of the starting parent antibodies and the library was subjected to rounds of affinity pressure similar to Cycle 1. Terminal round output monoclonal antibodies were sequenced, produced, and characterized. All of the clones selected from the second cycle of affinity maturation showed high affinity binding to cell-surface CD3 (see Figure 16), and had mutations in both the VH and VK regions relative to the parent clones (i.e., ADI-18589 and ADI-18590). Each exhibited Fab monovalent affinities to Hu CD3εδ Fc in the 13-142 nM K_D range and Fab monovalent affinities to Cy CD3εδ Fc in the 15-109 nM K_D range as determined by ForteBio Octet BLI measurement.

[0319] In order to ascertain the functional activity of the CD3 binders, a T-cell based IL-2 secretion assay– a measure of T-cell activation – was performed using two exemplary CD3 binders of the invention (ADI-20582 and ADI-20566) in comparison with I2C, an isotype control, and buffer alone (DPBS). The results, depicted in Figure 17, demonstrate that the exemplary CD3 binders elicited robust IL-2 release by CD3+ Jurkat T-cells relative to CD3- control T-cells, at a level meeting or exceeding that observed with the I2C control. Accordingly, CD3 binders of the present invention elicit potent T-cell activation.

[0320] *Optimization Cycle 3; CDR H3 mutagenesis and rational combination.* Subsequently, a single clone (ADI-20580) identified in the Cycle 2 optimization effort was selected for further optimization error ("Cycle 3") via H3 mutagenesis. H3 mutagenesis libraries were generated using standard oligo-based methods (e.g., NNK-based methods) and transformed into *Saccharomyces cerevisiae* using homologous recombination (see, e.g., Lee et al, *J. Mol. Biol.* Vol. 340, pages 1073-1093 (2004); WO 2009/036379; WO 2010/105256; and WO 2012/009569). Briefly, mutagenic oligonucleotides encoding site saturation (NNK nucleotide) mutagenesis at every pair of residues in combinatorial fashion were used to construct a library of theoretical diversity exceeding 2.6 x 10^4 (Figure 19). The library was subjected to two rounds of affinity pressure using titration of the CD3εN13 peptide from 100-10 nM by flow cytometry generally as described above (see Figure 20 for depiction of FACS results). Selected progeny were sequenced, produced, and characterized. Mutations observed in ADI-21970 and ADI-21961 and were rationally combined on the basis of observed affinity improvement. The mutation observed in ADI-21960 was also included based on H3 repeat frequency to generate rational, combinatorially combined variants based on mutations observed in five selected clones (Figure 22). Several clones showed improved binding affinity and cell staining compared to ADI-20580, while also showing a decrease in polyspecific reactivity (PSR) score (see Figures 21 and 22). ADI-21978 was chosen for scFv conversion and rational engineering of potential sequence degradation motifs.

[0321] *Optimization Cycle 4; rational mutagenesis of potential degradation sequence motifs.* ADI-21978 was observed potential sequence degradation motifs NG (Asn-Gly) and DP (Asp-Pro) in CDR H2, DG (Asp-Gly) in CDR H3, and NS (Asn-Ser) in CDR L1. These sites were rationally mutated to according to the following substitutions: NG -> EG (Glu-Gly) or NA (Asn-Ala), DP -> QP (Gln-Pro) or DA (Asp-Ala), DG -> EG or DA, and NS -> ES (Glu-Ser) or NA. The four sites were combined in a combinatorial matrix and the variant IgG were produced and characterized. Individual site substitutions were well tolerated, particularly mutations of the second position to Ala (i.e. NG->NA, DG->DA, etc.). Comparison of ADI-22523 (all four sequence liability sites) to individual VH Ala substitutions showed a < 2-fold reduction in monovalent (Fab) affinity for Cy CD3εδ and resolution of all four sites had a modest effect on avid (IgG) affinity for Hu CD3εδ (see Figures 23A and 23B). The resulting quadruple Ala variant ADI-25133 (ADI-26906) was used to compose a panel of bispecifics and for further CDR H3 mutagenesis.

[0322] Additionally, ADI-26906 was also converted to an scFv format using the same method as described for ADI-21978 and ADI-21952 and, as with those other scFv conversions, cell binding analysis revealed that conversion was well-tolerated. Optimized scFvs were tested for developability and thermostability.

[0323] *Optimization Cycle 5; CDR H3 mutagenesis focused on DG sequence motif.* ADI-21978 (ADI-22523) was diversified by site-saturation (NNK) mutagenesis targeting the degradation motif DG in CDR H3. In brief, every residue of the H3 was mutated in combination with the first or second position of the Asp-Gly site (Figure 24). A single round of FACS selection using the CD3εN13 peptide at 100 nM and 10 nM was conducted and the output sequenced, produced, and characterized. Only mutation of the Gly residues of the Asp-Gly motif produced binders, and all progeny showed some reduction in binding affinity relative to the parent (ADI-21978 (ADI-22523)).

[0324] *Cycle 6; Affinity modulation by rational combination.* ADI-25133 (ADI-26906) was rationally variegated by a matrix of CDR H2 and H3 sequences known to affect affinity with CDR L1 and L3 sequences known to affect affinity to yield a panel of 68 combinations (Figure 25A). The resulting sequence-confirmed antibodies were produced in yeast and characterized for recombinant antigen and cell binding. Monovalent Fab binding affinity spanned a range of nM-μM and correlated with cell binding median MFI at 100 nM IgG test concentration (Figures 25B and 25C). IFNγ production from PBMC was measured for both IgG and Fab formats, using two donors.

[0325] Clones derived from Cycles 5 and 6 were then tested for their ability to elicit T-cell stimulation and activation as deduced by measured cytokine levels as described below:

[0326] Cell lines/Primary human cells.

[0327] Frozen human peripheral blood mononuclear cells (PBMC) were purchased from AllCells Inc. (Alameda, CA)

[0328] Fresh peripheral blood mononuclear cells were purified from human whole blood from Scripps blood bank by Ficoll-Hypaque density gradient centrifugation.

[0329] Cell culture materials.

[0330] PBMC were cultured in RPMI-10% FBS consisted of RPMI-1640 serum-free medium supplemented with 10% fetal bovine serum (Hyclone FBS; catalog number SH30071.03IR, GE Healthcare, Logan, Utah), L-glutamine (catalog number 11875-093, ThermoFisher, Waltham, MA), 1% penicillin/streptomycin (catalog number 15070-063, ThermoFisher), 1 mM sodium pyruvate (catalog number 11360-070, ThermoFisher), 10 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES; catalog number 15630080, ThermoFisher), and 1X non-essential amino acid (catalog number 11140-50, ThermoFisher).

[0331] Previously frozen PBMC were quick thawed in 37°C water bath and added to pre-warmed RPMI-10% FBS media. Cells were pelleted at 300x g, re-suspended in pre-warmed media and counted before use.

[0332] **Determination of anti-CD3 clone activation of T cells in PBMCs in soluble IgG1 format and Fab format**

[0333] Cell stimulation procedure

[0334] Provided anti-CD3 IgG1 or anti-CD3 Fab were diluted in RPMI-10% FBS media to 2x final concentration (10 nM and 0.3 nM). Fifty microliters of 2x final concentration antibodies and 50 μL of donor PBMC at 2x10^5 cells/well were added to each well. Unstimulated control has RPMI-10% FBS media only, and positive control clone ADI-22523 and negative control ADI-03847 were also included in separate wells. Plates were incubated at 37°C for 48 hours supernatant was harvested for cytokine analysis.

[0335] Measurement of T cell activation by supernatant cytokine levels

[0336] After 48 hours of incubation, supernatant was collected for cytokine analysis by MesoScale discovery interferon-gamma tissue culture kit according to manufacturer's instruction. Supernatant was analyzed without dilution. Standard curve using recombinant cytokine was included in each plate for calculation of cytokine level in pg/ml.

[0337] Data analysis

[0338] Cytokine measurement by MSD.

Interferon gamma concentration (pg ml^{-1}) in supernatant was extrapolated using standard curve generated in MesoScale Discovery WorkBench software. Interferon gamma concentrations are listed as pg/ml. Antibody affinity data (Fab, IgG) to human CD3εδ was provided and are listed as Molar. Data is provided in the immediately following table (Table 1):

Table 1

ADI clone ID	**A4560 0.3nM Fab IFNg (pg ml^{-1})**	**A4560 0.3nM IgG1 IFNg (pg ml^{-1})**	**A4560 10nM Fab IFNg (pg ml^{-1})**	**A4560 10nM IgG1 IFNg (pg ml^{-1})**	**D5801 0.3nM Fab IFNg (pg ml^{-1})**	**D5801 0.3nM IgG1 IFNg (pg ml^{-1})**	**D5801 10nM Fab IFNg (pg ml^{-1})**	**D5801 10nM IgG1 IFNg (pg ml^{-1})**	Fab KD Human CD3εδ-Fc **(M) Monovalent**	Fab KD Cyno CD3εδ-Fc **(M) Monovalent**	IgG KD Human CD3ε **δ-Fc (M) Avid**	IgG KD Cyno CD3ε **δ-Fc (M) Avid**
ADI-03847	0	0	0	0	0	0	0	0	N.B.	N.B.	N.B.	N.B.

ADI-22523	0	2293.197	148.0116	4687.913	0	8857.269	698.8879	11887.59	5.9E-09	4.5E-09	2.0E-10	2.2E-10
ADI-23664	0	2725.718	239.8341	2131.418	0	4623.814	117.9867	5317.511	8.4E-09	8.9E-09	2.7E-10	2.8E-10
ADI-23672	0	1905.496	56.37432	2320.208	0	4121.787	172.223	4722.399	7.7E-09	8.8E-09	2.5E-10	2.4E-10
ADI-23673	0	2005.052	86.91475	4193.993	0	2627.311	185.1544	8565.428	7.6E-09	8.2E-09	2.7E-10	2.9E-10
ADI-26906	0	3849.833	70.52744	3983.237	0	9035.443	371.7809	9707.526	7.7E-09	8.1E-09	1.6E-09	2.5E-10
ADI-26907	0	1484.849	57.70298	5005.116	0	7885.667	335.9243	8561.689	9.6E-09	1.1E-08	1.8E-09	3.0E-10
ADI-26908	0	2629.234	20.6515	4618.489	0	8357.608	257.0513	7867.79	9.1E-09	1.0E-08	1.5E-09	3.1E-10
ADI-26909	0	3533.808	15.25265	3644.966	0	5777.494	101.2396	5639.143	1.4E-08	1.6E-08	1.9E-09	3.2E-10
ADI-26910	0	2128.518	37.69095	3142.977	0	5839.224	163.2046	5640.78	1.4E-08	1.6E-08	1.4E-09	2.6E-10
ADI-26912	0	0	0	0	0	0	0	0	1.3E-07	2.1E-07	3.0E-09	2.0E-09
ADI-26913	0	2235.181	0	3599.486	0	3239.355	0	4880.937	3.5E-08	3.8E-08	2.2E-09	4.0E-10
ADI-26915	0	0	2.579892	0	0	0	0	0	1.4E-07	P.F.	3.3E-09	2.6E-09
ADI-26916	0	0	0	14.77678	0	0	0	2.54948	1.7E-07	1.3E-07	2.9E-09	1.8E-09
ADI-26917	0	109.1881	0	895.5244	0	60.87033	0	1026.313	1.0E-07	1.2E-07	2.6E-09	1.0E-09
ADI-26918	0	0	0	0	0	0	0	0	1.4E-06	2.7E-07	3.0E-09	2.2E-09
ADI-26919	0	1221.756	0	1529.324	0	2607.514	0	2959.607	5.7E-08	5.4E-08	2.3E-09	5.9E-10
ADI-26920	0	710.0884	0	1667.536	0	787.9412	0	1783.751	7.6E-08	7.6E-08	3.4E-09	7.0E-10

ADI-26921	0	0	0	1496.688	0	86.26344	0	964.8354	9.5E-08	8.9E-08	3.7E-09	9.4E-10
ADI-26924	0	0	0	0	0	0	0	0	2.0E-07	2.8E-07	2.8E-09	2.1E-09
ADI-26925	0	0	0	0	0	0	0	0	N.B.	N.B.	1.1E-08	8.7E-09
ADI-26927	0	0	0	8.821052	0	0	0	8.597335	1.3E-07	1.5E-07	1.1E-09	1.1E-09
ADI-26928	0	0	0	0	0	0	0	0	N.B.	N.B.	2.8E-09	2.5E-09
ADI-26929	0	0	0	0	0	0	0	0	N.B.	N.B.	1.1E-08	9.7E-09
ADI-26930	0	0	0	0	0	0	0	0	N.B.	N.B.	1.0E-08	8.7E-09
ADI-26932	0	0	0	0	0	0	0	0	N.B.	N.B.	1.6E-08	1.3E-08
ADI-26933	0	1032.987	0	2752.275	0	660.8336	0	2100.075	5.9E-08	5.5E-08	6.7E-10	5.2E-10
ADI-26938	0	0	0	0	0	0	0	0	N.B.	N.B.	1.0E-08	1.0E-08
ADI-26939	0	0	0	0	0	0	0	0	3.5E-07	2.7E-07	1.9E-09	1.6E-09
ADI-26940	0	0	0	33.39678	0	0	0	2.8149	1.5E-07	1.5E-07	1.4E-09	1.2E-09
ADI-26941	0	0	0	0	0	0	0	0	1.1E-06	2.2E-07	1.7E-09	2.2E-09
ADI-26942	0	0	0	0	0	0	0	0	N.B.	N.B.	8.5E-09	7.8E-09
ADI-26943	0	0	0	0	0	0	0	0	N.B.	N.B.	7.6E-09	6.6E-09
ADI-26944	0	0	0	0	0	0	0	0	N.B.	N.B.	1.3E-08	1.2E-08
ADI-26945	0	0	0	0	0	0	0	0	N.B.	N.B.	2.0E-08	2.1E-08

ADI-26950	0	0	0	0	0	0	0	0	N.B.	N.B.	N.B.	N.B.
ADI-26954	0	0	0	521.1572	0	0	0	227.3743	N.B.	N.B.	N.B.	N.B.
Unstimulated	0	0	0	2.045886	0	0	0	0	#N/A	#N/A	#N/A	#N/A

[0339] A subset of the data is provided in graphic representation in Figure 25D. Among other things, a correlation of monovalent affinity with cytokine production was observed for both donors for 10 nM IgG having affinity for Hu and Cy CD3εδ Fc of at least 100 nM. Fab showed low IFNγ production by PBMC at 10 nM, but undetectable IFNγ production at 0.3 nM concentration (Figure 25D).

[0340] *scFv conversion of ADI-21978 (ADI-22523).* VH and VL were amplified and reassembled by overlap extension PCR to generate a matrix of scFv fused to IgG1 Fc (hereafter referred to as scFv-Fc and depicted in Figure 26A). In brief, the design matrix consisted of the VH/VK or VK/VH orientation, inclusion or exclusion of VH44-VK100 (Kabat numbering) disulfide (DS1) (Brinkmann U. *et al.* PNAS 1993), tether 5 or direct fusion, linker lengths of 15, 20, 25, and 30 amino acids. A modified VH44-VK100 disulfide (DS2) was also explored. Tether and linker sequences consisted of $(\text{Gly4Ser})_N$ repeats. The IgG1 upper hinge includes a Cys220Ser mutation in and scFv fusions were made to Glu216. Twenty-nine scFv-Fc from the ADI-21978 lineage were sequence confirmed, produced, and characterized (Figure 26B). Recombinant CD3 and cell binding analysis revealed that scFv conversion was well tolerated, with 2-4 fold affinity reduction compared to the IgG (Figure 26C). Many of the scFv-Fc designs exhibited a monomeric non-aggregated peak of 85-90% (Figure 26D). Thermal stability analysis by DSF showed that ADI-21978 scFv-Fc were generally stable, showing Tm in the range of 65-69°C (Figure 26E and Figure 26F). The inclusion of DS1 and DS2 yielded scFv-Fc with parent-like HIC retention time, whereas scFv-Fc without DS1/2 had a broad peak profile and delayed retention time (Figure 26G).

[0341] Example 2: Generation of SP34 (anti-CD3) variant antibodies: humanization and optimization SP34

[0342] *Humanization of SP34.* Humanization of SP34 was conducted by screening an initial panel of humanization designs produced in yeast (Figure 27). In brief, 28 designs representing combinations of four humanized VH and seven humanized Vκ or Vλ were produced in yeast and characterized for binding to Hu CD3εδ and Cy CD3εδ Fc. Due to relatively low expression titers, five selected HuSP34 designs were produced by transient HEK and evaluated for recombinant antigen binding, cell staining, and developability profiles (Figure 27). Of these, ADI-16606 (a combination of HC2 with LC3) was selected for having good binding and the cleanest developability profile, as indicated by AC-SINS and PSR data. Notably, background binding to CD3-expressing Jurkat cells (Jurkat CD3+), Jurkat cells not expressing CD3 (Jurkat CD3-), and Cyno HSC-F was comparable to chimeric SP34 (ChSP34).

[0343] *Affinity optimization from the HuSP34 effort leading to ADI-26956 and related antibody variants.* A first effort was undertaken to affinity-mature the human/cyno cross-reactive humanized anti-CD3 SP34 antibody (HuSP34) ADI-16606 (see Figure 28A for schematic of selection procedure and Figure 28B for exemplary flow cytometry selection plots). Briefly, a diversified antibody library was created by introducing stochastic diversity across the heavy and light chain variable domain regions. This resulted in a library exceeding 10^8 in realized diversity. Briefly, selection pressures for rounds 1 and 2 (R1 and R2) included biotinylated Hu CD3εδ Fc antigen titration from 50-5 nM, with selection of binders from the 10 nM condition gated for increased expression and antigen binding with respect to parent. In a third round (R3) antigen was titrated to 0.2 nM and selected binders, representing affinity-pressured progeny, were plated, sequenced, and produced. In a parallel effort, the R2 outputs were subjected to thermal pressure at R3. In brief, the enriched binding populations were subjected to thermal pressure by incubation of yeast at a range of temperature conditions spanning 53-65°C for 10 min in a thermocycler. After the yeast were cooled to 4°C, 50 nM CD3εN27 antigen was applied and the optimal condition for sorting was identified. Plasmids were released from sorted yeast using a Zymo Research kit, transformed into electrocompetent *E. coli*, mini-prepped from *E. coli*, and re-transformed into the cycle 1 parent HC or LC strains for Vλ and VH mutagenesis, respectively. Affinity and thermal pressures yielded divergent sequence collapse and consensus motifs (Figures 28C and 28D). Unique clones were produced and characterized for Fab and IgG binding to recombinant Hu and Cy CD3εδ Fc antigens, Hu and Cy cell binding, IL-2 production by Jurkat cells, polyspecific reactivity (PSR), self-interaction propensity (AC-SINS), and thermal stability by DSF.

[0344] *Optimization of HuSP34 Cycle 2; VH x Vλ chain shuffle and VH mutagenesis and Vλ mutagenesis.* Selected HC and LC from cycle 1 output were shuffled and diversified by error-prone PCR (Figure 29A). Selection were carried out utilizing similar affinity and thermal pressures as cycle 1 (Figure 29B). Unique output sequences were produced and characterized. ADI-20587, ADI-20607, and ADI-20590 were selected for another cycle of optimization.

[0345] *Optimization of HuSP34 Cycle 3; Vλ rational combination with 3X VH.* HC from ADI-20587, ADI-20607, and ADI-20590 were used to produce a matrix with 28 rationally-designed LC (Figure 30). The LC combined the most favorable mutations selected in cycles 1 and 2. In brief, Vλ mutations that increase thermal stability (F11L, T27A, T74I, A78V, D81E, S84A, and S93N), improve expression (R24G), decrease PSR (N52D), and improve affinity (A89V and L95H) were combined. Sequence-confirmed clones were produced and characterized. ADI-21952, a combination of the HC from ADI-20587 and a designed LC carrying the mutations F11L, R24G, N52D, D81E, S84A, and L95H, was selected for further due to a combination of affinity, cell binding, IL-2 production, thermal stability, and PSR.

[0346] *Optimization of HuSP34 Cycle 4; Rational mutation of potential degradation sequence motifs.* Potential degradation motifs in ADI-21952 were observed in VH FR3, NS (Asn-Ser) and CDR H3, NG (Asn-Gly). These sites were rationally mutated to according to the following substitutions: NG -> EG (Glu-Gly) or NA (Asn-Ala) and NS -> ES (Glu-Ser) or NA. The two sites were combined in a combinatorial matrix and the variant IgG were produced and characterized. Comparison of ADI-21952 (parent) and ADI-23634 and ADI-23637 showed that both rational mutations of the CDR H3 NG site significantly impacted affinity whereas mutations of the FR3 NS site as observed for ADI-23633 and ADI-23636 did not significantly impact properties (Figure 31).

[0347] *Optimization Cycle 5; CDR H3 mutagenesis to resolve the NG motif.* ADI-23633 was selected for diversification by site-saturation (NNK) mutagenesis targeting the degradation motif NG in CDR H3. A single round of affinity pressure using the CD3εN13 at 10 nM condition was performed. Selected progeny were produced and characterized, yielding at least two variants with comparable or improved affinity with respect to parent (Figure 32).

[0348] *Optimization Cycle 6; Affinity modulation by rational combination.* ADI-21952 was rationally variegated by a matrix of CDR H1, CDR H2, and CDR H3 sequences known to affect affinity with CDR L3 sequences known to affect affinity to yield a panel of 42 combinations (Figure 33A). The resulting sequence-confirmed antibodies were produced in yeast and characterized for recombinant antigen (Figure 33B) and cell binding (Figure 33C). Monovalent Fab binding affinity spanned a range of nM-μM and correlated with cell binding median MFI at 100 nM IgG test concentration (Figures 33B and 33C).

[0349] *scFv conversion of ADI-21952.* VH and VL were amplified and reassembled by overlap extension PCR to compose a matrix of scFv fused to IgG1 Fc. The design matrix was identical to that utilized for ADI-21978 conversion. Recombinant CD3 and cell binding analysis revealed a <2-fold reduction in affinity compared to the IgG for scFv that do not contain DS1 or DS2, but a significant decrease in affinity for disulfide-containing scFv (~8-fold) (Figure 34A). Many of the scFv-Fc designs exhibited a monomeric non-aggregated peak of 85-90%, a few designs showed >90% monomer content (Figure 34B). Thermal stability analysis by DSF showed that ADI-21952 scFv-Fc were metastable, showing Tm in the range of 59-66°C (Figure 34C). The inclusion of DS1 and DS2 yielded scFv-Fc with parent-like HIC retention time, whereas scFv-Fc without DS1/2 had a broad peak profile and delayed retention time (Figure 34D).

[0350] *HEK production panel of broad affinity for developability profiling.* A focused panel of variants representing a broad affinity range was selected for production in HEK. IgG and Fab were characterized for binding affinity to recombinant Hu and Cy CD3εδ Fc and human and cyno cell lines (Figure 35A). Developability assays included PSR, baculovirus particle assays, HIC, SEC, AC-SINS (self-interaction), Fab Tm by DSF, transient HEK titer. Chemical integrity was assessed by inspection of the intact HC peak breadth and symmetry (se Figure 35B). A literature control antibody, CTL-19672 (GNE 38E4 as disclosed in, e.g., US patent application publication number US 2015/0166661), and the novel lineage binder with unresolved potential degradation sites, ADI-22523, demonstrated succinimide intermediate formation under non-stress conditions (Figure 35B). ADI-26906, which has all predicted liability sites resolved, does not show peak broadening, supporting the beneficial role of these modifications for chemical stability of the antibody.

[0351] *HEK production of CD3 x TAA bispecifics.* Literature tumor associated antigen (TAA) binders targeting CD33 (Lintuzumab) and HER2 (Trastuzumab) were selected for assembly of bispecific molecules for functional validation, along with a negative control HEL binding antibody, ADI-03847 (Figure 36A). As a first step, antibodies were reformatted to scFv-Fc having the IgG4 isotype and stabilizing hinge mutation Ser228Phe, produced in HEK293ADI1, and purified by CaptureSelect FcXL (GE Healthcare LifeSciences). All scFv-Fc bound only the expected target antigen (see, e.g., Figure 36A, *bottom* panel). Bispecific CD3 x TAA antibodies were produced by co-transfection of HEK293ADI1 with both HC and the CD3 LC plasmids. Purification of heterodimer was achieved by pH gradient elution from POROS MabCapture A column, which was generally effective for resolving the heterodimer from the CD3 monospecific antibody (Figure 36B). CD3/HER2 bispecifics and TAA control were tested for their ability to activate T cells in the presence and absence of HER2 expressing cells SK-BR-3 as determined by percentage CD25+ CD69+ T (CD8) cells upon incubation with increasing amounts of the tested antibodies (Figure 36C). T cell activation was not observed in the absence of a HER2 binding arm except for a low level of activation observed with HuOKT3 (ADI-10390) as the CD3 arm. In the presence of target cells the ADI-21978/Trastuzumab and ADI-10390/Trastuzumab both activated T cells, but neither CD3 binder activated cells when paired with the HEL control arm.

[0352] *Analysis of T-cell activation and target cell killing.* Next, CD3/HER2 and CD3/HEL bispecifics were tested in a redirected T cell cytotoxicity assay (RTCC). ADI-21952 (ADI-24780) and ADI-21978 (ADI-24781) elicited dose-dependent target cell killing by incubated T cell effector cells at a potency (EC50) that was approximate to or better than positive controls. In particular, ADI-21978/Trastuzumab bispecific elicited target cell killing potency in the picomolar (pM) range (See, e.g., Figure 37).

[0353] A schematic representation of the selection, humanization, and optimization procedures and clone lineages generated thereby as described in Examples 1 and 2 are provided in Figure 38A and Figure 38B, respectively.

Variants

[0354] Applicant has found that introducing certain variations into CDR sequences in CD3 antibodies or antigen-binding polypeptides may confer beneficial properties, such as increased target binding affinity, resistance to degradation (e.g., by proteases), and improved developability (e.g., a reduction in polyspecificity). For example, it has been found herein that introducing a "T" at position one of CDRH3 can lead to increased target binding affinity. In some embodiments, CD3 antibodies or antigen-binding polypeptides are provided in which a "T" is introduced at position 1 of CDRH3 and are characterized by increased binding affinity to CD3 antigens.

[0355] Also, Applicant has found herein that avoiding certain consecutive amino acid sequences in CDRH2 (e.g.,"NG") and/or CDRH3 (e.g.,"DG") can increase resistance to degradation. In some embodiments, CD3 antibodies or antigen-binding polypeptides are provided in which particular amino acids are avoided at certain positions (e.g., avoiding a "G", "N", or "D") in CDRH2 and/or CDRH3 and are characterized by resistance to degradation.

[0356] Additionally, Applicant has found herein that introduction of certain amino acids (e.g., "L" or "I") in CDRL3 can improve developability (e.g., as measured by AC-SINS, HIC Retention Time, or binding to Polyspecificity Reagents). In some embodiments, CD3 antibodies or antigen-binding polypeptide are provided that have "L" or "I" substituted and are characterized by improved developability scores.

[0357] MATERIALS AND METHODS

[0358] In addition to the description provided above, the following Materials and Methods were employed in the Examples.

[0359] *Hu and Cy CD3εδ Fc heterodimer antigen production.* Recombinant heterodimeric CD3 Fc fusion antigens were produced in HEK 293 cells by co-transfection of plasmids encoding Hu CD3ε Fc (ectodomain, ECD, residues 22-126) and CD3δ Fc-HIS (ECD residues 22-100) or Cy CD3ε Fc (ECD residues 22-117) and CD3δ Fc-HIS (ECD residues 22-100) utilizing a heterologous signal peptide sequence. Chromatographic separations were performed on a computer controlled ÄKTA Avant 150 preparative chromatography system (GE Healthcare Life Sciences) equipped with an integrated conductivity sensor, enabling in-line salt concentration monitoring during the run. Clarified culture supernatants were purified by Ni

Sepharose 6 Fast Flow (GE Healthcare Life Sciences), which removes the CD3εε Fc-HIS homodimer. CD3εδ Fc-HIS heterodimer was resolved from CD3δδ Fc-HIS homodimer by Mono Q 10/100 GL by a linear Tris-buffered KCl gradient at pH 8.5.

[0360] *Peptides.* C-terminally biotinylated CD3ε N-terminal peptides were obtained from New England Peptide. All peptides were delivered with a purity of ≥95%. Peptides were designed based on the primary sequence of Hu CD3ε and the crystal structure of Hu CD3εδ bound to OKT3 (Kjer-Nielsen L. *et al.* PNAS 2004). The CD3εN27 peptide has the sequence H2N-QDGNEEMGSITQTPYQVSISGTTVILT[K/SCBiot(dPEG4)]-amide and the CD3εN13 peptide has the sequence H2N-QDGNEEMGGITQT[K/SCBiot(dPEG4)]-amide.

[0361] *Antigen biotinylation.* CD3 antigens were biotinylated using the EZ-Link Sulfo-NHS-Biotinylation Kit from Pierce. Goat anti-human F(ab')$_2$ kappa-FITC (LC-FITC), Extravidin-PE (EA-PE) and streptavidin-633 (SA-633) were obtained from Southern Biotech, Sigma and Molecular Probes, respectively. Streptavidin MicroBeads and MACS LC separation columns were purchased from Miltenyi Biotec.

[0362] *Cell line propagation and cell labeling assays.* Human Jurkat CD3+ cells (ATCC TIB-152) and Jurkat CD3- cells (ATCC TIB-153) were obtained from ATCC. Cyno HSC-F cells were obtained from the NIH Non-human Primate Reagent Resource. All cell lines were cultured in RPMI 1640 GlutaMax media supplemented with 10% fetal bovine serum (FBS).

[0363] Cell labeling was conducted by aliquoting 100,000-200,000 cells per well in a 96-well assay plate. Cells were centrifugated at 500 x g for 5 min at 4°C, then resuspended in 100 μl of 100 nM IgG and incubated at room temperature for 20 min. Cells were then washed in buffer (phosphate-buffered saline (PBS)/0.1% bovine serum albumin (BSA) three times and resuspended in secondary reagent, typically goat anti-human R-PE (Southern Biotech). The plate was assayed on a FACSCanto (BD Biosciences) using an HTS sample injector. Flow cytometry data was analyzed for median fluorescence intensity in the R-PE channel.

[0364] *Human PBMC sourcing and expansion.* Frozen human peripheral blood mononuclear cells (PBMC) were purchased from AllCells Inc. (Alameda, CA). Fresh peripheral blood mononuclear cells were purified from human whole blood from Scripps blood bank by Ficoll-Hypaque density gradient centrifugation.

[0365] PBMC were cultured in RPMI-10% FBS consisted of RPMI-1640 serum-free medium supplemented with 10% fetal bovine serum (Hyclone FBS; catalog number SH30071.03IR, GE Healthcare, Logan, Utah), L-glutamine (catalog number 11875-093, ThermoFisher, Waltham, MA), 1% penicillin/streptomycin (catalog number 15070-063, ThermoFisher), 1 mM sodium pyruvate (catalog number 11360-070, ThermoFisher), 10 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES; catalog number 15630080, ThermoFisher), and 1X non-essential amino acid (catalog number 11140-50, ThermoFisher).

[0366] Previously frozen PBMC were quick thawed in 37°C water bath and added to pre-warmed RPMI-10% FBS media. Cells were pelleted at 300xg, re-suspended in pre-warmed media and counted before use.

[0367] *Peripheral blood mononuclear cells (PBMC) activation by CD3 antibodies.* CD3 IgG and Fab were diluted in RPMI-10% FBS media to 2x final concentration (10 nM and 0.3 nM). Fifty microliters of 2x final concentration antibodies and 50 µL of donor PBMC at 2×10^5 cells/well were added to each well. Unstimulated control has RPMI-10% FBS media only, and positive control clone ADI-22523 and negative control ADI-03847 were also included in separate wells. Plates were incubated at 37°C for 48 hours supernatant was harvested for cytokine analysis.

[0368] *Measurement of T cell activation by supernatant cytokine.* After 48 hours of incubation, supernatant was collected for cytokine analysis by MesoScale discovery interferon-gamma tissue culture kit according to manufacturer's instruction. Supernatant was analyzed without dilution. Standard curve using recombinant cytokine was included in each plate for calculation of cytokine level in pg/ml.

[0369] Interferon gamma concentration (pg/mL) in supernatant was extrapolated using standard curve generated in MesoScale Discovery WorkBench software. Interferon gamma concentrations are listed as pg/ml. Antibody affinity data (Fab, IgG) to human CD3εδ was provided and are listed as Molar.

[0370] *FACS affinity pressured selection methods.* Briefly, yeast cells (at least ~2×10^7 cells/labeling condition) were incubated with a volume of biotinylated antigen sufficient to represent a stoichiometric excess with respect to the average IgG presentation number. Antigen labeling conditions are 100 to 1 nM under equilibrium conditions, typically carried out for 20 min to several hours at room temperature in FACS wash buffer (phosphate-buffered saline (PBS)/0.1% bovine serum albumin (BSA)). After washing three times with wash buffer, yeast were then stained with secondary reagents anti-human light chain FITC conjugate (LC-FITC) diluted 1:100 and either streptavidin-633 (SA-633) diluted 1:500 or extravidin-phycoerythrin (EA-PE) diluted 1:50 for 15 min at 4°C. After washing twice with ice-cold wash buffer, the cell pellets were resuspended in wash buffer in a typical volume of at least 1 mL per 1 x 10^7 yeast and transferred to strainer-capped sort tubes. Sorting is performed using a FACS ARIA sorter (BD Biosciences) and sort gates were determined to select for binders. After the final round of sorting, yeast were plated and individual colonies picked for characterization.

[0371] *FACS thermal pressured selection methods.* The parent antibody was diversified by error-prone PCR to derive an optimization library in yeast. This yeast library first proceeds through a positive antigen selection round to select for expressing binders, using CD3εN27. This enriched population then proceeded through a series of thermally pressured conditions ranging from ~50°C up to 65°C for 10 min with room temperature as a control. Optimally pressured conditions were gated on LC presentation (anti-human lambda PE) and antigen binding (SA-APC), reflecting the residual folded IgG competent to bind the selection reagents. Sorted cells are pelleted and the plasmids extracted using a commercial yeast plasmid purification kit (Zymo Research) in which the yeast cell walls are disrupted with Zymolase and the DNA is subsequently purified by a DNA mini-column. Plasmid DNA is then transformed into *E.coli* for amplification, followed by mini-prep isolation of the plasmid DNA with an *E. coli* plasmid purification kit (Qiagen). Plasmid DNA is then prepared for transformation into the appropriate yeast strain for subsequent cycles selection or sequencing and IgG production.

[0372] *Error-prone PCR optimization.* Error-prone PCR-based mutagenesis of the heavy chain (VH) and/or light chain (VL) using standard molecular biology techniques introduced stochastic diversity. Briefly, mutagenic nucleotide analogues dPTP and 8-oxo-dGTP were incorporated into the VH and VL amplification process at 1 uM concentration to increase the base mis-incorporation frequency up to approx. 0.01 bp. The mutated PCR product was recombined *in situ* by homologous recombination with a linearized vector containing the HC or LC constant region sequences. This typically results in a library of 1 x $10^{7\text{-}8}$ diversity. Affinity and expression co-pressures were applied by incubating the antigen antibody yeast complex at decreasing concentrations of antigen (equilibrium pressure) or with parental Fab competition (equilibrium and kinetic pressures) for varying amounts of time to select for the highest affinity antibodies on FACS over successive rounds of selection.

[0373] *Oligonucleotide-based CDR H3 mutagenesis.* Discovered or previously optimized antibodies can progress through additional optimization by diversification of the CDR H3 sequence. To do so, the light chain variable region of the starting antibody is PCR amplified, and then, using yeast homologous recombination, is inserted into a yeast strain containing the light chain empty vector. This constitutes the parental light chain yeast strain. The heavy chain of the starting antibody is used as PCR input in combination with germline specific primers that generate a PCR product that contains from framework 1 through framework three of the heavy chain. This amplification is perform using the mutagenic nucleotide 8-oxo-dGTP to provide additional low levels of mutagenesis in the amplified heavy chain region. In order to create designed diversity in the CDR H3 region of the starting antibody, a library of CDR H3 oligos is generated/ordered (i.e. from IDT). The oligo pool is amplified with primers containing 5’ tails that allow for germline specific recombination with the amplified FW1-FW3 region and the empty. A universal 3’ primer is used for FW4. Alternatively, mutagenic PCR can be performed that incorporates 8-oxo-dGTP into a PCR reaction using germline specific 5’ primers, the universal 3’ primer and VH DNA. Once the LC strain, HC FW1-FW3 and diversified CDR H3-FW4 inputs have been generated, a three piece transformation is performed by introducing the two HC components along with a HC empty vector into the LC strain. Subsequently, the cells are grown out under selective pressure to ensure HC and LC components are present.

[0374] *Antibody yeast production and purification.* Yeast clones were grown to saturation and then induced for 48 h at 30°C with shaking. After induction, yeast cells were pelleted and the supernatants were harvested for purification. IgGs were purified using a Protein A column and eluted with acetic acid, pH 2.0. Fab fragments were generated by papain digestion and purified over KappaSelect or CaptureSelect IgG-CH1 (GE Healthcare LifeSciences).

[0375] *Antibody HEK production and purification.* Mammalian expression of IgG was done by sub-cloning antibodies into a new expression vector followed by transient transfection and expression in HEK293ADI1, a monoclonal cell line derived from HEK293 (DSMZ) selected for clump-free growth, growth rate, and transfectability. Briefly, expression vectors containing the antibody of interest were transfected by complexing with a transfection reagent followed by exposure to HEK cells for one hour followed by dilution of culture media to a final density of 4 million cells per mL. The cells were then cultured for 7 days with fresh feed media every 48 hours. After 7 days, the supernatant was collected following centrifugation and purification was performed using protein A. If necessary, a CHT column purification was added to reach > 95 % monomer.

[0376] *Bispecific antibody HEK production and purification.* IgG4 scFv-Fc molecules carrying the ProA non-binding His435->Arg, Tyr436->Phe ("RF") mutations were purified by CaptureSelect™ FcXL (GE HealthCare) and eluted with acetic acid pH 3.5.

[0377] Bispecific antibodies were expressed in HEK293ADI1 cells grown in shake flasks. To obtain clearance of the ProA non-binding RF homodimer, primary capture was performed using a Mab Select SuRE column, eluted with acetic acid, pH 3.5 and neutralized with 2M HEPES pH 8.0. Heterodimer was then isolated by a secondary purification on a POROS MabCapture A column, and linear gradient elution of 40 mM acetic acid, 500 mM NaCl from pH 6.0 to pH 3.0. Fractions were neutralized with 2M HEPES pH 8.0, pooled to avoid inclusion of aggregates appearing at the tail of the heterodimer peak, and analyzed by LCMS to ensure heterodimer purity.

[0378] *ForteBio KD measurements (Biolayer interferometry; BLI).* ForteBio affinity measurements were performed generally as previously described (Estep, P., *et al.*, High throughput solution-based measurement of antibody-antigen affinity and epitope binning. MAbs, 2013. 5(2): p. 270-8.). Briefly, ForteBio affinity measurements were performed by loading IgGs online onto AHQ sensors. Sensors were equilibrated off-line in assay buffer for 30 min and then monitored on-line for 60 seconds for baseline establishment. Sensors with loaded IgGs were exposed to 100 nM antigen for 5 min, afterwards they were transferred to assay buffer for 5 min for off-rate measurement. Kinetics was analyzed using the 1:1 binding model.

[0379] *BiaCore KD measurements (Surface plasmon resonance; SPR).* Biosensor analysis was conducted at 25 °C in a HBS-EP buffer system (10 mM HEPES pH 7.3, 150 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20) using a Biacore 8K optical biosensor docked with a CM5 sensor chip (GE Healthcare, Marlboro, MA). The sample hotel was maintained at

10°C. Goat anti-human IgG capture antibody (Jackson ImmunoResearch Laboratories, Inc., West Grove, PA; 109-005-098) was immobilized (11700 +/- 400 RU) to both flow cells of the sensor chip using standard amine coupling chemistry. This surface type provided a format for reproducibly capturing fresh analysis antigen after each regeneration step. Flow cell 2 was used to analyze captured antigen (35.7 +/-0.8 RU) while flow cell 1 was used as a reference flow cell. Fab concentrations ranging from 100 to 0.412 nM (3-fold dilutions) were prepared in running buffer. Each of the Fab sample concentrations were run as a single replicate. Two blank (buffer) injections also were run and used to assess and subtract system artifacts. The association and dissociation phases for all Fab concentrations were monitored for 180 s each, at a flow rate of 30 μL/min. The surface was regenerated with 10 mM glycine, pH 1.5 for 30 s, at a flow rate of 30 μL/min. The data was aligned, double referenced, and fit using Biacore 8K Evaluation Software, version 1.0.

[0380] *Octet Red384 Epitope Binning/ligand blocking.* Epitope binning/ligand blocking was performed using a standard sandwich format cross-blocking assay. Control anti-target IgG was loaded onto AHQ sensors and unoccupied Fc-binding sites on the sensor were blocked with an irrelevant human IgG1 antibody. The sensors were then exposed to 100 nM target antigen followed by a second anti-target antibody or ligand. Data was processed using ForteBio's Data Analysis Software 7.0. Additional binding by the second antibody or ligand after antigen association indicates an unoccupied epitope (non-competitor), while no binding indicates epitope blocking (competitor or ligand blocking).

[0381] *Size Exclusion Chromatography.* A TSKgel SuperSW mAb HTP column (22855) was used for fast SEC analysis of yeast and mammalian produced mAbs at 0.4 mL/min with a cycle time of 6 min/run. 200 mM Sodium Phosphate and 250 mM Sodium Chloride was used as the mobile phase.

[0382] *Dynamic Scanning Fluorimetry (DSF).* 10 μL of 20x Sypro Orange is added to 20 μL of 0.2-1mg/mL mAb or Fab solution. A RT-PCR instrument (BioRad CFX96 RT PCR) is used to ramp the sample plate temperature from 40 to 95°C at 0.5°C increments, with 2 min equilibrate at each temperature. The negative of first derivative for the raw data is used to extract Tm.

[0383] *PSR Preparation.* Polyspecific reactivity reagent (PSR) was prepared as described in, e.g., WO 2014/179363 and Xu et al., *mAbs*, 2013. In brief, 2.5 liters CHO-S cells were used as starting material. The cells were pelleted at 2,400 x g for 5 min in 500 mL centrifuge bottles filled to 400 mL. Cell pellets were combined and then resuspended in 25 ml Buffer B and pelleted at 2,400 x g for 3 min. The buffer was decanted and the wash repeated one time. Cell pellets were resuspend in 3x the pellet volume of Buffer B containing 1 x protease inhibitors (Roche, Complete, EDTA-free) using a polytron homogenizer with the cells maintained on ice. The homogenate was then centrifuged at 2,400 x g for 5 min and the supernatant retained and pelleted one additional time (2,400 x g/5min) to ensure the removal of unbroken cells, cell debris and nuclei; the resultant supernatant is the total protein preparation. The supernatant was then transferred into two Nalgene Oak Ridge 45 mL centrifuge tubes and pelleted at 40,000 x g for 40 min at 4°C. The supernatants containing the Separated Cytosolic Proteins (SCPs) were then transferred into clean Oak Ridge tubes, and centrifuged at 40,000 x g one more time. In parallel, the pellets containing the membrane fraction (EMF) were retained and centrifuged at 40,000 for 20 min to remove residual supernatant. The EMF pellets were then rinsed with Buffer B. 8 mL Buffer B was then added to the membrane pellets to dislodge the pellets and transfer into a Dounce Homogenizer. After the pellets were homogenized, they were transferred to a 50 mL conical tube and represented the final EMF preparation.

[0384] One billion mammalian cells (e.g. CHO, HEK293, Sf9) at ~10^6 – 10^7 cells/mL were transferred from tissue culture environment into 4x 250 mL conical tubes and pelleted at 550 x g for 3 min. All subsequent steps were performed at 4°C or on ice with ice-cold buffers. Cells were washed with 100 mL of PBSF (1x PBS + 1 mg/mL BSA) and combined into one conical tube. After removing the supernatant, the cell pellet was then re-suspended in 30 mL Buffer B (50 mM HEPES, 0.15 M NaCl, 2 mM $CaCl_2$, 5 mM KCl, 5 mM $MgCl_2$, 10 % Glycerol, pH 7.2) and pelleted at 550 x g for 3 min. Buffer B supernatant was decanted and cells re-suspended in 3x pellet volume of Buffer B plus 2.5x protease inhibitor (Roche, cOmplete, EDTA-free). Protease inhibitors in Buffer B were included from here on forward. Cells were homogenized four times for 30 sec pulses (Polyton homogenizer, PT1200E) and the membrane fraction was pelleted at 40,000 x g for 1 hour at 4°C. The pellet is rinsed with 1 mL Buffer B; the supernatant is retained and represents the s. The pellet is transferred into a Dounce homogenizer with 3 mL of Buffer B and re-suspended by moving the pestle slowly up and down for 30-35 strokes. The enriched membrane fraction (EMF) is moved into a new collection tube, rinsing the pestle to collect all potential protein. Determine the protein concentration of the purified EMF using the Dc-protein assay kit (BioRad). To solubilize the EMF, transfer into Solubilization Buffer (50 mM HEPES, 0.15 M NaCl, 2 mM $CaCl_2$, 5 mM KCl, 5 mM $MgCl_2$, 1 % n-Dodecyl-b-D-Maltopyranoside (DDM), 1x protease inhibitor, pH 7.2) to a final concentration of 1 mg/mL. Rotate the mixture overnight at 4°C rotating followed by centrifugation in a 50 mL Oak Ridge tube (Fisher Scientific, 050529-ID) at 40,000 x g for 1 hour. Collect the supernatant which represents the soluble membrane proteins (SMPs) and quantify the protein yield as described above.

[0385] For biotinylation, prepare the NHS-LC-Biotin stock solution according to manufacturer's protocol (Pierce, Thermo Fisher). In brief, 20 µl of biotin reagent is added for every 1 mg of EMF sample and incubated at 4°C for 3 hours with gentle agitation. Adjust the volume to 25 mL with Buffer B and transfer to an Oak Ridge centrifuge tube. Pellet the biotinylated EMF (b-EMF) at 40,000 x g for 1 hour, and rinse two times with 3 mL of Buffer C (Buffer B minus the glycerol) without disturbing the pellet. Remove the residual solution. Re-suspended the pellet with a Dounce homogenizer in 3 mL of Buffer C as described previously. The re-suspended pellet now represents biotinylated EMF (b-EMF). Solubilized as described above to prepare b-SMPs.

[0386] *PSR Binding Analyses.* Assays were performed generally as described in, e.g., Xu et al. To characterize the PSR profile of monoclonal antibodies presented on yeast, two million IgG-presenting yeast were transferred into a 96-well assay plate and pellet at 3000 x g for 3 min to remove supernatant. Re-suspend the pellet in 50 µl of freshly prepared 1:10 dilution of stock b-PSRs and incubate on ice for 20 minutes. Wash the cells twice with 200 µl of cold PBSF and pellet re-suspended in 50 µl of secondary labeling mix (Extravidin-R-PE, anti-human LC-FITC, and propidium iodide). Incubate the mix on ice for 20 minutes followed by two washes with 200 ul ice-cold PBSF. Re-suspend the cells in 100 µl of ice-cold PBSF and run the plate on a FACSCanto (BD Biosciences) using HTS sample injector. Flow cytometry data was analyzed for mean fluorescence intensity in the R-PE channel and normalized to proper controls in order to assess non-specific binding. Numerous methods for presentation or display of antibodies or antibody fragments on the surface of yeast have been described previously, all of which are consistent with this protocol (Blaise et al., 2004, Boder and Wittrup, 1997, Kuroda and Ueda, 2011, Orcutt and Wittrup, 2010, Rakestraw et al., 2011, Sazinsky et al., 2008, Tasumi et al., 2009, Vasquez et al., 2009).

[0387] *Baculovirus particle assay (BVP).* BVPs (BlueSky Biotech) were incubated on ELISA plates by adding 50 µl of 1:1 BVP stock: 50 mM sodium carbonate (pH 9.6) per well and placed at 4°C for 16–24 h. The next day, unbound BVPs were aspirated from the wells. All remaining steps were performed at room temperature (22°C). One hundred microliters of blocking buffer (PBS with 0.5% BSA) was added and let incubate for 1 h prior to three washes with 100 µl of PBS. Next, 50 µl of 1 µM primary antibodies (i.e. test antibodies) in blocking buffer was added to the wells and incubated for 1 h followed by six washes with 100 µl of PBS. Fifty microliters of anti-Human-IgG-HRP (Promega W4038, prepared in PBS) was added to the wells and incubated for 1 h followed by six washes as before. Finally, 50 µl of TMB substrate (Fisher Scientific, 34021) was added to each well and incubated for 10–15 min. The reactions were stopped by adding 50 µl of 2 M sulfuric acid to each well. The absorbance was read at 450 nm and BVP score determined by normalizing absorbance by control wells with no test antibody.

[0388] *ForteBio Kinetics.* FortBio Octet HTX instruments were used in 12 channel mode (8 sensors per channel, 96 sensors per experiment) with either AHC, SA, or AHQ sensors. Instrumentation was driven by manufacturer supplied software (versions 8.2 and 9.0). Sample names and concentrations were input into the plate data page, and sensor associated proteins were identified in the “information” column on the sensor data page. Kinetic experiments are collected with either a 90 or 180 s baseline, 180 s association phase, and 180 s dissociation phase. Binning experiments were collected in 5 steps: 90 s of baseline1, 90 s of a sensor binding check with the secondary binder, 90 s of baseline2, 180 s of association, and 180 s of dissociation in the well containing the secondary mAb. All files were saved into a shared network drive with a naming convention that identifies the format of the experiment.

[0389] *HIC.* IgG1 samples were buffer exchanged into 1 M ammonium sulfate and 0.1 M sodium phosphate at pH 6.5 using a Zeba 40 kDa 0.5 mL spin column (Thermo Pierce, cat # 87766). A salt gradient was established on a Dionex ProPac HIC-10 column from 1.8 M ammonium sulfate, 0.1 M sodium phosphate at pH 6.5 to the same condition without ammonium sulfate. The gradient ran for 17 min at a flow rate of 0.75 ml/min. An acetonitrile wash step was added at the end of the run to remove any remaining protein and the column was re-equilibrated over 7 column volumes before the next injection cycle. Peak retention times were monitored at A280 absorbance and concentrations of ammonium sulfate at elution were calculated based on gradient and flow rate.

[0390] *LCMS.* mAb samples were reduced by DTT, followed by middle down LCMS analysis on a Bruker maXis4G mass spectrometer coupled with an Agilent 1100 HPLC (Agilent). A POROS R2 10 µm (2.1 x 30 mm) reversed phase column was used to remove salt in the samples. A fast LC flow at 2 mL/min allows the separation between sample and salt and elution of samples and regeneration of column to finish within a 2.1 min cycle. A T-junction is used to deliver only 0.15 mL/min sample flow into the mass spectrometer for sample analysis. The Bruker maXis 4G mass spectrometer was run in positive ion mode with detection in the range of 750 to 2500 m/z. The remaining source parameters were set as follows; the capillary was set at 5500V, the Nebulizer at 4.0 Bar, dry gas at 4.0 l/min, and dry temp set at 200°C.

[0391] The MS spectra were analyzed using Bruker Data Analysis version 4.1 and the deconvolution was accomplished using maximum entropy deconvolution with a mass range of 20 to 30 kDa.

[0392] *IL2 Secretion.* Coat a flat-bottom 96-well culture plate (Thermo Scientific, 446612) with 200 ul per well of anti-CD3 antibody at 10 µg/mL concentration in sterile DPBS; cover with lid and incubate overnight at 4°C. Just before adding cells the following day, wash the 96-well culture plate 3 times with 200 µl of ice-cold sterile DPBS. In parallel, prepare the cells. Measure the cell density, and calculate the total number of CD3+ and CD3- cells to achieve $1x10^6$ cells/well. Aliquot the required amount of cells into a 50 mL conical tube, and then wash cells 3X in 50 mL of warm (37°C) RPMI 1640 GlutaMAX (Gibco, 61870-127). Resuspend the cells in warm culture media containing soluble anti-CD28 antibody (BioLegend) at a concentration of 2 µg/mL, for a cell density of $1x10^7$ cells/mL. Dispense 100 ul, containing $1.0x10^6$ cells, per well onto anti-CD3-coated cell culture plate. Cover the plate with the hard plastic plate lid and incubate in stationary incubator at 37°C for 14-16 h. The next day, harvest the contents of each well by carefully pipetting, and then transfer the cells and supernatants to a 96-well plate (Thermo Scientific, 264623). Centrifuge the plate at 500 x g for 3 min to pellet the cells. Without disturbing the pellet, carefully transfer the supernatant to a new Eppendorf tube or

Canto plate. Gather and prepare all reagents to be used in the MSD kit (Meso Scale Discovery IL-2 V-Plex Kit, K151QQD-2). Serially dilute the IL-2 calibrator with Diluent 2 to generate a set of 7 points for a standard curve, in addition to a zero sample containing only Diluent 2. Transfer 50 µl of each standard to each well in one column of an MSD plate, ensuring the entire bottom of the well is coated. Transfer 50 µl of sample from each well to the MSD plate. Ensure the liquid completely coats the entire bottom of each well, including both electrodes. Cover the MSD plate with clear film, and incubate it on a plate shaker for 2 h at 700 rpm at room temperature (22-25°C). After 2 h, flick and blot the plate on a paper towel, and wash three times with 150 ul wash buffer, flicking to get rid of buffer between washes. After the final wash, blot the plate on a paper towel to remove any remaining buffer. Add 25 µl of IL-2 detection antibody solution to the bottom of each well. Cover the MSD plate with clear film, and incubate it on a plate shaker for 1-2 h at 700 rpm at room temperature. After 2 h, flick and blot the plate on a paper towel, and then wash three times with 150 ul wash buffer. Add 150 µl of 2X read buffer with surfactant to each well, and analyze the plate (or selected wells of the plate) on the MSD instrument.

[0393] An informal sequence listing is provided in Table 2, below. The informal sequence listing provides the following sixteen (16) sequence elements contained in each of 405 antibodies, identified as described above and designated as Antibody Numbers (Ab #) 1 through 405, in the following order:

- Heavy chain variable region (“HC”) nucleic acid sequence
- Heavy chain variable region ("HC") amino acid sequence
- Heavy chain variable region CDR H1 ("H1") amino acid sequence
- Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
- Heavy chain variable region CDR H2 ("H2") amino acid sequence
- Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
- Heavy chain variable region CDR H3 ("H3") amino acid sequence
- Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
- Light chain variable region("LC") nucleic acid sequence
- Light chain variable region ("LC") amino acid sequence
- Light chain variable region CDR L1 ("L1") amino acid sequence
- Light chain variable region CDR L1 ("L1") nucleic acid sequence

- Light chain variable region CDR L2 ("L2") amino acid sequence
- Light chain variable region CDR L2 ("L2") nucleic acid sequence
- Light chain variable region CDR L3 ("L3") amino acid sequence
- Light chain variable region CDR L3 ("L3") nucleic acid sequence

Table 2: Antibody sequences

Antibody No.	SEQ ID NO:	Sequence	Clone # (ADI)	Descriptors
Ab 1	1	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-16606 LAD2189_P03_F02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 1	2	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS	ADI-16606 LAD2189_P03_F02	Heavy chain variable region ("HC") amino acid sequence
Ab 1	3	FTFNTYAMN	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 1	4	TTCACCTTTAACACATATGCCATGAAT	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 1	5	RIRSKYNNYATYYADSVKD	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 1	6	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 1	7	VRHGNFGNSYVSWFAY	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 1	8	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTAT	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 1	9	CAGACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-16606 LAD2189_P03_F02	Light chain variable region("LC") nucleic acid sequence
Ab 1	10	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL	ADI-16606 LAD2189_P03_F02	Light chain variable region ("LC") amino acid sequence
Ab 1	11	RSSTGAVTTSNYAN	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 1	12	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 1	13	GTNKRAP	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 1	14	GGCACAAACAAGCGCGCTCCT	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 1	15	ALWYSNLWV	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 1	16	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 2	17	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-20587 SAD5519_P01_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 2	18	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-20587 SAD5519_P01_B02	Heavy chain variable region ("HC") amino acid sequence
Ab 2	19	FTFDTYAMN	ADI-20587 SAD5519_P01_B02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 2	20	TTCACCTTTGACACATATGCCATGAAT	ADI-20587 SAD5519_P01_B02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 2	21	RIRSKYNNYATYYADSVKD	ADI-20587 SAD5519_P01_B02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 2	22	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20587 SAD5519_P01_B02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 2	23	VRHGNFGNGYVSWFAH	ADI-20587 SAD5519_P01_B02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 2	24	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-20587 SAD5519_P01_B02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 2	25	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20587 SAD5519_P01_B02	Light chain variable region("LC") nucleic acid sequence
Ab 2	26	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDESDYYCALWYSNLWVFGGGTKLTVL	ADI-20587 SAD5519_P01_B02	Light chain variable region ("LC") amino acid sequence
Ab 2	27	RSSTGAVTTSNYAN	ADI-20587 SAD5519_P01_B02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 2	28	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20587 SAD5519_P01_B02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 2	29	GTDKRAP	ADI-20587 SAD5519_P01_B02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 2	30	GGCACAGACAAGCGCGCTCCC	ADI-20587 SAD5519_P01_B02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 2	31	ALWYSNLWV	ADI-20587 SAD5519_P01_B02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 2	32	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20587 SAD5519_P01_B02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 3	33	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-20588 SAD5520_P01_E08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 3	34	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-20588 SAD5520_P01_E08	Heavy chain variable region ("HC") amino acid sequence
Ab 3	35	FTFDTYAMN	ADI-20588 SAD5520_P01_E08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 3	36	TTCACCTTTGACACATATGCCATGAAT	ADI-20588 SAD5520_P01_E08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 3	37	RIRSKYNNYATYYADSVKD	ADI-20588 SAD5520_P01_E08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 3	38	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20588 SAD5520_P01_E08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 3	39	VRHGNFGNGYVSWFAH	ADI-20588 SAD5520_P01_E08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 3	40	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-20588 SAD5520_P01_E08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 3	41	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20588 SAD5520_P01_E08	Light chain variable region("LC") nucleic acid sequence
Ab 3	42	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-20588 SAD5520_P01_E08	Light chain variable region ("LC") amino acid sequence
Ab 3	43	RSSTGAVTTSNYAN	ADI-20588 SAD5520_P01_E08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 3	44	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20588 SAD5520_P01_E08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 3	45	GTNKRAP	ADI-20588 SAD5520_P01_E08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 3	46	GGCACAAACAAGCGCGCTCCT	ADI-20588 SAD5520_P01_E08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 3	47	ALWYSNLWV	ADI-20588 SAD5520_P01_E08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 3	48	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20588 SAD5520_P01_E08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 4	49	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGGCTCTCCTGTGCAGCCTCTGGATTCACCTTTAACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGGTCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACGGTTATGTATCCTGGTTTGCTTACTG	ADI-20589 SAD5519_P02_D03	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 4	50	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNGYVSWFAYWGQGTLVTVSS	ADI-20589 SAD5519_P02_D03	Heavy chain variable region ("HC") amino acid sequence
Ab 4	51	FTFNTYAMN	ADI-20589 SAD5519_P02_D03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 4	52	TTCACCTTTAACACATATGCCATGAAT	ADI-20589 SAD5519_P02_D03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 4	53	RIRSKYNNYATYYADSVKD	ADI-20589 SAD5519_P02_D03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 4	54	AGGATTAGGTCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20589 SAD5519_P02_D03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 4	55	VRHSNFGNGYVSWFAY	ADI-20589 SAD5519_P02_D03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 4	56	GTCAGGCACAGTAACTTCGGGAACGGTTATGTATCCTGGTTTGCTTAC	ADI-20589 SAD5519_P02_D03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 4	57	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20589 SAD5519_P02_D03	Light chain variable region("LC") nucleic acid sequence
Ab 4	58	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDESDYYCALWYSNLWVFGGGTKLTVL	ADI-20589 SAD5519_P02_D03	Light chain variable region ("LC") amino acid sequence
Ab 4	59	RSSTGAVTTSNYAN	ADI-20589 SAD5519_P02_D03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 4	60	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20589 SAD5519_P02_D03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 4	61	GTDKRAP	ADI-20589 SAD5519_P02_D03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 4	62	GGCACAGACAAGCGCGCTCCC	ADI-20589 SAD5519_P02_D03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 4	63	ALWYSNLWV	ADI-20589 SAD5519_P02_D03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 4	64	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20589 SAD5519_P02_D03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 5	65	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20590 SAD5519_P05_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 5	66	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-20590 SAD5519_P05_C08	Heavy chain variable region ("HC") amino acid sequence
Ab 5	67	FTFDTYAMN	ADI-20590 SAD5519_P05_C08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 5	68	TTCACCTTTGACACATATGCCATGAAT	ADI-20590 SAD5519_P05_C08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 5	69	RIRSKYNNYATYYADSVKG	ADI-20590 SAD5519_P05_C08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 5	70	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-20590 SAD5519_P05_C08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 5	71	VRHGNFGNSYVSWFAH	ADI-20590 SAD5519_P05_C08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 5	72	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-20590 SAD5519_P05_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 5	73	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20590 SAD5519_P05_C08	Light chain variable region("LC") nucleic acid sequence
Ab 5	74	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDESDYYCALWYSNLWVFGGGTKLTVL	ADI-20590 SAD5519_P05_C08	Light chain variable region ("LC") amino acid sequence
Ab 5	75	RSSTGAVTTSNYAN	ADI-20590 SAD5519_P05_C08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 5	76	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20590 SAD5519_P05_C08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 5	77	GTDKRAP	ADI-20590 SAD5519_P05_C08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 5	78	GGCACAGACAAGCGCGCTCCC	ADI-20590 SAD5519_P05_C08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 5	79	ALWYSNLWV	ADI-20590 SAD5519_P05_C08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 5	80	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20590 SAD5519_P05_C08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 6	81	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20594 SAD5523_P02_D07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 6	82	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-20594 SAD5523_P02_D07	Heavy chain variable region ("HC") amino acid sequence
Ab 6	83	FTFDTYAMN	ADI-20594 SAD5523_P02_D07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 6	84	TTCACCTTTGACACATATGCCATGAAT	ADI-20594 SAD5523_P02_D07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 6	85	RIRSKYNNYATYYADSVKD	ADI-20594 SAD5523_P02_D07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 6	86	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20594 SAD5523_P02_D07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 6	87	VRHGNFGNSYVSWFAH	ADI-20594 SAD5523_P02_D07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 6	88	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-20594 SAD5523_P02_D07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 6	89	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGATCCAGCAGACCCCAGGCCAGGCCCCGCGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCCTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20594 SAD5523_P02_D07	Light chain variable region("LC") nucleic acid sequence
Ab 6	90	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWIQQTPGQAPRGLIGGTNKRAPGVPDRLSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-20594 SAD5523_P02_D07	Light chain variable region ("LC") amino acid sequence
Ab 6	91	RSSTGAVTTSNYAN	ADI-20594 SAD5523_P02_D07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 6	92	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20594 SAD5523_P02_D07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 6	93	GTNKRAP	ADI-20594 SAD5523_P02_D07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 6	94	GGCACAAACAAGCGCGCTCCT	ADI-20594 SAD5523_P02_D07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 6	95	ALWYSNLWV	ADI-20594 SAD5523_P02_D07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 6	96	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20594 SAD5523_P02_D07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 7	97	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCGGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACGTACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTACCTGCAAATAAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20596 SAD5519_P03_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAGCCCTGGTCACCGTCTCCTCA		
Ab 7	98	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQINSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGALVTVSS	ADI-20596 SAD5519_P03_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 7	99	FTFDTYAMN	ADI-20596 SAD5519_P03_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 7	100	TTCACCTTTGACACATATGCCATGAAT	ADI-20596 SAD5519_P03_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 7	101	RIRSKYNNYATYYADSVKD	ADI-20596 SAD5519_P03_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 7	102	AGGATTAGATCCAAGTATAACAATTACGCTACGTACTACGCAGACTCCGTGAAGGAT	ADI-20596 SAD5519_P03_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 7	103	VRHGNFGNSYVSWFAH	ADI-20596 SAD5519_P03_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 7	104	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-20596 SAD5519_P03_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 7	105	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20596 SAD5519_P03_E05	Light chain variable region("LC") nucleic acid sequence
Ab 7	106	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDESDYYCALWYSNLWVFGGGTKLTVL	ADI-20596 SAD5519_P03_E05	Light chain variable region ("LC") amino acid sequence
Ab 7	107	RSSTGAVTTSNYAN	ADI-20596 SAD5519_P03_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 7	108	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20596 SAD5519_P03_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 7	109	GTDKRAP	ADI-20596 SAD5519_P03_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 7	110	GGCACAGACAAGCGCGCTCCC	ADI-20596 SAD5519_P03_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 7	111	ALWYSNLWV	ADI-20596 SAD5519_P03_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 7	112	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20596 SAD5519_P03_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 8	113	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20599 SAD5522_P03_C02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 8	114	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-20599 SAD5522_P03_C02	Heavy chain variable region ("HC") amino acid sequence
Ab 8	115	FTFDTYAMN	ADI-20599 SAD5522_P03_C02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 8	116	TTCACCTTTGACACATATGCCATGAAT	ADI-20599 SAD5522_P03_C02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 8	117	RIRSKYNNYATYYADSVKD	ADI-20599 SAD5522_P03_C02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 8	118	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20599 SAD5522_P03_C02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 8	119	VRHGNFGNSYVSWFAH	ADI-20599 SAD5522_P03_C02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 8	120	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-20599 SAD5522_P03_C02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 8	121	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCCGGGGTCCCTGAGCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20599 SAD5522_P03_C02	Light chain variable region("LC") nucleic acid sequence
Ab 8	122	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPERFSGSLLGDKAALTITGAQAEDESDYYCVLWYSNLWVFGGGTKLTVL	ADI-20599 SAD5522_P03_C02	Light chain variable region ("LC") amino acid sequence
Ab 8	123	RSSTGAVTTSNYAN	ADI-20599 SAD5522_P03_C02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 8	124	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20599 SAD5522_P03_C02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 8	125	GTDKRAP	ADI-20599 SAD5522_P03_C02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 8	126	GGCACAGACAAGCGCGCTCCC	ADI-20599 SAD5522_P03_C02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 8	127	VLWYSNLWV	ADI-20599 SAD5522_P03_C02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 8	128	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-20599 SAD5522_P03_C02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 9	129	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20605 SAD5522_P01_E11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 9	130	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-20605 SAD5522_P01_E11	Heavy chain variable region ("HC") amino acid sequence
Ab 9	131	FTFDTYAMN	ADI-20605 SAD5522_P01_E11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 9	132	TTCACCTTTGACACATATGCCATGAAT	ADI-20605 SAD5522_P01_E11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 9	133	RIRSKYNNYATYYADSVKD	ADI-20605 SAD5522_P01_E11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 9	134	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20605 SAD5522_P01_E11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 9	135	VRHGNFGNSYVSWFAH	ADI-20605 SAD5522_P01_E11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 9	136	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-20605 SAD5522_P01_E11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 9	137	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTCGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20605 SAD5522_P01_E11	Light chain variable region("LC") nucleic acid sequence
Ab 9	138	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDESDYYCALWYSNHWVFGGGTKLTVL	ADI-20605 SAD5522_P01_E11	Light chain variable region ("LC") amino acid sequence
Ab 9	139	RSSTGAVTTSNYAN	ADI-20605 SAD5522_P01_E11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 9	140	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20605 SAD5522_P01_E11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 9	141	GTDKRAP	ADI-20605 SAD5522_P01_E11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 9	142	GGCACAGACAAGCGCGCTCCC	ADI-20605 SAD5522_P01_E11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 9	143	ALWYSNHWV	ADI-20605 SAD5522_P01_E11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 9	144	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-20605 SAD5522_P01_E11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 10	145	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20607 SAD5520_P02_C11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 10	146	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-20607 SAD5520_P02_C11	Heavy chain variable region ("HC") amino acid sequence
Ab 10	147	FTFDTYAMN	ADI-20607 SAD5520_P02_C11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 10	148	TTCACCTTTGACACATATGCCATGAAT	ADI-20607 SAD5520_P02_C11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 10	149	RIRSKYNNYATYYADSVKD	ADI-20607 SAD5520_P02_C11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 10	150	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20607 SAD5520_P02_C11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 10	151	VRHSNFGNSYVSWFAH	ADI-20607 SAD5520_P02_C11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 10	152	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-20607 SAD5520_P02_C11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 10	153	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20607 SAD5520_P02_C11	Light chain variable region("LC") nucleic acid sequence
Ab 10	154	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-20607 SAD5520_P02_C11	Light chain variable region ("LC") amino acid sequence
Ab 10	155	RSSTGAVTTSNYAN	ADI-20607 SAD5520_P02_C11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 10	156	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20607 SAD5520_P02_C11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 10	157	GTNKRAP	ADI-20607 SAD5520_P02_C11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 10	158	GGCACAAACAAGCGCGCTCCT	ADI-20607 SAD5520_P02_C11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 10	159	ALWYSNLWV	ADI-20607 SAD5520_P02_C11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 10	160	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20607 SAD5520_P02_C11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 11	161	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTCTGCCACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTCACGTATCCTGGTTTGCTCATTGG	ADI-20608 SAD5520_P06_G02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 11	162	EVQLLESGGGLVQPGGSLRLSCAASGFTSATYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSHVSWFAHWGQGTLVTVSS	ADI-20608 SAD5520_P06_G02	Heavy chain variable region ("HC") amino acid sequence
Ab 11	163	FTSATYAMN	ADI-20608 SAD5520_P06_G02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 11	164	TTCACCTCTGCCACATATGCCATGAAT	ADI-20608 SAD5520_P06_G02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 11	165	RIRSKYNNYATYYADSVKD	ADI-20608 SAD5520_P06_G02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 11	166	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20608 SAD5520_P06_G02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 11	167	VRHGNFGNSHVSWFAH	ADI-20608 SAD5520_P06_G02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 11	168	GTCAGGCACGGTAACTTCGGGAACAGTCACGTATCCTGGTTTGCTCAT	ADI-20608 SAD5520_P06_G02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 11	169	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20608 SAD5520_P06_G02	Light chain variable region("LC") nucleic acid sequence
Ab 11	170	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-20608 SAD5520_P06_G02	Light chain variable region ("LC") amino acid sequence
Ab 11	171	RSSTGAVTTSNYAN	ADI-20608 SAD5520_P06_G02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 11	172	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20608 SAD5520_P06_G02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 11	173	GTNKRAP	ADI-20608 SAD5520_P06_G02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 11	174	GGCACAAACAAGCGCGCTCCT	ADI-20608 SAD5520_P06_G02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 11	175	ALWYSNLWV	ADI-20608 SAD5520_P06_G02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 11	176	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20608 SAD5520_P06_G02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 12	177	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTCTTGG	ADI-20609 SAD5521_P01_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 12	178	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFASWGQGTLVTVSS	ADI-20609 SAD5521_P01_E04	Heavy chain variable region ("HC") amino acid sequence
Ab 12	179	FTFNTYAMN	ADI-20609 SAD5521_P01_E04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 12	180	TTCACCTTTAACACATATGCCATGAAT	ADI-20609 SAD5521_P01_E04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 12	181	RIRSKYNNYATYYADSVKD	ADI-20609 SAD5521_P01_E04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 12	182	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-20609 SAD5521_P01_E04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 12	183	VRHGNFGNSYVSWFAS	ADI-20609 SAD5521_P01_E04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 12	184	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTCT	ADI-20609 SAD5521_P01_E04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 12	185	CAGACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGCTCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-20609 SAD5521_P01_E04	Light chain variable region("LC") nucleic acid sequence
Ab 12	186	QTVVTQEPSFSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL	ADI-20609 SAD5521_P01_E04	Light chain variable region ("LC") amino acid sequence
Ab 12	187	GSSTGAVTTSNYAN	ADI-20609 SAD5521_P01_E04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 12	188	GGCTCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-20609 SAD5521_P01_E04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 12	189	GTDKRAP	ADI-20609 SAD5521_P01_E04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 12	190	GGCACAGACAAGCGCGCTCCT	ADI-20609 SAD5521_P01_E04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 12	191	ALWYSNLWV	ADI-20609 SAD5521_P01_E04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 12	192	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-20609 SAD5521_P01_E04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 13	193	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21943 LAD4204_P01_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 13	194	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21943 LAD4204_P01_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 13	195	FTFDTYAMN	ADI-21943 LAD4204_P01_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 13	196	TTCACCTTTGACACATATGCCATGAAT	ADI-21943 LAD4204_P01_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 13	197	RIRSKYNNYATYYADSVKD	ADI-21943 LAD4204_P01_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 13	198	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21943 LAD4204_P01_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 13	199	VRHGNFGNGYVSWFAH	ADI-21943 LAD4204_P01_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 13	200	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21943 LAD4204_P01_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 13	201	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21943 LAD4204_P01_E02	Light chain variable region("LC") nucleic acid sequence
Ab 13	202	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-21943 LAD4204_P01_E02	Light chain variable region ("LC") amino acid sequence
Ab 13	203	GSSTGAVTTSNYAN	ADI-21943 LAD4204_P01_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 13	204	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21943 LAD4204_P01_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 13	205	GTDKRAP	ADI-21943 LAD4204_P01_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 13	206	GGCACAGACAAGCGCGCTCCT	ADI-21943 LAD4204_P01_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 13	207	ALWYSNHWV	ADI-21943 LAD4204_P01_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 13	208	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-21943 LAD4204_P01_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 14	209	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21944 LAD4204_P01_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 14	210	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21944 LAD4204_P01_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 14	211	FTFDTYAMN	ADI-21944 LAD4204_P01_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 14	212	TTCACCTTTGACACATATGCCATGAAT	ADI-21944 LAD4204_P01_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 14	213	RIRSKYNNYATYYADSVKD	ADI-21944 LAD4204_P01_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 14	214	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21944 LAD4204_P01_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 14	215	VRHGNFGNGYVSWFAH	ADI-21944 LAD4204_P01_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 14	216	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21944 LAD4204_P01_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 14	217	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21944 LAD4204_P01_E05	Light chain variable region("LC") nucleic acid sequence
Ab 14	218	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-21944 LAD4204_P01_E05	Light chain variable region ("LC") amino acid sequence
Ab 14	219	GSSTGAVTTSNYAN	ADI-21944 LAD4204_P01_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 14	220	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21944 LAD4204_P01_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 14	221	GTDKRAP	ADI-21944 LAD4204_P01_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 14	222	GGCACAGACAAGCGCGCTCCT	ADI-21944 LAD4204_P01_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 14	223	ALWYSNHWV	ADI-21944 LAD4204_P01_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 14	224	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-21944 LAD4204_P01_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 15	225	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21945 LAD4204_P01_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 15	226	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21945 LAD4204_P01_D06	Heavy chain variable region ("HC") amino acid sequence
Ab 15	227	FTFDTYAMN	ADI-21945 LAD4204_P01_D06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 15	228	TTCACCTTTGACACATATGCCATGAAT	ADI-21945 LAD4204_P01_D06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 15	229	RIRSKYNNYATYYADSVKD	ADI-21945 LAD4204_P01_D06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 15	230	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21945 LAD4204_P01_D06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 15	231	VRHGNFGNGYVSWFAH	ADI-21945 LAD4204_P01_D06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 15	232	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21945 LAD4204_P01_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 15	233	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21945 LAD4204_P01_D06	Light chain variable region("LC") nucleic acid sequence
Ab 15	234	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-21945 LAD4204_P01_D06	Light chain variable region ("LC") amino acid sequence
Ab 15	235	GSSAGAVTTSNYAN	ADI-21945 LAD4204_P01_D06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 15	236	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21945 LAD4204_P01_D06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 15	237	GTDKRAP	ADI-21945 LAD4204_P01_D06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 15	238	GGCACAGACAAGCGCGCTCCT	ADI-21945 LAD4204_P01_D06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 15	239	VLWYSNLWV	ADI-21945 LAD4204_P01_D06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 15	240	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-21945 LAD4204_P01_D06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 16	241	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21946 LAD4204_P01_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 16	242	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21946 LAD4204_P01_F06	Heavy chain variable region ("HC") amino acid sequence
Ab 16	243	FTFDTYAMN	ADI-21946 LAD4204_P01_F06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 16	244	TTCACCTTTGACACATATGCCATGAAT	ADI-21946 LAD4204_P01_F06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 16	245	RIRSKYNNYATYYADSVKD	ADI-21946 LAD4204_P01_F06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 16	246	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21946 LAD4204_P01_F06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 16	247	VRHGNFGNGYVSWFAH	ADI-21946 LAD4204_P01_F06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 16	248	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21946 LAD4204_P01_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 16	249	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21946 LAD4204_P01_F06	Light chain variable region("LC") nucleic acid sequence
Ab 16	250	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-21946 LAD4204_P01_F06	Light chain variable region ("LC") amino acid sequence
Ab 16	251	GSSAGAVTTSNYAN	ADI-21946 LAD4204_P01_F06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 16	252	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21946 LAD4204_P01_F06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 16	253	GTDKRAP	ADI-21946 LAD4204_P01_F06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 16	254	GGCACAGACAAGCGCGCTCCT	ADI-21946 LAD4204_P01_F06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 16	255	ALWYSNHWV	ADI-21946 LAD4204_P01_F06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 16	256	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-21946 LAD4204_P01_F06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 17	257	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21947 LAD4204_P01_H07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 17	258	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21947 LAD4204_P01_H07	Heavy chain variable region ("HC") amino acid sequence
Ab 17	259	FTFDTYAMN	ADI-21947 LAD4204_P01_H07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 17	260	TTCACCTTTGACACATATGCCATGAAT	ADI-21947 LAD4204_P01_H07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 17	261	RIRSKYNNYATYYADSVKD	ADI-21947 LAD4204_P01_H07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 17	262	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21947 LAD4204_P01_H07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 17	263	VRHGNFGNGYVSWFAH	ADI-21947 LAD4204_P01_H07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 17	264	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21947 LAD4204_P01_H07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 17	265	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21947 LAD4204_P01_H07	Light chain variable region("LC") nucleic acid sequence
Ab 17	266	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNHWVFGGGTKLTVL	ADI-21947 LAD4204_P01_H07	Light chain variable region ("LC") amino acid sequence
Ab 17	267	GSSTGAVTTSNYAN	ADI-21947 LAD4204_P01_H07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 17	268	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21947 LAD4204_P01_H07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 17	269	GTDKRAP	ADI-21947 LAD4204_P01_H07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 17	270	GGCACAGACAAGCGCGCTCCT	ADI-21947 LAD4204_P01_H07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 17	271	ALWYNNHWV	ADI-21947 LAD4204_P01_H07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 17	272	GCGCTGTGGTACAATAACCATTGGGTG	ADI-21947 LAD4204_P01_H07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 18	273	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21948 LAD4206_P01_D10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 18	274	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-21948 LAD4206_P01_D10	Heavy chain variable region ("HC") amino acid sequence
Ab 18	275	FTFDTYAMN	ADI-21948 LAD4206_P01_D10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 18	276	TTCACCTTTGACACATATGCCATGAAT	ADI-21948 LAD4206_P01_D10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 18	277	RIRSKYNNYATYYADSVKD	ADI-21948 LAD4206_P01_D10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 18	278	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21948 LAD4206_P01_D10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 18	279	VRHSNFGNSYVSWFAH	ADI-21948 LAD4206_P01_D10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 18	280	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-21948 LAD4206_P01_D10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 18	281	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21948 LAD4206_P01_D10	Light chain variable region("LC") nucleic acid sequence
Ab 18	282	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-21948 LAD4206_P01_D10	Light chain variable region ("LC") amino acid sequence
Ab 18	283	GSSAGAVTTSNYAN	ADI-21948 LAD4206_P01_D10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 18	284	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21948 LAD4206_P01_D10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 18	285	GTDKRAP	ADI-21948 LAD4206_P01_D10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 18	286	GGCACAGACAAGCGCGCTCCT	ADI-21948 LAD4206_P01_D10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 18	287	VLWYSNLWV	ADI-21948 LAD4206_P01_D10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 18	288	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-21948 LAD4206_P01_D10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 19	289	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21949 LAD4206_P01_F10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 19	290	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-21949 LAD4206_P01_F10	Heavy chain variable region ("HC") amino acid sequence
Ab 19	291	FTFDTYAMN	ADI-21949 LAD4206_P01_F10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 19	292	TTCACCTTTGACACATATGCCATGAAT	ADI-21949 LAD4206_P01_F10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 19	293	RIRSKYNNYATYYADSVKD	ADI-21949 LAD4206_P01_F10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 19	294	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21949 LAD4206_P01_F10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 19	295	VRHSNFGNSYVSWFAH	ADI-21949 LAD4206_P01_F10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 19	296	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-21949 LAD4206_P01_F10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 19	297	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21949 LAD4206_P01_F10	Light chain variable region("LC") nucleic acid sequence
Ab 19	298	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-21949 LAD4206_P01_F10	Light chain variable region ("LC") amino acid sequence
Ab 19	299	GSSAGAVTTSNYAN	ADI-21949 LAD4206_P01_F10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 19	300	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21949 LAD4206_P01_F10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 19	301	GTDKRAP	ADI-21949 LAD4206_P01_F10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 19	302	GGCACAGACAAGCGCGCTCCT	ADI-21949 LAD4206_P01_F10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 19	303	ALWYSNHWV	ADI-21949 LAD4206_P01_F10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 19	304	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-21949 LAD4206_P01_F10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 20	305	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21950 LAD4206_P01_D11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 20	306	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-21950 LAD4206_P01_D11	Heavy chain variable region ("HC") amino acid sequence
Ab 20	307	FTFDTYAMN	ADI-21950 LAD4206_P01_D11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 20	308	TTCACCTTTGACACATATGCCATGAAT	ADI-21950 LAD4206_P01_D11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 20	309	RIRSKYNNYATYYADSVKD	ADI-21950 LAD4206_P01_D11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 20	310	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21950 LAD4206_P01_D11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 20	311	VRHSNFGNSYVSWFAH	ADI-21950 LAD4206_P01_D11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 20	312	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-21950 LAD4206_P01_D11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 20	313	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21950 LAD4206_P01_D11	Light chain variable region("LC") nucleic acid sequence
Ab 20	314	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNHWVFGGGTKLTVL	ADI-21950 LAD4206_P01_D11	Light chain variable region ("LC") amino acid sequence
Ab 20	315	GSSTGAVTTSNYAN	ADI-21950 LAD4206_P01_D11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 20	316	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21950 LAD4206_P01_D11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 20	317	GTDKRAP	ADI-21950 LAD4206_P01_D11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 20	318	GGCACAGACAAGCGCGCTCCT	ADI-21950 LAD4206_P01_D11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 20	319	ALWYNNHWV	ADI-21950 LAD4206_P01_D11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 20	320	GCGCTGTGGTACAATAACCATTGGGTG	ADI-21950 LAD4206_P01_D11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 21	321	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21951 LAD4204_P02_F04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 21	322	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21951 LAD4204_P02_F04	Heavy chain variable region ("HC") amino acid sequence
Ab 21	323	FTFDTYAMN	ADI-21951 LAD4204_P02_F04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 21	324	TTCACCTTTGACACATATGCCATGAAT	ADI-21951 LAD4204_P02_F04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 21	325	RIRSKYNNYATYYADSVKD	ADI-21951 LAD4204_P02_F04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 21	326	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21951 LAD4204_P02_F04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 21	327	VRHGNFGNGYVSWFAH	ADI-21951 LAD4204_P02_F04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 21	328	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21951 LAD4204_P02_F04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 21	329	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21951 LAD4204_P02_F04	Light chain variable region("LC") nucleic acid sequence
Ab 21	330	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-21951 LAD4204_P02_F04	Light chain variable region ("LC") amino acid sequence
Ab 21	331	GSSTGAVTTSNYAN	ADI-21951 LAD4204_P02_F04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 21	332	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21951 LAD4204_P02_F04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 21	333	GTDKRAP	ADI-21951 LAD4204_P02_F04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 21	334	GGCACAGACAAGCGCGCTCCT	ADI-21951 LAD4204_P02_F04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 21	335	VLWYSNLWV	ADI-21951 LAD4204_P02_F04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 21	336	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-21951 LAD4204_P02_F04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 22	337	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21952 LAD4204_P02_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 22	338	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21952 LAD4204_P02_B05	Heavy chain variable region ("HC") amino acid sequence
Ab 22	339	FTFDTYAMN	ADI-21952 LAD4204_P02_B05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 22	340	TTCACCTTTGACACATATGCCATGAAT	ADI-21952 LAD4204_P02_B05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 22	341	RIRSKYNNYATYYADSVKD	ADI-21952 LAD4204_P02_B05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 22	342	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21952 LAD4204_P02_B05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 22	343	VRHGNFGNGYVSWFAH	ADI-21952 LAD4204_P02_B05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 22	344	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21952 LAD4204_P02_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 22	345	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21952 LAD4204_P02_B05	Light chain variable region("LC") nucleic acid sequence
Ab 22	346	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-21952 LAD4204_P02_B05	Light chain variable region ("LC") amino acid sequence
Ab 22	347	GSSTGAVTTSNYAN	ADI-21952 LAD4204_P02_B05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 22	348	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21952 LAD4204_P02_B05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 22	349	GTDKRAP	ADI-21952 LAD4204_P02_B05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 22	350	GGCACAGACAAGCGCGCTCCT	ADI-21952 LAD4204_P02_B05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 22	351	ALWYSNHWV	ADI-21952 LAD4204_P02_B05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 22	352	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-21952 LAD4204_P02_B05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 23	353	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21953 LAD4204_P02_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 23	354	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21953 LAD4204_P02_F01	Heavy chain variable region ("HC") amino acid sequence
Ab 23	355	FTFDTYAMN	ADI-21953 LAD4204_P02_F01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 23	356	TTCACCTTTGACACATATGCCATGAAT	ADI-21953 LAD4204_P02_F01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 23	357	RIRSKYNNYATYYADSVKD	ADI-21953 LAD4204_P02_F01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 23	358	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21953 LAD4204_P02_F01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 23	359	VRHGNFGNGYVSWFAH	ADI-21953 LAD4204_P02_F01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 23	360	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21953 LAD4204_P02_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 23	361	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21953 LAD4204_P02_F01	Light chain variable region("LC") nucleic acid sequence
Ab 23	362	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-21953 LAD4204_P02_F01	Light chain variable region ("LC") amino acid sequence
Ab 23	363	GSSAGAVTTSNYAN	ADI-21953 LAD4204_P02_F01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 23	364	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21953 LAD4204_P02_F01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 23	365	GTDKRAP	ADI-21953 LAD4204_P02_F01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 23	366	GGCACAGACAAGCGCGCTCCT	ADI-21953 LAD4204_P02_F01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 23	367	ALWYSNLWV	ADI-21953 LAD4204_P02_F01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 23	368	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-21953 LAD4204_P02_F01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 24	369	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21954 LAD4204_P02_D03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 24	370	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-21954 LAD4204_P02_D03	Heavy chain variable region ("HC") amino acid sequence
Ab 24	371	FTFDTYAMN	ADI-21954 LAD4204_P02_D03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 24	372	TTCACCTTTGACACATATGCCATGAAT	ADI-21954 LAD4204_P02_D03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 24	373	RIRSKYNNYATYYADSVKD	ADI-21954 LAD4204_P02_D03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 24	374	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21954 LAD4204_P02_D03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 24	375	VRHGNFGNGYVSWFAH	ADI-21954 LAD4204_P02_D03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 24	376	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-21954 LAD4204_P02_D03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 24	377	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21954 LAD4204_P02_D03	Light chain variable region("LC") nucleic acid sequence
Ab 24	378	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-21954 LAD4204_P02_D03	Light chain variable region ("LC") amino acid sequence
Ab 24	379	GSSAGAVTTSNYAN	ADI-21954 LAD4204_P02_D03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 24	380	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21954 LAD4204_P02_D03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 24	381	GTDKRAP	ADI-21954 LAD4204_P02_D03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 24	382	GGCACAGACAAGCGCGCTCCT	ADI-21954 LAD4204_P02_D03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 24	383	ALWYNNLWV	ADI-21954 LAD4204_P02_D03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 24	384	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-21954 LAD4204_P02_D03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 25	385	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21955 LAD4206_P02_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 25	386	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-21955 LAD4206_P02_G01	Heavy chain variable region ("HC") amino acid sequence
Ab 25	387	FTFDTYAMN	ADI-21955 LAD4206_P02_G01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 25	388	TTCACCTTTGACACATATGCCATGAAT	ADI-21955 LAD4206_P02_G01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 25	389	RIRSKYNNYATYYADSVKD	ADI-21955 LAD4206_P02_G01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 25	390	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21955 LAD4206_P02_G01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 25	391	VRHSNFGNSYVSWFAH	ADI-21955 LAD4206_P02_G01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 25	392	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-21955 LAD4206_P02_G01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 25	393	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21955 LAD4206_P02_G01	Light chain variable region("LC") nucleic acid sequence
Ab 25	394	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-21955 LAD4206_P02_G01	Light chain variable region ("LC") amino acid sequence
Ab 25	395	GSSAGAVTTSNYAN	ADI-21955 LAD4206_P02_G01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 25	396	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21955 LAD4206_P02_G01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 25	397	GTDKRAP	ADI-21955 LAD4206_P02_G01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 25	398	GGCACAGACAAGCGCGCTCCT	ADI-21955 LAD4206_P02_G01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 25	399	ALWYSNLWV	ADI-21955 LAD4206_P02_G01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 25	400	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-21955 LAD4206_P02_G01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 26	401	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21956 LAD4206_P02_D03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 26	402	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-21956 LAD4206_P02_D03	Heavy chain variable region ("HC") amino acid sequence
Ab 26	403	FTFDTYAMN	ADI-21956 LAD4206_P02_D03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 26	404	TTCACCTTTGACACATATGCCATGAAT	ADI-21956 LAD4206_P02_D03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 26	405	RIRSKYNNYATYYADSVKD	ADI-21956 LAD4206_P02_D03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 26	406	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-21956 LAD4206_P02_D03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 26	407	VRHSNFGNSYVSWFAH	ADI-21956 LAD4206_P02_D03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 26	408	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-21956 LAD4206_P02_D03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 26	409	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-21956 LAD4206_P02_D03	Light chain variable region("LC") nucleic acid sequence
Ab 26	410	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-21956 LAD4206_P02_D03	Light chain variable region ("LC") amino acid sequence
Ab 26	411	GSSAGAVTTSNYAN	ADI-21956 LAD4206_P02_D03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 26	412	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-21956 LAD4206_P02_D03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 26	413	GTDKRAP	ADI-21956 LAD4206_P02_D03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 26	414	GGCACAGACAAGCGCGCTCCT	ADI-21956 LAD4206_P02_D03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 26	415	ALWYNNLWV	ADI-21956 LAD4206_P02_D03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 26	416	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-21956 LAD4206_P02_D03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 27	417	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23629 LAD4692_P01_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 27	418	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-23629 LAD4692_P01_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 27	419	FTFDAYAMN	ADI-23629 LAD4692_P01_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 27	420	TTCACCTTTGACGCTTATGCCATGAAT	ADI-23629 LAD4692_P01_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 27	421	RIRSKYNDYATYYADSVKD	ADI-23629 LAD4692_P01_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 27	422	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23629 LAD4692_P01_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 27	423	VRHGNFGNGYVSWFAH	ADI-23629 LAD4692_P01_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 27	424	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-23629 LAD4692_P01_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 27	425	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23629 LAD4692_P01_A06	Light chain variable region("LC") nucleic acid sequence
Ab 27	426	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-23629 LAD4692_P01_A06	Light chain variable region ("LC") amino acid sequence
Ab 27	427	GSSTGAVTTSNYAN	ADI-23629 LAD4692_P01_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 27	428	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23629 LAD4692_P01_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 27	429	GTDKRAP	ADI-23629 LAD4692_P01_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 27	430	GGCACAGACAAGCGCGCTCCT	ADI-23629 LAD4692_P01_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 27	431	ALWYSDLWV	ADI-23629 LAD4692_P01_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 27	432	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-23629 LAD4692_P01_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 28	433	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23632 LAD4695_P01_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 28	434	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-23632 LAD4695_P01_E09	Heavy chain variable region ("HC") amino acid sequence
Ab 28	435	FTFDTYAMN	ADI-23632 LAD4695_P01_E09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 28	436	TTCACCTTTGACACATATGCCATGAAT	ADI-23632 LAD4695_P01_E09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 28	437	RIRSKYNNYATYYADSVKD	ADI-23632 LAD4695_P01_E09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 28	438	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23632 LAD4695_P01_E09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 28	439	VRHGNFGNGYVSWFAH	ADI-23632 LAD4695_P01_E09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 28	440	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-23632 LAD4695_P01_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 28	441	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23632 LAD4695_P01_E09	Light chain variable region("LC") nucleic acid sequence
Ab 28	442	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-23632 LAD4695_P01_E09	Light chain variable region ("LC") amino acid sequence
Ab 28	443	GSSTGAVTTSNYAN	ADI-23632 LAD4695_P01_E09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 28	444	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23632 LAD4695_P01_E09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 28	445	GTDKRAP	ADI-23632 LAD4695_P01_E09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 28	446	GGCACAGACAAGCGCGCTCCT	ADI-23632 LAD4695_P01_E09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 28	447	ALWYSDLWV	ADI-23632 LAD4695_P01_E09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 28	448	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-23632 LAD4695_P01_E09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 29	449	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23633 LAD4773_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 29	450	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-23633 LAD4773_P02_A05	Heavy chain variable region ("HC") amino acid sequence
Ab 29	451	FTFDTYAMN	ADI-23633 LAD4773_P02_A05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 29	452	TTCACCTTTGACACATATGCCATGAAT	ADI-23633 LAD4773_P02_A05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 29	453	RIRSKYNNYATYYADSVKD	ADI-23633 LAD4773_P02_A05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 29	454	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23633 LAD4773_P02_A05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 29	455	VRHGNFGNGYVSWFAH	ADI-23633 LAD4773_P02_A05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 29	456	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-23633 LAD4773_P02_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 29	457	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23633 LAD4773_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 29	458	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-23633 LAD4773_P02_A05	Light chain variable region ("LC") amino acid sequence
Ab 29	459	GSSTGAVTTSNYAN	ADI-23633 LAD4773_P02_A05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 29	460	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23633 LAD4773_P02_A05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 29	461	GTDKRAP	ADI-23633 LAD4773_P02_A05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 29	462	GGCACAGACAAGCGCGCTCCT	ADI-23633 LAD4773_P02_A05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 29	463	ALWYSNHWV	ADI-23633 LAD4773_P02_A05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 29	464	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-23633 LAD4773_P02_A05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 30	465	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23634 LAD4774_P02_C06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 30	466	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-23634 LAD4774_P02_C06	Heavy chain variable region ("HC") amino acid sequence
Ab 30	467	FTFDTYAMN	ADI-23634 LAD4774_P02_C06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 30	468	TTCACCTTTGACACATATGCCATGAAT	ADI-23634 LAD4774_P02_C06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 30	469	RIRSKYNNYATYYADSVKD	ADI-23634 LAD4774_P02_C06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 30	470	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23634 LAD4774_P02_C06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 30	471	VRHGNFGEGYVSWFAH	ADI-23634 LAD4774_P02_C06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 30	472	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-23634 LAD4774_P02_C06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 30	473	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23634 LAD4774_P02_C06	Light chain variable region("LC") nucleic acid sequence
Ab 30	474	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-23634 LAD4774_P02_C06	Light chain variable region ("LC") amino acid sequence
Ab 30	475	GSSTGAVTTSNYAN	ADI-23634 LAD4774_P02_C06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 30	476	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23634 LAD4774_P02_C06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 30	477	GTDKRAP	ADI-23634 LAD4774_P02_C06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 30	478	GGCACAGACAAGCGCGCTCCT	ADI-23634 LAD4774_P02_C06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 30	479	ALWYSNHWV	ADI-23634 LAD4774_P02_C06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 30	480	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-23634 LAD4774_P02_C06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 31	481	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23635 LAD4775_P02_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 31	482	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-23635 LAD4775_P02_F07	Heavy chain variable region ("HC") amino acid sequence
Ab 31	483	FTFDTYAMN	ADI-23635 LAD4775_P02_F07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 31	484	TTCACCTTTGACACATATGCCATGAAT	ADI-23635 LAD4775_P02_F07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 31	485	RIRSKYNNYATYYADSVKD	ADI-23635 LAD4775_P02_F07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 31	486	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23635 LAD4775_P02_F07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 31	487	VRHGNFGEGYVSWFAH	ADI-23635 LAD4775_P02_F07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 31	488	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-23635 LAD4775_P02_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 31	489	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23635 LAD4775_P02_F07	Light chain variable region("LC") nucleic acid sequence
Ab 31	490	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-23635 LAD4775_P02_F07	Light chain variable region ("LC") amino acid sequence
Ab 31	491	GSSTGAVTTSNYAN	ADI-23635 LAD4775_P02_F07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 31	492	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23635 LAD4775_P02_F07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 31	493	GTDKRAP	ADI-23635 LAD4775_P02_F07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 31	494	GGCACAGACAAGCGCGCTCCT	ADI-23635 LAD4775_P02_F07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 31	495	ALWYSNHWV	ADI-23635 LAD4775_P02_F07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 31	496	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-23635 LAD4775_P02_F07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 32	497	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACGCTCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23636 LAD4776_P01_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 32	498	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNALRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-23636 LAD4776_P01_C01	Heavy chain variable region ("HC") amino acid sequence
Ab 32	499	FTFDTYAMN	ADI-23636 LAD4776_P01_C01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 32	500	TTCACCTTTGACACATATGCCATGAAT	ADI-23636 LAD4776_P01_C01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 32	501	RIRSKYNNYATYYADSVKD	ADI-23636 LAD4776_P01_C01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 32	502	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23636 LAD4776_P01_C01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 32	503	VRHGNFGNGYVSWFAH	ADI-23636 LAD4776_P01_C01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 32	504	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-23636 LAD4776_P01_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 32	505	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23636 LAD4776_P01_C01	Light chain variable region("LC") nucleic acid sequence
Ab 32	506	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-23636 LAD4776_P01_C01	Light chain variable region ("LC") amino acid sequence
Ab 32	507	GSSTGAVTTSNYAN	ADI-23636 LAD4776_P01_C01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 32	508	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23636 LAD4776_P01_C01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 32	509	GTDKRAP	ADI-23636 LAD4776_P01_C01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 32	510	GGCACAGACAAGCGCGCTCCT	ADI-23636 LAD4776_P01_C01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 32	511	ALWYSNHWV	ADI-23636 LAD4776_P01_C01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 32	512	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-23636 LAD4776_P01_C01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 33	513	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGCTTACGTATCCTGGTTTGCTCATTGG	ADI-23637 LAD4777_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 33	514	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNAYVSWFAHWGQGTLVTVSS	ADI-23637 LAD4777_P01_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 33	515	FTFDTYAMN	ADI-23637 LAD4777_P01_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 33	516	TTCACCTTTGACACATATGCCATGAAT	ADI-23637 LAD4777_P01_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 33	517	RIRSKYNNYATYYADSVKD	ADI-23637 LAD4777_P01_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 33	518	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23637 LAD4777_P01_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 33	519	VRHGNFGNAYVSWFAH	ADI-23637 LAD4777_P01_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 33	520	GTCAGGCACGGTAACTTCGGGAACGCTTACGTATCCTGGTTTGCTCAT	ADI-23637 LAD4777_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 33	521	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23637 LAD4777_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 33	522	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-23637 LAD4777_P01_A02	Light chain variable region ("LC") amino acid sequence
Ab 33	523	GSSTGAVTTSNYAN	ADI-23637 LAD4777_P01_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 33	524	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23637 LAD4777_P01_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 33	525	GTDKRAP	ADI-23637 LAD4777_P01_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 33	526	GGCACAGACAAGCGCGCTCCT	ADI-23637 LAD4777_P01_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 33	527	ALWYSNHWV	ADI-23637 LAD4777_P01_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 33	528	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-23637 LAD4777_P01_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 34	529	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACGCTCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGCTTACGTATCCTGGTTTGCTCATTGG	ADI-23638 LAD4778_P01_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 34	530	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNALRAEDTAVYYCVRHGNFGNAYVSWFAHWGQGTLVTVSS	ADI-23638 LAD4778_P01_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 34	531	FTFDTYAMN	ADI-23638 LAD4778_P01_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 34	532	TTCACCTTTGACACATATGCCATGAAT	ADI-23638 LAD4778_P01_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 34	533	RIRSKYNNYATYYADSVKD	ADI-23638 LAD4778_P01_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 34	534	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-23638 LAD4778_P01_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 34	535	VRHGNFGNAYVSWFAH	ADI-23638 LAD4778_P01_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 34	536	GTCAGGCACGGTAACTTCGGGAACGCTTACGTATCCTGGTTTGCTCAT	ADI-23638 LAD4778_P01_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 34	537	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-23638 LAD4778_P01_A03	Light chain variable region("LC") nucleic acid sequence
Ab 34	538	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-23638 LAD4778_P01_A03	Light chain variable region ("LC") amino acid sequence
Ab 34	539	GSSTGAVTTSNYAN	ADI-23638 LAD4778_P01_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 34	540	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-23638 LAD4778_P01_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 34	541	GTDKRAP	ADI-23638 LAD4778_P01_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 34	542	GGCACAGACAAGCGCGCTCCT	ADI-23638 LAD4778_P01_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 34	543	ALWYSNHWV	ADI-23638 LAD4778_P01_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 34	544	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-23638 LAD4778_P01_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 35	545	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24388 BAD24629_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 35	546	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24388 BAD24629_C01	Heavy chain variable region ("HC") amino acid sequence
Ab 35	547	FTFDTYAMN	ADI-24388 BAD24629_C01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 35	548	TTCACCTTTGACACATATGCCATGAAT	ADI-24388 BAD24629_C01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 35	549	RIRSKYNNYATYYADSVKD	ADI-24388 BAD24629_C01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 35	550	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24388 BAD24629_C01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 35	551	VRHGNFGNGYVSWFAH	ADI-24388 BAD24629_C01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 35	552	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24388 BAD24629_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 35	553	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24388 BAD24629_C01	Light chain variable region("LC") nucleic acid sequence
Ab 35	554	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24388 BAD24629_C01	Light chain variable region ("LC") amino acid sequence
Ab 35	555	GSSTGAVTTSNYAN	ADI-24388 BAD24629_C01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 35	556	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24388 BAD24629_C01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 35	557	GTDKRAP	ADI-24388 BAD24629_C01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 35	558	GGCACAGACAAGCGCGCTCCT	ADI-24388 BAD24629_C01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 35	559	ALWYSNHWV	ADI-24388 BAD24629_C01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 35	560	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24388 BAD24629_C01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 36	561	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24389 BAD24629_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 36	562	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24389 BAD24629_G01	Heavy chain variable region ("HC") amino acid sequence
Ab 36	563	FTFDTYAMN	ADI-24389 BAD24629_G01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 36	564	TTCACCTTTGACACATATGCCATGAAT	ADI-24389 BAD24629_G01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 36	565	RIRSKYNNYATYYADSVKD	ADI-24389 BAD24629_G01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 36	566	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24389 BAD24629_G01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 36	567	VRHGNFGNGYVSWFAH	ADI-24389 BAD24629_G01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 36	568	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24389 BAD24629_G01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 36	569	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24389 BAD24629_G01	Light chain variable region("LC") nucleic acid sequence
Ab 36	570	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24389 BAD24629_G01	Light chain variable region ("LC") amino acid sequence
Ab 36	571	GSSTGAVTTSNYAN	ADI-24389 BAD24629_G01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 36	572	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24389 BAD24629_G01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 36	573	GTDKRAP	ADI-24389 BAD24629_G01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 36	574	GGCACAGACAAGCGCGCTCCT	ADI-24389 BAD24629_G01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 36	575	ALWYSNHWV	ADI-24389 BAD24629_G01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 36	576	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24389 BAD24629_G01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 37	577	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24390 BAD24629_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 37	578	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24390 BAD24629_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 37	579	FTFDTYAMN	ADI-24390 BAD24629_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 37	580	TTCACCTTTGACACATATGCCATGAAT	ADI-24390 BAD24629_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 37	581	RIRSKYNNYATYYADSVKD	ADI-24390 BAD24629_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 37	582	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24390 BAD24629_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 37	583	VRHGNFGNGYVSWFAH	ADI-24390 BAD24629_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 37	584	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24390 BAD24629_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 37	585	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24390 BAD24629_A02	Light chain variable region("LC") nucleic acid sequence
Ab 37	586	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24390 BAD24629_A02	Light chain variable region ("LC") amino acid sequence
Ab 37	587	GSSTGAVTTSNYAN	ADI-24390 BAD24629_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 37	588	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24390 BAD24629_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 37	589	GTDKRAP	ADI-24390 BAD24629_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 37	590	GGCACAGACAAGCGCGCTCCT	ADI-24390 BAD24629_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 37	591	ALWYSNHWV	ADI-24390 BAD24629_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 37	592	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24390 BAD24629_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 38	593	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24391 BAD24629_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 38	594	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24391 BAD24629_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 38	595	FTFDTYAMN	ADI-24391 BAD24629_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 38	596	TTCACCTTTGACACATATGCCATGAAT	ADI-24391 BAD24629_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 38	597	RIRSKYNNYATYYADSVKD	ADI-24391 BAD24629_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 38	598	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24391 BAD24629_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 38	599	VRHGNFGNGYVSWFAH	ADI-24391 BAD24629_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 38	600	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24391 BAD24629_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 38	601	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24391 BAD24629_A03	Light chain variable region("LC") nucleic acid sequence
Ab 38	602	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24391 BAD24629_A03	Light chain variable region ("LC") amino acid sequence
Ab 38	603	GSSTGAVTTSNYAN	ADI-24391 BAD24629_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 38	604	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24391 BAD24629_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 38	605	GTDKRAP	ADI-24391 BAD24629_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 38	606	GGCACAGACAAGCGCGCTCCT	ADI-24391 BAD24629_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 38	607	ALWYSNHWV	ADI-24391 BAD24629_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 38	608	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24391 BAD24629_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 39	609	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24392 BAD24629_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 39	610	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24392 BAD24629_H03	Heavy chain variable region ("HC") amino acid sequence
Ab 39	611	FTFDTYAMN	ADI-24392 BAD24629_H03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 39	612	TTCACCTTTGACACATATGCCATGAAT	ADI-24392 BAD24629_H03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 39	613	RIRSKYNNYATYYADSVKD	ADI-24392 BAD24629_H03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 39	614	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24392 BAD24629_H03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 39	615	VRHGNFGNGYVSWFAH	ADI-24392 BAD24629_H03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 39	616	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24392 BAD24629_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 39	617	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24392 BAD24629_H03	Light chain variable region("LC") nucleic acid sequence
Ab 39	618	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24392 BAD24629_H03	Light chain variable region ("LC") amino acid sequence
Ab 39	619	GSSTGAVTTSNYAN	ADI-24392 BAD24629_H03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 39	620	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24392 BAD24629_H03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 39	621	GTDKRAP	ADI-24392 BAD24629_H03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 39	622	GGCACAGACAAGCGCGCTCCT	ADI-24392 BAD24629_H03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 39	623	ALWYSNHWV	ADI-24392 BAD24629_H03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 39	624	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24392 BAD24629_H03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 40	625	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24393 BAD24629_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 40	626	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24393 BAD24629_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 40	627	FTFDTYAMN	ADI-24393 BAD24629_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 40	628	TTCACCTTTGACACATATGCCATGAAT	ADI-24393 BAD24629_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 40	629	RIRSKYNNYATYYADSVKD	ADI-24393 BAD24629_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 40	630	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24393 BAD24629_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 40	631	VRHGNFGNGYVSWFAH	ADI-24393 BAD24629_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 40	632	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24393 BAD24629_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 40	633	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24393 BAD24629_A04	Light chain variable region("LC") nucleic acid sequence
Ab 40	634	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24393 BAD24629_A04	Light chain variable region ("LC") amino acid sequence
Ab 40	635	GSSTGAVTTSNYAN	ADI-24393 BAD24629_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 40	636	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24393 BAD24629_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 40	637	GTDKRAP	ADI-24393 BAD24629_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 40	638	GGCACAGACAAGCGCGCTCCT	ADI-24393 BAD24629_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 40	639	ALWYSNHWV	ADI-24393 BAD24629_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 40	640	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24393 BAD24629_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 41	641	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACTCATACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24394 BAD24702_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 41	642	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYSYSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	ADI-24394 BAD24702_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 41	643	FTFDTYAMN	ADI-24394 BAD24702_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 41	644	TTCACCTTTGACACATATGCCATGAAT	ADI-24394 BAD24702_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 41	645	RIRSKYNNYATYYSYSVKD	ADI-24394 BAD24702_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 41	646	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC TCATACTCCGTGAAGGAT	ADI-24394 BAD24702_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 41	647	VRHGNFGNGYVSWFAH	ADI-24394 BAD24702_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 41	648	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24394 BAD24702_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 41	649	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24394 BAD24702_A01	Light chain variable region("LC") nucleic acid sequence
Ab 41	650	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24394 BAD24702_A01	Light chain variable region ("LC") amino acid sequence
Ab 41	651	GSSTGAVTTSNYAN	ADI-24394 BAD24702_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 41	652	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24394 BAD24702_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 41	653	GTDKRAP	ADI-24394 BAD24702_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 41	654	GGCACAGACAAGCGCGCTCCT	ADI-24394 BAD24702_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 41	655	ALWYSNHWV	ADI-24394 BAD24702_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 41	656	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24394 BAD24702_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 42	657	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24395 BAD24629_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 42	658	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24395 BAD24629_B05	Heavy chain variable region ("HC") amino acid sequence
Ab 42	659	FTFDTYAMN	ADI-24395 BAD24629_B05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 42	660	TTCACCTTTGACACATATGCCATGAAT	ADI-24395 BAD24629_B05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 42	661	RIRSKYNNYATYYADSVKD	ADI-24395 BAD24629_B05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 42	662	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24395 BAD24629_B05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 42	663	VRHGNFGNGYVSWFAH	ADI-24395 BAD24629_B05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 42	664	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24395 BAD24629_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 42	665	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24395 BAD24629_B05	Light chain variable region("LC") nucleic acid sequence
Ab 42	666	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24395 BAD24629_B05	Light chain variable region ("LC") amino acid sequence
Ab 42	667	GSSTGAVTTSNYAN	ADI-24395 BAD24629_B05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 42	668	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24395 BAD24629_B05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 42	669	GTDKRAP	ADI-24395 BAD24629_B05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 42	670	GGCACAGACAAGCGCGCTCCT	ADI-24395 BAD24629_B05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 42	671	ALWYSNHWV	ADI-24395 BAD24629_B05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 42	672	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24395 BAD24629_B05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 43	673	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24396 BAD24629_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 43	674	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24396 BAD24629_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 43	675	FTFDTYAMN	ADI-24396 BAD24629_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 43	676	TTCACCTTTGACACATATGCCATGAAT	ADI-24396 BAD24629_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 43	677	RIRSKYNNYATYYADSVKD	ADI-24396 BAD24629_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 43	678	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24396 BAD24629_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 43	679	VRHGNFGNGYVSWFAH	ADI-24396 BAD24629_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 43	680	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24396 BAD24629_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 43	681	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24396 BAD24629_E05	Light chain variable region("LC") nucleic acid sequence
Ab 43	682	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24396 BAD24629_E05	Light chain variable region ("LC") amino acid sequence
Ab 43	683	GSSTGAVTTSNYAN	ADI-24396 BAD24629_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 43	684	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24396 BAD24629_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 43	685	GTDKRAP	ADI-24396 BAD24629_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 43	686	GGCACAGACAAGCGCGCTCCT	ADI-24396 BAD24629_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 43	687	ALWYSNHWV	ADI-24396 BAD24629_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 43	688	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24396 BAD24629_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 44	689	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24397 BAD24629_B06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 44	690	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24397 BAD24629_B06	Heavy chain variable region ("HC") amino acid sequence
Ab 44	691	FTFDTYAMN	ADI-24397 BAD24629_B06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 44	692	TTCACCTTTGACACATATGCCATGAAT	ADI-24397 BAD24629_B06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 44	693	RIRSKYNNYATYYADSVKD	ADI-24397 BAD24629_B06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 44	694	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24397 BAD24629_B06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 44	695	VRHGNFGNGYVSWFAH	ADI-24397 BAD24629_B06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 44	696	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24397 BAD24629_B06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 44	697	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24397 BAD24629_B06	Light chain variable region("LC") nucleic acid sequence
Ab 44	698	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24397 BAD24629_B06	Light chain variable region ("LC") amino acid sequence
Ab 44	699	GSSTGAVTTSNYAN	ADI-24397 BAD24629_B06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 44	700	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24397 BAD24629_B06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 44	701	GTDKRAP	ADI-24397 BAD24629_B06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 44	702	GGCACAGACAAGCGCGCTCCT	ADI-24397 BAD24629_B06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 44	703	ALWYSNHWV	ADI-24397 BAD24629_B06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 44	704	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24397 BAD24629_B06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 45	705	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24398 BAD24734_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 45	706	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24398 BAD24734_D01	Heavy chain variable region ("HC") amino acid sequence
Ab 45	707	FTFDTYAMN	ADI-24398 BAD24734_D01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 45	708	TTCACCTTTGACACATATGCCATGAAT	ADI-24398 BAD24734_D01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 45	709	RIRSKYNNYATYYADSVKD	ADI-24398 BAD24734_D01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 45	710	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24398 BAD24734_D01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 45	711	VRHGNFGNGYVSWFAH	ADI-24398 BAD24734_D01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 45	712	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24398 BAD24734_D01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 45	713	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24398 BAD24734_D01	Light chain variable region("LC") nucleic acid sequence
Ab 45	714	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24398 BAD24734_D01	Light chain variable region ("LC") amino acid sequence
Ab 45	715	GSSTGAVTTSNYAN	ADI-24398 BAD24734_D01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 45	716	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24398 BAD24734_D01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 45	717	GTDKRAP	ADI-24398 BAD24734_D01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 45	718	GGCACAGACAAGCGCGCTCCT	ADI-24398 BAD24734_D01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 45	719	ALWYSNHWV	ADI-24398 BAD24734_D01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 45	720	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24398 BAD24734_D01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 46	721	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24399 BAD24702_F02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 46	722	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24399 BAD24702_F02	Heavy chain variable region ("HC") amino acid sequence
Ab 46	723	FTFDTYAMN	ADI-24399 BAD24702_F02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 46	724	TTCACCTTTGACACATATGCCATGAAT	ADI-24399 BAD24702_F02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 46	725	RIRSKYNNYATYYADSVKD	ADI-24399 BAD24702_F02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 46	726	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24399 BAD24702_F02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 46	727	VRHGNFGNGYVSWFAH	ADI-24399 BAD24702_F02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 46	728	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24399 BAD24702_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 46	729	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24399 BAD24702_F02	Light chain variable region("LC") nucleic acid sequence
Ab 46	730	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24399 BAD24702_F02	Light chain variable region ("LC") amino acid sequence
Ab 46	731	GSSTGAVTTSNYAN	ADI-24399 BAD24702_F02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 46	732	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24399 BAD24702_F02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 46	733	GTDKRAP	ADI-24399 BAD24702_F02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 46	734	GGCACAGACAAGCGCGCTCCT	ADI-24399 BAD24702_F02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 46	735	ALWYSNHWV	ADI-24399 BAD24702_F02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 46	736	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24399 BAD24702_F02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 47	737	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24400 BAD24629_G07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 47	738	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24400 BAD24629_G07	Heavy chain variable region ("HC") amino acid sequence
Ab 47	739	FTFDTYAMN	ADI-24400 BAD24629_G07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 47	740	TTCACCTTTGACACATATGCCATGAAT	ADI-24400 BAD24629_G07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 47	741	RIRSKYNNYATYYADSVKD	ADI-24400 BAD24629_G07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 47	742	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24400 BAD24629_G07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 47	743	VRHGNFGNGYVSWFAH	ADI-24400 BAD24629_G07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 47	744	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24400 BAD24629_G07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 47	745	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGTTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24400 BAD24629_G07	Light chain variable region("LC") nucleic acid sequence
Ab 47	746	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24400 BAD24629_G07	Light chain variable region ("LC") amino acid sequence
Ab 47	747	GSSTGAVTTSNYAN	ADI-24400 BAD24629_G07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 47	748	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24400 BAD24629_G07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 47	749	GTDKRAP	ADI-24400 BAD24629_G07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 47	750	GGCACAGACAAGCGCGCTCCT	ADI-24400 BAD24629_G07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 47	751	ALWYSNHWV	ADI-24400 BAD24629_G07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 47	752	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24400 BAD24629_G07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 48	753	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24401 BAD24629_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 48	754	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24401 BAD24629_A08	Heavy chain variable region ("HC") amino acid sequence
Ab 48	755	FTFDTYAMN	ADI-24401 BAD24629_A08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 48	756	TTCACCTTTGACACATATGCCATGAAT	ADI-24401 BAD24629_A08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 48	757	RIRSKYNNYATYYADSVKD	ADI-24401 BAD24629_A08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 48	758	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24401 BAD24629_A08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 48	759	VRHGNFGNGYVSWFAH	ADI-24401 BAD24629_A08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 48	760	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24401 BAD24629_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 48	761	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24401 BAD24629_A08	Light chain variable region("LC") nucleic acid sequence
Ab 48	762	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24401 BAD24629_A08	Light chain variable region ("LC") amino acid sequence
Ab 48	763	GSSTGAVTTSNYAN	ADI-24401 BAD24629_A08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 48	764	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24401 BAD24629_A08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 48	765	GTDKRAP	ADI-24401 BAD24629_A08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 48	766	GGCACAGACAAGCGCGCTCCT	ADI-24401 BAD24629_A08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 48	767	ALWYSNHWV	ADI-24401 BAD24629_A08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 48	768	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24401 BAD24629_A08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 49	769	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24402 BAD24629_E08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 49	770	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24402 BAD24629_E08	Heavy chain variable region ("HC") amino acid sequence
Ab 49	771	FTFDTYAMN	ADI-24402 BAD24629_E08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 49	772	TTCACCTTTGACACATATGCCATGAAT	ADI-24402 BAD24629_E08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 49	773	RIRSKYNNYATYYADSVKD	ADI-24402 BAD24629_E08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 49	774	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24402 BAD24629_E08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 49	775	VRHGNFGNGYVSWFAH	ADI-24402 BAD24629_E08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 49	776	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24402 BAD24629_E08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 49	777	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-24402 BAD24629_E08	Light chain variable region("LC") nucleic acid sequence
Ab 49	778	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-24402 BAD24629_E08	Light chain variable region ("LC") amino acid sequence
Ab 49	779	GSSTGAVTTSNYAN	ADI-24402 BAD24629_E08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 49	780	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24402 BAD24629_E08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 49	781	GTDKRAP	ADI-24402 BAD24629_E08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 49	782	GGCACAGACAAGCGCGCTCCT	ADI-24402 BAD24629_E08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 49	783	ALWYSNHWV	ADI-24402 BAD24629_E08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 49	784	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24402 BAD24629_E08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 50	785	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24419 BAD24630_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 50	786	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24419 BAD24630_D05	Heavy chain variable region ("HC") amino acid sequence
Ab 50	787	FTFDTYAMN	ADI-24419 BAD24630_D05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 50	788	TTCACCTTTGACACATATGCCATGAAT	ADI-24419 BAD24630_D05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 50	789	RIRSKYNNYATYYADSVKD	ADI-24419 BAD24630_D05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 50	790	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24419 BAD24630_D05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 50	791	VRHGNFGNGYVSWFAH	ADI-24419 BAD24630_D05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 50	792	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24419 BAD24630_D05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 50	793	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24419 BAD24630_D05	Light chain variable region("LC") nucleic acid sequence
Ab 50	794	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24419 BAD24630_D05	Light chain variable region ("LC") amino acid sequence
Ab 50	795	GSSTGAVTTSNYAN	ADI-24419 BAD24630_D05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 50	796	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24419 BAD24630_D05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 50	797	GTDKRAP	ADI-24419 BAD24630_D05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 50	798	GGCACAGACAAGCGCGCTCCT	ADI-24419 BAD24630_D05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 50	799	ALWYSNHWV	ADI-24419 BAD24630_D05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 50	800	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24419 BAD24630_D05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 51	801	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24420 BAD24630_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 51	802	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24420 BAD24630_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 51	803	FTFDTYAMN	ADI-24420 BAD24630_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 51	804	TTCACCTTTGACACATATGCCATGAAT	ADI-24420 BAD24630_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 51	805	RIRSKYNNYATYYADSVKD	ADI-24420 BAD24630_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 51	806	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24420 BAD24630_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 51	807	VRHGNFGNGYVSWFAH	ADI-24420 BAD24630_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 51	808	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24420 BAD24630_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 51	809	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24420 BAD24630_E05	Light chain variable region("LC") nucleic acid sequence
Ab 51	810	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24420 BAD24630_E05	Light chain variable region ("LC") amino acid sequence
Ab 51	811	GSSTGAVTTSNYAN	ADI-24420 BAD24630_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 51	812	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24420 BAD24630_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 51	813	GTDKRAP	ADI-24420 BAD24630_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 51	814	GGCACAGACAAGCGCGCTCCT	ADI-24420 BAD24630_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 51	815	ALWYSNHWV	ADI-24420 BAD24630_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 51	816	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24420 BAD24630_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 52	817	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24421 BAD24630_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 52	818	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24421 BAD24630_D06	Heavy chain variable region ("HC") amino acid sequence
Ab 52	819	FTFDTYAMN	ADI-24421 BAD24630_D06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 52	820	TTCACCTTTGACACATATGCCATGAAT	ADI-24421 BAD24630_D06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 52	821	RIRSKYNNYATYYADSVKD	ADI-24421 BAD24630_D06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 52	822	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24421 BAD24630_D06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 52	823	VRHGNFGNGYVSWFAH	ADI-24421 BAD24630_D06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 52	824	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24421 BAD24630_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 52	825	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24421 BAD24630_D06	Light chain variable region("LC") nucleic acid sequence
Ab 52	826	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24421 BAD24630_D06	Light chain variable region ("LC") amino acid sequence
Ab 52	827	GSSTGAVTTSNYAN	ADI-24421 BAD24630_D06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 52	828	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24421 BAD24630_D06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 52	829	GTDKRAP	ADI-24421 BAD24630_D06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 52	830	GGCACAGACAAGCGCGCTCCT	ADI-24421 BAD24630_D06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 52	831	ALWYSNHWV	ADI-24421 BAD24630_D06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 52	832	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24421 BAD24630_D06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 53	833	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24422 BAD24702_D07	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 53	834	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24422 BAD24702_D07	Heavy chain variable region ("HC") amino acid sequence
Ab 53	835	FTFDTYAMN	ADI-24422 BAD24702_D07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 53	836	TTCACCTTTGACACATATGCCATGAAT	ADI-24422 BAD24702_D07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 53	837	RIRSKYNNYATYYADSVKD	ADI-24422 BAD24702_D07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 53	838	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24422 BAD24702_D07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 53	839	VRHGNFGNGYVSWFAH	ADI-24422 BAD24702_D07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 53	840	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24422 BAD24702_D07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 53	841	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24422 BAD24702_D07	Light chain variable region("LC") nucleic acid sequence
Ab 53	842	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24422 BAD24702_D07	Light chain variable region ("LC") amino acid sequence
Ab 53	843	GSSTGAVTTSNYAN	ADI-24422 BAD24702_D07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 53	844	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24422 BAD24702_D07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 53	845	GTDKRAP	ADI-24422 BAD24702_D07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 53	846	GGCACAGACAAGCGCGCTCCT	ADI-24422 BAD24702_D07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 53	847	ALWYSNHWV	ADI-24422 BAD24702_D07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 53	848	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24422 BAD24702_D07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 54	849	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24423 BAD24702_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 54	850	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24423 BAD24702_C08	Heavy chain variable region ("HC") amino acid sequence
Ab 54	851	FTFDTYAMN	ADI-24423 BAD24702_C08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 54	852	TTCACCTTTGACACATATGCCATGAAT	ADI-24423 BAD24702_C08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 54	853	RIRSKYNNYATYYADSVKD	ADI-24423 BAD24702_C08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 54	854	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24423 BAD24702_C08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 54	855	VRHGNFGNGYVSWFAH	ADI-24423 BAD24702_C08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 54	856	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24423 BAD24702_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 54	857	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24423 BAD24702_C08	Light chain variable region("LC") nucleic acid sequence
Ab 54	858	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24423 BAD24702_C08	Light chain variable region ("LC") amino acid sequence
Ab 54	859	GSSTGAVTTSNYAN	ADI-24423 BAD24702_C08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 54	860	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24423 BAD24702_C08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 54	861	GTDKRAP	ADI-24423 BAD24702_C08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 54	862	GGCACAGACAAGCGCGCTCCT	ADI-24423 BAD24702_C08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 54	863	ALWYSNHWV	ADI-24423 BAD24702_C08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 54	864	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24423 BAD24702_C08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 55	865	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24424 BAD24630_E07	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 55	866	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24424 BAD24630_E07	Heavy chain variable region ("HC") amino acid sequence
Ab 55	867	FTFDTYAMN	ADI-24424 BAD24630_E07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 55	868	TTCACCTTTGACACATATGCCATGAAT	ADI-24424 BAD24630_E07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 55	869	RIRSKYNNYATYYADSVKD	ADI-24424 BAD24630_E07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 55	870	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24424 BAD24630_E07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 55	871	VRHGNFGNGYVSWFAH	ADI-24424 BAD24630_E07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 55	872	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24424 BAD24630_E07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 55	873	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24424 BAD24630_E07	Light chain variable region("LC") nucleic acid sequence
Ab 55	874	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24424 BAD24630_E07	Light chain variable region ("LC") amino acid sequence
Ab 55	875	GSSTGAVTTSNYAN	ADI-24424 BAD24630_E07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 55	876	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24424 BAD24630_E07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 55	877	GTDKRAP	ADI-24424 BAD24630_E07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 55	878	GGCACAGACAAGCGCGCTCCT	ADI-24424 BAD24630_E07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 55	879	ALWYSNHWV	ADI-24424 BAD24630_E07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 55	880	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24424 BAD24630_E07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 56	881	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24425 BAD24630_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 56	882	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24425 BAD24630_C08	Heavy chain variable region ("HC") amino acid sequence
Ab 56	883	FTFDTYAMN	ADI-24425 BAD24630_C08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 56	884	TTCACCTTTGACACATATGCCATGAAT	ADI-24425 BAD24630_C08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 56	885	RIRSKYNNYATYYADSVKD	ADI-24425 BAD24630_C08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 56	886	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24425 BAD24630_C08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 56	887	VRHGNFGNGYVSWFAH	ADI-24425 BAD24630_C08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 56	888	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24425 BAD24630_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 56	889	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24425 BAD24630_C08	Light chain variable region("LC") nucleic acid sequence
Ab 56	890	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24425 BAD24630_C08	Light chain variable region ("LC") amino acid sequence
Ab 56	891	GSSTGAVTTSNYAN	ADI-24425 BAD24630_C08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 56	892	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24425 BAD24630_C08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 56	893	GTDKRAP	ADI-24425 BAD24630_C08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 56	894	GGCACAGACAAGCGCGCTCCT	ADI-24425 BAD24630_C08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 56	895	ALWYSNHWV	ADI-24425 BAD24630_C08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 56	896	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24425 BAD24630_C08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 57	897	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24426 BAD24702_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 57	898	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24426 BAD24702_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 57	899	FTFDTYAMN	ADI-24426 BAD24702_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 57	900	TTCACCTTTGACACATATGCCATGAAT	ADI-24426 BAD24702_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 57	901	RIRSKYNNYATYYADSVKD	ADI-24426 BAD24702_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 57	902	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24426 BAD24702_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 57	903	VRHGNFGNGYVSWFAH	ADI-24426 BAD24702_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 57	904	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24426 BAD24702_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 57	905	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24426 BAD24702_A09	Light chain variable region("LC") nucleic acid sequence
Ab 57	906	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24426 BAD24702_A09	Light chain variable region ("LC") amino acid sequence
Ab 57	907	GSSTGAVTTSNYAN	ADI-24426 BAD24702_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 57	908	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24426 BAD24702_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 57	909	GTDKRAP	ADI-24426 BAD24702_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 57	910	GGCACAGACAAGCGCGCTCCT	ADI-24426 BAD24702_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 57	911	ALWYSNHWV	ADI-24426 BAD24702_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 57	912	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24426 BAD24702_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 58	913	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24427 BAD24630_C09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 58	914	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24427 BAD24630_C09	Heavy chain variable region ("HC") amino acid sequence
Ab 58	915	FTFDTYAMN	ADI-24427 BAD24630_C09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 58	916	TTCACCTTTGACACATATGCCATGAAT	ADI-24427 BAD24630_C09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 58	917	RIRSKYNNYATYYADSVKD	ADI-24427 BAD24630_C09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 58	918	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24427 BAD24630_C09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 58	919	VRHGNFGNGYVSWFAH	ADI-24427 BAD24630_C09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 58	920	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24427 BAD24630_C09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 58	921	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24427 BAD24630_C09	Light chain variable region("LC") nucleic acid sequence
Ab 58	922	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24427 BAD24630_C09	Light chain variable region ("LC") amino acid sequence
Ab 58	923	GSSTGAVTTSNYAN	ADI-24427 BAD24630_C09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 58	924	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24427 BAD24630_C09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 58	925	GTDKRAP	ADI-24427 BAD24630_C09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 58	926	GGCACAGACAAGCGCGCTCCT	ADI-24427 BAD24630_C09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 58	927	ALWYSNHWV	ADI-24427 BAD24630_C09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 58	928	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24427 BAD24630_C09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 59	929	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24428 BAD24630_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 59	930	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24428 BAD24630_F09	Heavy chain variable region ("HC") amino acid sequence
Ab 59	931	FTFDTYAMN	ADI-24428 BAD24630_F09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 59	932	TTCACCTTTGACACATATGCCATGAAT	ADI-24428 BAD24630_F09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 59	933	RIRSKYNNYATYYADSVKD	ADI-24428 BAD24630_F09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 59	934	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24428 BAD24630_F09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 59	935	VRHGNFGNGYVSWFAH	ADI-24428 BAD24630_F09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 59	936	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24428 BAD24630_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 59	937	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24428 BAD24630_F09	Light chain variable region("LC") nucleic acid sequence
Ab 59	938	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24428 BAD24630_F09	Light chain variable region ("LC") amino acid sequence
Ab 59	939	GSSTGAVTTSNYAN	ADI-24428 BAD24630_F09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 59	940	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24428 BAD24630_F09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 59	941	GTDKRAP	ADI-24428 BAD24630_F09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 59	942	GGCACAGACAAGCGCGCTCCT	ADI-24428 BAD24630_F09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 59	943	ALWYSNHWV	ADI-24428 BAD24630_F09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 59	944	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24428 BAD24630_F09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 60	945	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24429 BAD24630_C10	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 60	946	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24429 BAD24630_C10	Heavy chain variable region ("HC") amino acid sequence
Ab 60	947	FTFDTYAMN	ADI-24429 BAD24630_C10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 60	948	TTCACCTTTGACACATATGCCATGAAT	ADI-24429 BAD24630_C10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 60	949	RIRSKYNNYATYYADSVKD	ADI-24429 BAD24630_C10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 60	950	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24429 BAD24630_C10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 60	951	VRHGNFGNGYVSWFAH	ADI-24429 BAD24630_C10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 60	952	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24429 BAD24630_C10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 60	953	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCTCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24429 BAD24630_C10	Light chain variable region("LC") nucleic acid sequence
Ab 60	954	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDLFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24429 BAD24630_C10	Light chain variable region ("LC") amino acid sequence
Ab 60	955	GSSTGAVTTSNYAN	ADI-24429 BAD24630_C10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 60	956	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24429 BAD24630_C10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 60	957	GTDKRAP	ADI-24429 BAD24630_C10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 60	958	GGCACAGACAAGCGCGCTCCT	ADI-24429 BAD24630_C10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 60	959	ALWYSNHWV	ADI-24429 BAD24630_C10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 60	960	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24429 BAD24630_C10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 61	961	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24430 BAD24702_D09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 61	962	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24430 BAD24702_D09	Heavy chain variable region ("HC") amino acid sequence
Ab 61	963	FTFDTYAMN	ADI-24430 BAD24702_D09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 61	964	TTCACCTTTGACACATATGCCATGAAT	ADI-24430 BAD24702_D09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 61	965	RIRSKYNNYATYYADSVKD	ADI-24430 BAD24702_D09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 61	966	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24430 BAD24702_D09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 61	967	VRHGNFGNGYVSWFAH	ADI-24430 BAD24702_D09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 61	968	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24430 BAD24702_D09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 61	969	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24430 BAD24702_D09	Light chain variable region("LC") nucleic acid sequence
Ab 61	970	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24430 BAD24702_D09	Light chain variable region ("LC") amino acid sequence
Ab 61	971	GSSTGAVTTSNYAN	ADI-24430 BAD24702_D09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 61	972	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24430 BAD24702_D09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 61	973	GTDKRAP	ADI-24430 BAD24702_D09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 61	974	GGCACAGACAAGCGCGCTCCT	ADI-24430 BAD24702_D09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 61	975	ALWYSNHWV	ADI-24430 BAD24702_D09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 61	976	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24430 BAD24702_D09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 62	977	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24431 BAD24702_B11	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 62	978	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24431 BAD24702_B11	Heavy chain variable region ("HC") amino acid sequence
Ab 62	979	FTFDTYAMN	ADI-24431 BAD24702_B11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 62	980	TTCACCTTTGACACATATGCCATGAAT	ADI-24431 BAD24702_B11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 62	981	RIRSKYNNYATYYADSVKD	ADI-24431 BAD24702_B11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 62	982	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24431 BAD24702_B11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 62	983	VRHGNFGNGYVSWFAH	ADI-24431 BAD24702_B11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 62	984	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24431 BAD24702_B11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 62	985	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24431 BAD24702_B11	Light chain variable region("LC") nucleic acid sequence
Ab 62	986	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24431 BAD24702_B11	Light chain variable region ("LC") amino acid sequence
Ab 62	987	GSSTGAVTTSNYAN	ADI-24431 BAD24702_B11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 62	988	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24431 BAD24702_B11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 62	989	GTDKRAP	ADI-24431 BAD24702_B11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 62	990	GGCACAGACAAGCGCGCTCCT	ADI-24431 BAD24702_B11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 62	991	ALWYSNHWV	ADI-24431 BAD24702_B11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 62	992	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24431 BAD24702_B11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 63	993	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24432 BAD24630_D12	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 63	994	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24432 BAD24630_D12	Heavy chain variable region ("HC") amino acid sequence
Ab 63	995	FTFDTYAMN	ADI-24432 BAD24630_D12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 63	996	TTCACCTTTGACACATATGCCATGAAT	ADI-24432 BAD24630_D12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 63	997	RIRSKYNNYATYYADSVKD	ADI-24432 BAD24630_D12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 63	998	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24432 BAD24630_D12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 63	999	VRHGNFGNGYVSWFAH	ADI-24432 BAD24630_D12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 63	1000	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24432 BAD24630_D12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 63	1001	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24432 BAD24630_D12	Light chain variable region("LC") nucleic acid sequence
Ab 63	1002	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24432 BAD24630_D12	Light chain variable region ("LC") amino acid sequence
Ab 63	1003	GSSTGAVTTSNYAN	ADI-24432 BAD24630_D12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 63	1004	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24432 BAD24630_D12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 63	1005	GTDKRAP	ADI-24432 BAD24630_D12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 63	1006	GGCACAGACAAGCGCGCTCCT	ADI-24432 BAD24630_D12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 63	1007	ALWYSNHWV	ADI-24432 BAD24630_D12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 63	1008	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24432 BAD24630_D12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 64	1009	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24433 BAD24702_C12	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 64	1010	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24433 BAD24702_C12	Heavy chain variable region ("HC") amino acid sequence
Ab 64	1011	FTFDTYAMN	ADI-24433 BAD24702_C12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 64	1012	TTCACCTTTGACACATATGCCATGAAT	ADI-24433 BAD24702_C12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 64	1013	RIRSKYNNYATYYADSVKD	ADI-24433 BAD24702_C12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 64	1014	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24433 BAD24702_C12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 64	1015	VRHGNFGNGYVSWFAH	ADI-24433 BAD24702_C12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 64	1016	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24433 BAD24702_C12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 64	1017	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24433 BAD24702_C12	Light chain variable region("LC") nucleic acid sequence
Ab 64	1018	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24433 BAD24702_C12	Light chain variable region ("LC") amino acid sequence
Ab 64	1019	GSSTGAVTTSNYAN	ADI-24433 BAD24702_C12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 64	1020	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24433 BAD24702_C12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 64	1021	GTDKRAP	ADI-24433 BAD24702_C12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 64	1022	GGCACAGACAAGCGCGCTCCT	ADI-24433 BAD24702_C12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 64	1023	ALWYSNHWV	ADI-24433 BAD24702_C12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 64	1024	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24433 BAD24702_C12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 65	1025	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGGGATGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24447 BAD24734_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 65	1026	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGGCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24447 BAD24734_F09	Heavy chain variable region ("HC") amino acid sequence
Ab 65	1027	FTFDTYAMN	ADI-24447 BAD24734_F09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 65	1028	TTCACCTTTGACACATATGCCATGAAT	ADI-24447 BAD24734_F09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 65	1029	RIRSKYNNYATYYADSVKD	ADI-24447 BAD24734_F09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 65	1030	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24447 BAD24734_F09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 65	1031	VRHGNFGNGYVSWFAH	ADI-24447 BAD24734_F09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 65	1032	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24447 BAD24734_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 65	1033	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24447 BAD24734_F09	Light chain variable region("LC") nucleic acid sequence
Ab 65	1034	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24447 BAD24734_F09	Light chain variable region ("LC") amino acid sequence
Ab 65	1035	GSSTGAVTTSNYAN	ADI-24447 BAD24734_F09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 65	1036	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24447 BAD24734_F09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 65	1037	GTDKRAP	ADI-24447 BAD24734_F09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 65	1038	GGCACAGACAAGCGCGCTCCT	ADI-24447 BAD24734_F09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 65	1039	ALWYSNHWV	ADI-24447 BAD24734_F09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 65	1040	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24447 BAD24734_F09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 66	1041	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGGGATGTCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24448 BAD24734_A10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 66	1042	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGGCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-24448 BAD24734_A10	Heavy chain variable region ("HC") amino acid sequence
Ab 66	1043	FTFDTYAMN	ADI-24448 BAD24734_A10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 66	1044	TTCACCTTTGACACATATGCCATGAAT	ADI-24448 BAD24734_A10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 66	1045	RIRSKYNNYATYYADSVKD	ADI-24448 BAD24734_A10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 66	1046	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-24448 BAD24734_A10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 66	1047	VRHGNFGNGYVSWFAH	ADI-24448 BAD24734_A10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 66	1048	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-24448 BAD24734_A10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 66	1049	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCTTGATCTCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGGGACCAAGCTGACCGTCCTA	ADI-24448 BAD24734_A10	Light chain variable region("LC") nucleic acid sequence
Ab 66	1050	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVLDLFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVL	ADI-24448 BAD24734_A10	Light chain variable region ("LC") amino acid sequence
Ab 66	1051	GSSTGAVTTSNYAN	ADI-24448 BAD24734_A10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 66	1052	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-24448 BAD24734_A10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 66	1053	GTDKRAP	ADI-24448 BAD24734_A10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 66	1054	GGCACAGACAAGCGCGCTCCT	ADI-24448 BAD24734_A10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 66	1055	ALWYSNHWV	ADI-24448 BAD24734_A10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 66	1056	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-24448 BAD24734_A10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 67	1057	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26955 LAD5221_P05_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 67	1058	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQGTLVTVSS	ADI-26955 LAD5221_P05_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 67	1059	FTFDTYAMN	ADI-26955 LAD5221_P05_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 67	1060	TTCACCTTTGACACATATGCCATGAAC	ADI-26955 LAD5221_P05_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 67	1061	RIRSKYNNYATYYADSVKD	ADI-26955 LAD5221_P05_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 67	1062	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26955 LAD5221_P05_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 67	1063	VRHGNFQGGYVSWFAH	ADI-26955 LAD5221_P05_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 67	1064	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-26955 LAD5221_P05_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 67	1065	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26955 LAD5221_P05_A01	Light chain variable region("LC") nucleic acid sequence
Ab 67	1066	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26955 LAD5221_P05_A01	Light chain variable region ("LC") amino acid sequence
Ab 67	1067	GSSTGAVTTSNYAN	ADI-26955 LAD5221_P05_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 67	1068	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26955 LAD5221_P05_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 67	1069	GTDKRAP	ADI-26955 LAD5221_P05_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 67	1070	GGCACAGACAAGCGCGCTCCT	ADI-26955 LAD5221_P05_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 67	1071	ALWYSNHWV	ADI-26955 LAD5221_P05_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 67	1072	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26955 LAD5221_P05_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 68	1073	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGCTTGGTG	ADI-26956 LAD5221_P05_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 68	1074	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFAWWGQGTLVTVSS	ADI-26956 LAD5221_P05_F01	Heavy chain variable region ("HC") amino acid sequence
Ab 68	1075	FTFDTYAMN	ADI-26956 LAD5221_P05_F01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 68	1076	TTCACCTTTGACACATATGCCATGAAC	ADI-26956 LAD5221_P05_F01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 68	1077	RIRSKYNNYATYYADSVKD	ADI-26956 LAD5221_P05_F01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 68	1078	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26956 LAD5221_P05_F01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 68	1079	VRHGNFGGGYVSWFAW	ADI-26956 LAD5221_P05_F01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 68	1080	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGCTTGG	ADI-26956 LAD5221_P05_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 68	1081	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26956 LAD5221_P05_F01	Light chain variable region("LC") nucleic acid sequence
Ab 68	1082	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26956 LAD5221_P05_F01	Light chain variable region ("LC") amino acid sequence
Ab 68	1083	GSSTGAVTTSNYAN	ADI-26956 LAD5221_P05_F01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 68	1084	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26956 LAD5221_P05_F01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 68	1085	GTDKRAP	ADI-26956 LAD5221_P05_F01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 68	1086	GGCACAGACAAGCGCGCTCCT	ADI-26956 LAD5221_P05_F01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 68	1087	ALWYSNHWV	ADI-26956 LAD5221_P05_F01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 68	1088	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26956 LAD5221_P05_F01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 69	1089	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26957 LAD5221_P05_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 69	1090	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHANFGAGYVSWFAHWGQGTLVTVSS	ADI-26957 LAD5221_P05_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 69	1091	FTFDTYAMN	ADI-26957 LAD5221_P05_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 69	1092	TTCACCTTTGACACATATGCCATGAAC	ADI-26957 LAD5221_P05_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 69	1093	RIRSKYNNYATYYADSVKD	ADI-26957 LAD5221_P05_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 69	1094	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26957 LAD5221_P05_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 69	1095	VRHANFGAGYVSWFAH	ADI-26957 LAD5221_P05_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 69	1096	GTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTGGTTTGCTCAT	ADI-26957 LAD5221_P05_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 69	1097	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26957 LAD5221_P05_A02	Light chain variable region("LC") nucleic acid sequence
Ab 69	1098	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26957 LAD5221_P05_A02	Light chain variable region ("LC") amino acid sequence
Ab 69	1099	GSSTGAVTTSNYAN	ADI-26957 LAD5221_P05_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 69	1100	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26957 LAD5221_P05_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 69	1101	GTDKRAP	ADI-26957 LAD5221_P05_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 69	1102	GGCACAGACAAGCGCGCTCCT	ADI-26957 LAD5221_P05_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 69	1103	ALWYSNHWV	ADI-26957 LAD5221_P05_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 69	1104	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26957 LAD5221_P05_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 70	1105	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26958 LAD5221_P05_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 70	1106	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-26958 LAD5221_P05_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 70	1107	FTFDTYAMN	ADI-26958 LAD5221_P05_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 70	1108	TTCACCTTTGACACATATGCCATGAAC	ADI-26958 LAD5221_P05_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 70	1109	RIRSKYNNYATYYADSVKD	ADI-26958 LAD5221_P05_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 70	1110	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26958 LAD5221_P05_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 70	1111	VRHGNFGEGYVSWFAH	ADI-26958 LAD5221_P05_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 70	1112	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-26958 LAD5221_P05_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 70	1113	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26958 LAD5221_P05_E02	Light chain variable region("LC") nucleic acid sequence
Ab 70	1114	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26958 LAD5221_P05_E02	Light chain variable region ("LC") amino acid sequence
Ab 70	1115	GSSTGAVTTSNYAN	ADI-26958 LAD5221_P05_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 70	1116	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26958 LAD5221_P05_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 70	1117	GTDKRAP	ADI-26958 LAD5221_P05_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 70	1118	GGCACAGACAAGCGCGCTCCT	ADI-26958 LAD5221_P05_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 70	1119	ALWYSNHWV	ADI-26958 LAD5221_P05_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 70	1120	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26958 LAD5221_P05_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 71	1121	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26959 LAD5221_P05_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 71	1122	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQGTLVTVSS	ADI-26959 LAD5221_P05_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 71	1123	FTFDTYAMN	ADI-26959 LAD5221_P05_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 71	1124	TTCACCTTTGACACATATGCCATGAAC	ADI-26959 LAD5221_P05_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 71	1125	RIRSKYNNYATYYADSVKD	ADI-26959 LAD5221_P05_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 71	1126	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26959 LAD5221_P05_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 71	1127	VRHDNFGAGYVSWFAH	ADI-26959 LAD5221_P05_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 71	1128	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCAT	ADI-26959 LAD5221_P05_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 71	1129	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26959 LAD5221_P05_A03	Light chain variable region("LC") nucleic acid sequence
Ab 71	1130	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26959 LAD5221_P05_A03	Light chain variable region ("LC") amino acid sequence
Ab 71	1131	GSSTGAVTTSNYAN	ADI-26959 LAD5221_P05_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 71	1132	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26959 LAD5221_P05_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 71	1133	GTDKRAP	ADI-26959 LAD5221_P05_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 71	1134	GGCACAGACAAGCGCGCTCCT	ADI-26959 LAD5221_P05_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 71	1135	ALWYSNHWV	ADI-26959 LAD5221_P05_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 71	1136	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26959 LAD5221_P05_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 72	1137	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26960 LAD5221_P05_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 72	1138	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQGTLVTVSS	ADI-26960 LAD5221_P05_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 72	1139	FTFDTYAMN	ADI-26960 LAD5221_P05_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 72	1140	TTCACCTTTGACACATATGCCATGAAC	ADI-26960 LAD5221_P05_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 72	1141	RIRSKYNNYATYYADSVKD	ADI-26960 LAD5221_P05_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 72	1142	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26960 LAD5221_P05_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 72	1143	VRHGNFGVGYVSWFAS	ADI-26960 LAD5221_P05_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 72	1144	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCT	ADI-26960 LAD5221_P05_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 72	1145	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26960 LAD5221_P05_E03	Light chain variable region("LC") nucleic acid sequence
Ab 72	1146	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26960 LAD5221_P05_E03	Light chain variable region ("LC") amino acid sequence
Ab 72	1147	GSSTGAVTTSNYAN	ADI-26960 LAD5221_P05_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 72	1148	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26960 LAD5221_P05_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 72	1149	GTDKRAP	ADI-26960 LAD5221_P05_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 72	1150	GGCACAGACAAGCGCGCTCCT	ADI-26960 LAD5221_P05_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 72	1151	ALWYSNHWV	ADI-26960 LAD5221_P05_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 72	1152	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26960 LAD5221_P05_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 73	1153	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26962 LAD5221_P05_G04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 73	1154	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-26962 LAD5221_P05_G04	Heavy chain variable region ("HC") amino acid sequence
Ab 73	1155	FTFDTYAMN	ADI-26962 LAD5221_P05_G04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 73	1156	TTCACCTTTGACACATATGCCATGAAC	ADI-26962 LAD5221_P05_G04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 73	1157	RIRSKYNDYATYYADSVKD	ADI-26962 LAD5221_P05_G04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 73	1158	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26962 LAD5221_P05_G04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 73	1159	VRHGNFGEGYVSWFAH	ADI-26962 LAD5221_P05_G04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 73	1160	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-26962 LAD5221_P05_G04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 73	1161	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26962 LAD5221_P05_G04	Light chain variable region("LC") nucleic acid sequence
Ab 73	1162	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26962 LAD5221_P05_G04	Light chain variable region ("LC") amino acid sequence
Ab 73	1163	GSSTGAVTTSNYAN	ADI-26962 LAD5221_P05_G04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 73	1164	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26962 LAD5221_P05_G04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 73	1165	GTDKRAP	ADI-26962 LAD5221_P05_G04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 73	1166	GGCACAGACAAGCGCGCTCCT	ADI-26962 LAD5221_P05_G04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 73	1167	ALWYSNHWV	ADI-26962 LAD5221_P05_G04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 73	1168	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26962 LAD5221_P05_G04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 74	1169	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26963 LAD5221_P05_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 74	1170	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQGTLVTVSS	ADI-26963 LAD5221_P05_B05	Heavy chain variable region ("HC") amino acid sequence
Ab 74	1171	FTFDTYAMN	ADI-26963 LAD5221_P05_B05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 74	1172	TTCACCTTTGACACATATGCCATGAAC	ADI-26963 LAD5221_P05_B05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 74	1173	RIRSKYNDYATYYADSVKD	ADI-26963 LAD5221_P05_B05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 74	1174	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26963 LAD5221_P05_B05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 74	1175	VRHDNFGAGYVSWFAH	ADI-26963 LAD5221_P05_B05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 74	1176	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCAT	ADI-26963 LAD5221_P05_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 74	1177	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26963 LAD5221_P05_B05	Light chain variable region("LC") nucleic acid sequence
Ab 74	1178	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26963 LAD5221_P05_B05	Light chain variable region ("LC") amino acid sequence
Ab 74	1179	GSSTGAVTTSNYAN	ADI-26963 LAD5221_P05_B05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 74	1180	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26963 LAD5221_P05_B05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 74	1181	GTDKRAP	ADI-26963 LAD5221_P05_B05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 74	1182	GGCACAGACAAGCGCGCTCCT	ADI-26963 LAD5221_P05_B05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 74	1183	ALWYSNHWV	ADI-26963 LAD5221_P05_B05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 74	1184	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26963 LAD5221_P05_B05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 75	1185	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26964 LAD5221_P05_H05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 75	1186	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQG TLVTVSS	ADI-26964 LAD5221_P05_H05	Heavy chain variable region ("HC") amino acid sequence
Ab 75	1187	FTFDTYAMN	ADI-26964 LAD5221_P05_H05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 75	1188	TTCACCTTTGACACATATGCCATGAAC	ADI-26964 LAD5221_P05_H05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 75	1189	RIRSKYNDYATYYADSVKD	ADI-26964 LAD5221_P05_H05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 75	1190	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	ADI-26964 LAD5221_P05_H05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 75	1191	VRHGNFGVGYVSWFAS	ADI-26964 LAD5221_P05_H05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 75	1192	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTG GTTTGCTTCT	ADI-26964 LAD5221_P05_H05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 75	1193	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26964 LAD5221_P05_H05	Light chain variable region("LC") nucleic acid sequence
Ab 75	1194	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26964 LAD5221_P05_H05	Light chain variable region ("LC") amino acid sequence
Ab 75	1195	GSSTGAVTTSNYAN	ADI-26964 LAD5221_P05_H05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 75	1196	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26964 LAD5221_P05_H05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 75	1197	GTDKRAP	ADI-26964 LAD5221_P05_H05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 75	1198	GGCACAGACAAGCGCGCTCCT	ADI-26964 LAD5221_P05_H05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 75	1199	ALWYSNHWV	ADI-26964 LAD5221_P05_H05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 75	1200	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26964 LAD5221_P05_H05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 76	1201	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26965 LAD5221_P05_C06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 76	1202	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQGTLVTVSS	ADI-26965 LAD5221_P05_C06	Heavy chain variable region ("HC") amino acid sequence
Ab 76	1203	FTFDTYAMN	ADI-26965 LAD5221_P05_C06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 76	1204	TTCACCTTTGACACATATGCCATGAAC	ADI-26965 LAD5221_P05_C06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 76	1205	RIRSKYNDYATYYADSVKD	ADI-26965 LAD5221_P05_C06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 76	1206	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26965 LAD5221_P05_C06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 76	1207	VRHGNFGGAYVSWFAH	ADI-26965 LAD5221_P05_C06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 76	1208	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCAT	ADI-26965 LAD5221_P05_C06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 76	1209	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26965 LAD5221_P05_C06	Light chain variable region("LC") nucleic acid sequence
Ab 76	1210	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26965 LAD5221_P05_C06	Light chain variable region ("LC") amino acid sequence
Ab 76	1211	GSSTGAVTTSNYAN	ADI-26965 LAD5221_P05_C06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 76	1212	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26965 LAD5221_P05_C06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 76	1213	GTDKRAP	ADI-26965 LAD5221_P05_C06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 76	1214	GGCACAGACAAGCGCGCTCCT	ADI-26965 LAD5221_P05_C06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 76	1215	ALWYSNHWV	ADI-26965 LAD5221_P05_C06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 76	1216	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26965 LAD5221_P05_C06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 77	1217	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGGGCATTG	ADI-26966 LAD5221_P05_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 77	1218	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFGHWGQGTLVTVSS	ADI-26966 LAD5221_P05_F06	Heavy chain variable region ("HC") amino acid sequence
Ab 77	1219	FTFDAYAMN	ADI-26966 LAD5221_P05_F06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 77	1220	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26966 LAD5221_P05_F06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 77	1221	RIRSKYNDYATYYADSVKD	ADI-26966 LAD5221_P05_F06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 77	1222	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26966 LAD5221_P05_F06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 77	1223	VRHGNFGGGYVSWFGH	ADI-26966 LAD5221_P05_F06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 77	1224	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGGGCAT	ADI-26966 LAD5221_P05_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 77	1225	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26966 LAD5221_P05_F06	Light chain variable region("LC") nucleic acid sequence
Ab 77	1226	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26966 LAD5221_P05_F06	Light chain variable region ("LC") amino acid sequence
Ab 77	1227	GSSTGAVTTSNYAN	ADI-26966 LAD5221_P05_F06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 77	1228	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26966 LAD5221_P05_F06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 77	1229	GTDKRAP	ADI-26966 LAD5221_P05_F06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 77	1230	GGCACAGACAAGCGCGCTCCT	ADI-26966 LAD5221_P05_F06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 77	1231	ALWYSNHWV	ADI-26966 LAD5221_P05_F06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 77	1232	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26966 LAD5221_P05_F06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 78	1233	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCATTGG	ADI-26968 LAD5221_P05_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 78	1234	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQGTLVTVSS	ADI-26968 LAD5221_P05_F07	Heavy chain variable region ("HC") amino acid sequence
Ab 78	1235	FTFDAYAMN	ADI-26968 LAD5221_P05_F07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 78	1236	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26968 LAD5221_P05_F07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 78	1237	RIRSKYNDYATYYADSVKD	ADI-26968 LAD5221_P05_F07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 78	1238	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26968 LAD5221_P05_F07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 78	1239	VRHGNFGNYAVSWFAH	ADI-26968 LAD5221_P05_F07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 78	1240	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCAT	ADI-26968 LAD5221_P05_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 78	1241	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26968 LAD5221_P05_F07	Light chain variable region("LC") nucleic acid sequence
Ab 78	1242	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-26968 LAD5221_P05_F07	Light chain variable region ("LC") amino acid sequence
Ab 78	1243	GSSTGAVTTSNYAN	ADI-26968 LAD5221_P05_F07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 78	1244	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26968 LAD5221_P05_F07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 78	1245	GTDKRAP	ADI-26968 LAD5221_P05_F07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 78	1246	GGCACAGACAAGCGCGCTCCT	ADI-26968 LAD5221_P05_F07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 78	1247	ALWYSNHWV	ADI-26968 LAD5221_P05_F07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 78	1248	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-26968 LAD5221_P05_F07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 79	1249	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26969 LAD5222_P05_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 79	1250	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQGTLVTVSS	ADI-26969 LAD5222_P05_A08	Heavy chain variable region ("HC") amino acid sequence
Ab 79	1251	FTFDTYAMN	ADI-26969 LAD5222_P05_A08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 79	1252	TTCACCTTTGACACATATGCCATGAAC	ADI-26969 LAD5222_P05_A08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 79	1253	RIRSKYNNYATYYADSVKD	ADI-26969 LAD5222_P05_A08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 79	1254	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26969 LAD5222_P05_A08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 79	1255	VRHGNFQGGYVSWFAH	ADI-26969 LAD5222_P05_A08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 79	1256	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-26969 LAD5222_P05_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 79	1257	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26969 LAD5222_P05_A08	Light chain variable region("LC") nucleic acid sequence
Ab 79	1258	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26969 LAD5222_P05_A08	Light chain variable region ("LC") amino acid sequence
Ab 79	1259	GSSTGAVTTSNYAN	ADI-26969 LAD5222_P05_A08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 79	1260	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26969 LAD5222_P05_A08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 79	1261	GTDKRAP	ADI-26969 LAD5222_P05_A08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 79	1262	GGCACAGACAAGCGCGCTCCT	ADI-26969 LAD5222_P05_A08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 79	1263	ALWYSNLWV	ADI-26969 LAD5222_P05_A08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 79	1264	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26969 LAD5222_P05_A08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 80	1265	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26971 LAD5222_P05_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 80	1266	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHANFGAGYVSWFAHWGQGTLVTVSS	ADI-26971 LAD5222_P05_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 80	1267	FTFDTYAMN	ADI-26971 LAD5222_P05_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 80	1268	TTCACCTTTGACACATATGCCATGAAC	ADI-26971 LAD5222_P05_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 80	1269	RIRSKYNNYATYYADSVKD	ADI-26971 LAD5222_P05_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 80	1270	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26971 LAD5222_P05_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 80	1271	VRHANFGAGYVSWFAH	ADI-26971 LAD5222_P05_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 80	1272	GTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTGGTTTGCTCAT	ADI-26971 LAD5222_P05_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 80	1273	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26971 LAD5222_P05_A09	Light chain variable region("LC") nucleic acid sequence
Ab 80	1274	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26971 LAD5222_P05_A09	Light chain variable region ("LC") amino acid sequence
Ab 80	1275	GSSTGAVTTSNYAN	ADI-26971 LAD5222_P05_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 80	1276	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26971 LAD5222_P05_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 80	1277	GTDKRAP	ADI-26971 LAD5222_P05_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 80	1278	GGCACAGACAAGCGCGCTCCT	ADI-26971 LAD5222_P05_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 80	1279	ALWYSNLWV	ADI-26971 LAD5222_P05_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 80	1280	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26971 LAD5222_P05_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 81	1281	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26972 LAD5222_P05_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 81	1282	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-26972 LAD5222_P05_F09	Heavy chain variable region ("HC") amino acid sequence
Ab 81	1283	FTFDTYAMN	ADI-26972 LAD5222_P05_F09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 81	1284	TTCACCTTTGACACATATGCCATGAAC	ADI-26972 LAD5222_P05_F09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 81	1285	RIRSKYNNYATYYADSVKD	ADI-26972 LAD5222_P05_F09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 81	1286	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26972 LAD5222_P05_F09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 81	1287	VRHGNFGEGYVSWFAH	ADI-26972 LAD5222_P05_F09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 81	1288	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-26972 LAD5222_P05_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 81	1289	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26972 LAD5222_P05_F09	Light chain variable region("LC") nucleic acid sequence
Ab 81	1290	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26972 LAD5222_P05_F09	Light chain variable region ("LC") amino acid sequence
Ab 81	1291	GSSTGAVTTSNYAN	ADI-26972 LAD5222_P05_F09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 81	1292	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26972 LAD5222_P05_F09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 81	1293	GTDKRAP	ADI-26972 LAD5222_P05_F09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 81	1294	GGCACAGACAAGCGCGCTCCT	ADI-26972 LAD5222_P05_F09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 81	1295	ALWYSNLWV	ADI-26972 LAD5222_P05_F09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 81	1296	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26972 LAD5222_P05_F09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 82	1297	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26973 LAD5222_P05_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 82	1298	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQGTLVTVSS	ADI-26973 LAD5222_P05_E10	Heavy chain variable region ("HC") amino acid sequence
Ab 82	1299	FTFDTYAMN	ADI-26973 LAD5222_P05_E10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 82	1300	TTCACCTTTGACACATATGCCATGAAC	ADI-26973 LAD5222_P05_E10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 82	1301	RIRSKYNNYATYYADSVKD	ADI-26973 LAD5222_P05_E10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 82	1302	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26973 LAD5222_P05_E10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 82	1303	VRHDNFGAGYVSWFAH	ADI-26973 LAD5222_P05_E10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 82	1304	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCAT	ADI-26973 LAD5222_P05_E10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 82	1305	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26973 LAD5222_P05_E10	Light chain variable region("LC") nucleic acid sequence
Ab 82	1306	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26973 LAD5222_P05_E10	Light chain variable region ("LC") amino acid sequence
Ab 82	1307	GSSTGAVTTSNYAN	ADI-26973 LAD5222_P05_E10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 82	1308	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26973 LAD5222_P05_E10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 82	1309	GTDKRAP	ADI-26973 LAD5222_P05_E10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 82	1310	GGCACAGACAAGCGCGCTCCT	ADI-26973 LAD5222_P05_E10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 82	1311	ALWYSNLWV	ADI-26973 LAD5222_P05_E10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 82	1312	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26973 LAD5222_P05_E10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 83	1313	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26974 LAD5222_P05_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 83	1314	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQGTLVTVSS	ADI-26974 LAD5222_P05_A11	Heavy chain variable region ("HC") amino acid sequence
Ab 83	1315	FTFDTYAMN	ADI-26974 LAD5222_P05_A11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 83	1316	TTCACCTTTGACACATATGCCATGAAC	ADI-26974 LAD5222_P05_A11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 83	1317	RIRSKYNNYATYYADSVKD	ADI-26974 LAD5222_P05_A11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 83	1318	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26974 LAD5222_P05_A11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 83	1319	VRHGNFGGAYVSWFAH	ADI-26974 LAD5222_P05_A11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 83	1320	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCAT	ADI-26974 LAD5222_P05_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 83	1321	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26974 LAD5222_P05_A11	Light chain variable region("LC") nucleic acid sequence
Ab 83	1322	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26974 LAD5222_P05_A11	Light chain variable region ("LC") amino acid sequence
Ab 83	1323	GSSTGAVTTSNYAN	ADI-26974 LAD5222_P05_A11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 83	1324	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26974 LAD5222_P05_A11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 83	1325	GTDKRAP	ADI-26974 LAD5222_P05_A11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 83	1326	GGCACAGACAAGCGCGCTCCT	ADI-26974 LAD5222_P05_A11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 83	1327	ALWYSNLWV	ADI-26974 LAD5222_P05_A11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 83	1328	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26974 LAD5222_P05_A11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 84	1329	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26975 LAD5222_P05_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 84	1330	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-26975 LAD5222_P05_F11	Heavy chain variable region ("HC") amino acid sequence
Ab 84	1331	FTFDTYAMN	ADI-26975 LAD5222_P05_F11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 84	1332	TTCACCTTTGACACATATGCCATGAAC	ADI-26975 LAD5222_P05_F11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 84	1333	RIRSKYNDYATYYADSVKD	ADI-26975 LAD5222_P05_F11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 84	1334	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26975 LAD5222_P05_F11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 84	1335	VRHGNFGEGYVSWFAH	ADI-26975 LAD5222_P05_F11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 84	1336	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-26975 LAD5222_P05_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 84	1337	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26975 LAD5222_P05_F11	Light chain variable region("LC") nucleic acid sequence
Ab 84	1338	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26975 LAD5222_P05_F11	Light chain variable region ("LC") amino acid sequence
Ab 84	1339	GSSTGAVTTSNYAN	ADI-26975 LAD5222_P05_F11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 84	1340	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26975 LAD5222_P05_F11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 84	1341	GTDKRAP	ADI-26975 LAD5222_P05_F11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 84	1342	GGCACAGACAAGCGCGCTCCT	ADI-26975 LAD5222_P05_F11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 84	1343	ALWYSNLWV	ADI-26975 LAD5222_P05_F11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 84	1344	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26975 LAD5222_P05_F11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 85	1345	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGATAACTTCGGGGCTGGTTACGTATCATGGTTTGCTCATTGG	ADI-26976 LAD5222_P05_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTATCCTCA		
Ab 85	1346	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQGTLVTVSS	ADI-26976 LAD5222_P05_A12	Heavy chain variable region ("HC") amino acid sequence
Ab 85	1347	FTFDTYAMN	ADI-26976 LAD5222_P05_A12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 85	1348	TTCACCTTTGACACATATGCCATGAAC	ADI-26976 LAD5222_P05_A12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 85	1349	RIRSKYNDYATYYADSVKD	ADI-26976 LAD5222_P05_A12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 85	1350	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26976 LAD5222_P05_A12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 85	1351	VRHDNFGAGYVSWFAH	ADI-26976 LAD5222_P05_A12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 85	1352	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCATGGTTTGCTCAT	ADI-26976 LAD5222_P05_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 85	1353	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26976 LAD5222_P05_A12	Light chain variable region("LC") nucleic acid sequence
Ab 85	1354	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26976 LAD5222_P05_A12	Light chain variable region ("LC") amino acid sequence
Ab 85	1355	GSSTGAVTTSNYAN	ADI-26976 LAD5222_P05_A12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 85	1356	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26976 LAD5222_P05_A12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 85	1357	GTDKRAP	ADI-26976 LAD5222_P05_A12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 85	1358	GGCACAGACAAGCGCGCTCCT	ADI-26976 LAD5222_P05_A12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 85	1359	ALWYSNLWV	ADI-26976 LAD5222_P05_A12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 85	1360	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26976 LAD5222_P05_A12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 86	1361	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26977 LAD5222_P05_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 86	1362	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQGTLVTVSS	ADI-26977 LAD5222_P05_F12	Heavy chain variable region ("HC") amino acid sequence
Ab 86	1363	FTFDTYAMN	ADI-26977 LAD5222_P05_F12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 86	1364	TTCACCTTTGACACATATGCCATGAAC	ADI-26977 LAD5222_P05_F12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 86	1365	RIRSKYNDYATYYADSVKD	ADI-26977 LAD5222_P05_F12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 86	1366	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26977 LAD5222_P05_F12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 86	1367	VRHGNFGVGYVSWFAS	ADI-26977 LAD5222_P05_F12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 86	1368	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCT	ADI-26977 LAD5222_P05_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 86	1369	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26977 LAD5222_P05_F12	Light chain variable region("LC") nucleic acid sequence
Ab 86	1370	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26977 LAD5222_P05_F12	Light chain variable region ("LC") amino acid sequence
Ab 86	1371	GSSTGAVTTSNYAN	ADI-26977 LAD5222_P05_F12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 86	1372	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26977 LAD5222_P05_F12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 86	1373	GTDKRAP	ADI-26977 LAD5222_P05_F12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 86	1374	GGCACAGACAAGCGCGCTCCT	ADI-26977 LAD5222_P05_F12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 86	1375	ALWYSNLWV	ADI-26977 LAD5222_P05_F12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 86	1376	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26977 LAD5222_P05_F12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 87	1377	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26978 LAD5222_P06_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 87	1378	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQGTLVTVSS	ADI-26978 LAD5222_P06_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 87	1379	FTFDTYAMN	ADI-26978 LAD5222_P06_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 87	1380	TTCACCTTTGACACATATGCCATGAAC	ADI-26978 LAD5222_P06_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 87	1381	RIRSKYNDYATYYADSVKD	ADI-26978 LAD5222_P06_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 87	1382	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26978 LAD5222_P06_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 87	1383	VRHGNFGGAYVSWFAH	ADI-26978 LAD5222_P06_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 87	1384	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCAT	ADI-26978 LAD5222_P06_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 87	1385	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26978 LAD5222_P06_A01	Light chain variable region("LC") nucleic acid sequence
Ab 87	1386	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26978 LAD5222_P06_A01	Light chain variable region ("LC") amino acid sequence
Ab 87	1387	GSSTGAVTTSNYAN	ADI-26978 LAD5222_P06_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 87	1388	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26978 LAD5222_P06_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 87	1389	GTDKRAP	ADI-26978 LAD5222_P06_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 87	1390	GGCACAGACAAGCGCGCTCCT	ADI-26978 LAD5222_P06_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 87	1391	ALWYSNLWV	ADI-26978 LAD5222_P06_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 87	1392	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26978 LAD5222_P06_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 88	1393	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGGGCATTG	ADI-26979 LAD5222_P06_E01	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 88	1394	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFGHWGQGTLVTVSS	ADI-26979 LAD5222_P06_E01	Heavy chain variable region ("HC") amino acid sequence
Ab 88	1395	FTFDAYAMN	ADI-26979 LAD5222_P06_E01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 88	1396	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26979 LAD5222_P06_E01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 88	1397	RIRSKYNDYATYYADSVKD	ADI-26979 LAD5222_P06_E01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 88	1398	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26979 LAD5222_P06_E01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 88	1399	VRHGNFGGGYVSWFGH	ADI-26979 LAD5222_P06_E01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 88	1400	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGGGCAT	ADI-26979 LAD5222_P06_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 88	1401	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26979 LAD5222_P06_E01	Light chain variable region("LC") nucleic acid sequence
Ab 88	1402	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26979 LAD5222_P06_E01	Light chain variable region ("LC") amino acid sequence
Ab 88	1403	GSSTGAVTTSNYAN	ADI-26979 LAD5222_P06_E01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 88	1404	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26979 LAD5222_P06_E01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 88	1405	GTDKRAP	ADI-26979 LAD5222_P06_E01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 88	1406	GGCACAGACAAGCGCGCTCCT	ADI-26979 LAD5222_P06_E01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 88	1407	ALWYSNLWV	ADI-26979 LAD5222_P06_E01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 88	1408	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26979 LAD5222_P06_E01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 89	1409	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTGGTTTGCTCATTG	ADI-26980 LAD5222_P06_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 89	1410	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNVGGGYVSWFAHWGQGTLVTVSS	ADI-26980 LAD5222_P06_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 89	1411	FTFDAYAMN	ADI-26980 LAD5222_P06_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 89	1412	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26980 LAD5222_P06_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 89	1413	RIRSKYNDYATYYADSVKD	ADI-26980 LAD5222_P06_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 89	1414	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26980 LAD5222_P06_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 89	1415	VRHGNVGGGYVSWFAH	ADI-26980 LAD5222_P06_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 89	1416	GTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-26980 LAD5222_P06_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 89	1417	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26980 LAD5222_P06_A02	Light chain variable region("LC") nucleic acid sequence
Ab 89	1418	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26980 LAD5222_P06_A02	Light chain variable region ("LC") amino acid sequence
Ab 89	1419	GSSTGAVTTSNYAN	ADI-26980 LAD5222_P06_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 89	1420	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26980 LAD5222_P06_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 89	1421	GTDKRAP	ADI-26980 LAD5222_P06_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 89	1422	GGCACAGACAAGCGCGCTCCT	ADI-26980 LAD5222_P06_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 89	1423	ALWYSNLWV	ADI-26980 LAD5222_P06_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 89	1424	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26980 LAD5222_P06_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 90	1425	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCATTGG	ADI-26981 LAD5222_P06_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 90	1426	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQGTLVTVSS	ADI-26981 LAD5222_P06_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 90	1427	FTFDAYAMN	ADI-26981 LAD5222_P06_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 90	1428	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26981 LAD5222_P06_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 90	1429	RIRSKYNDYATYYADSVKD	ADI-26981 LAD5222_P06_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 90	1430	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26981 LAD5222_P06_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 90	1431	VRHGNFGNYAVSWFAH	ADI-26981 LAD5222_P06_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 90	1432	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCAT	ADI-26981 LAD5222_P06_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 90	1433	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26981 LAD5222_P06_E02	Light chain variable region("LC") nucleic acid sequence
Ab 90	1434	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-26981 LAD5222_P06_E02	Light chain variable region ("LC") amino acid sequence
Ab 90	1435	GSSTGAVTTSNYAN	ADI-26981 LAD5222_P06_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 90	1436	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26981 LAD5222_P06_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 90	1437	GTDKRAP	ADI-26981 LAD5222_P06_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 90	1438	GGCACAGACAAGCGCGCTCCT	ADI-26981 LAD5222_P06_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 90	1439	ALWYSNLWV	ADI-26981 LAD5222_P06_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 90	1440	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-26981 LAD5222_P06_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 91	1441	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26982 LAD5223_P05_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 91	1442	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQGTLVTVSS	ADI-26982 LAD5223_P05_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 91	1443	FTFDTYAMN	ADI-26982 LAD5223_P05_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 91	1444	TTCACCTTTGACACATATGCCATGAAC	ADI-26982 LAD5223_P05_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 91	1445	RIRSKYNNYATYYADSVKD	ADI-26982 LAD5223_P05_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 91	1446	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26982 LAD5223_P05_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 91	1447	VRHGNFQGGYVSWFAH	ADI-26982 LAD5223_P05_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 91	1448	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-26982 LAD5223_P05_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 91	1449	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26982 LAD5223_P05_A03	Light chain variable region("LC") nucleic acid sequence
Ab 91	1450	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26982 LAD5223_P05_A03	Light chain variable region ("LC") amino acid sequence
Ab 91	1451	GSSTGAVTTSNYAN	ADI-26982 LAD5223_P05_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 91	1452	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26982 LAD5223_P05_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 91	1453	GTDKRAP	ADI-26982 LAD5223_P05_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 91	1454	GGCACAGACAAGCGCGCTCCT	ADI-26982 LAD5223_P05_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 91	1455	ALWYSDLWV	ADI-26982 LAD5223_P05_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 91	1456	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26982 LAD5223_P05_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 92	1457	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGCTTGGTG	ADI-26983 LAD5223_P05_C03	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 92	1458	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFAWWGQGTLVTVSS	ADI-26983 LAD5223_P05_C03	Heavy chain variable region ("HC") amino acid sequence
Ab 92	1459	FTFDTYAMN	ADI-26983 LAD5223_P05_C03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 92	1460	TTCACCTTTGACACATATGCCATGAAC	ADI-26983 LAD5223_P05_C03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 92	1461	RIRSKYNNYATYYADSVKD	ADI-26983 LAD5223_P05_C03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 92	1462	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26983 LAD5223_P05_C03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 92	1463	VRHGNFGGGYVSWFAW	ADI-26983 LAD5223_P05_C03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 92	1464	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGCTTGG	ADI-26983 LAD5223_P05_C03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 92	1465	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26983 LAD5223_P05_C03	Light chain variable region("LC") nucleic acid sequence
Ab 92	1466	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26983 LAD5223_P05_C03	Light chain variable region ("LC") amino acid sequence
Ab 92	1467	GSSTGAVTTSNYAN	ADI-26983 LAD5223_P05_C03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 92	1468	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26983 LAD5223_P05_C03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 92	1469	GTDKRAP	ADI-26983 LAD5223_P05_C03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 92	1470	GGCACAGACAAGCGCGCTCCT	ADI-26983 LAD5223_P05_C03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 92	1471	ALWYSDLWV	ADI-26983 LAD5223_P05_C03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 92	1472	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26983 LAD5223_P05_C03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 93	1473	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26984 LAD5223_P05_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 93	1474	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHANFGAGYVSWFAHWGQGTLVTVSS	ADI-26984 LAD5223_P05_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 93	1475	FTFDTYAMN	ADI-26984 LAD5223_P05_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 93	1476	TTCACCTTTGACACATATGCCATGAAC	ADI-26984 LAD5223_P05_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 93	1477	RIRSKYNNYATYYADSVKD	ADI-26984 LAD5223_P05_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 93	1478	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26984 LAD5223_P05_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 93	1479	VRHANFGAGYVSWFAH	ADI-26984 LAD5223_P05_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 93	1480	GTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTGGTTTGCTCAT	ADI-26984 LAD5223_P05_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 93	1481	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26984 LAD5223_P05_A04	Light chain variable region("LC") nucleic acid sequence
Ab 93	1482	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26984 LAD5223_P05_A04	Light chain variable region ("LC") amino acid sequence
Ab 93	1483	GSSTGAVTTSNYAN	ADI-26984 LAD5223_P05_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 93	1484	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26984 LAD5223_P05_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 93	1485	GTDKRAP	ADI-26984 LAD5223_P05_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 93	1486	GGCACAGACAAGCGCGCTCCT	ADI-26984 LAD5223_P05_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 93	1487	ALWYSDLWV	ADI-26984 LAD5223_P05_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 93	1488	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26984 LAD5223_P05_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 94	1489	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26985 LAD5223_P05_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 94	1490	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-26985 LAD5223_P05_D05	Heavy chain variable region ("HC") amino acid sequence
Ab 94	1491	FTFDTYAMN	ADI-26985 LAD5223_P05_D05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 94	1492	TTCACCTTTGACACATATGCCATGAAC	ADI-26985 LAD5223_P05_D05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 94	1493	RIRSKYNNYATYYADSVKD	ADI-26985 LAD5223_P05_D05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 94	1494	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26985 LAD5223_P05_D05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 94	1495	VRHGNFGEGYVSWFAH	ADI-26985 LAD5223_P05_D05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 94	1496	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-26985 LAD5223_P05_D05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 94	1497	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26985 LAD5223_P05_D05	Light chain variable region("LC") nucleic acid sequence
Ab 94	1498	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26985 LAD5223_P05_D05	Light chain variable region ("LC") amino acid sequence
Ab 94	1499	GSSTGAVTTSNYAN	ADI-26985 LAD5223_P05_D05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 94	1500	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26985 LAD5223_P05_D05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 94	1501	GTDKRAP	ADI-26985 LAD5223_P05_D05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 94	1502	GGCACAGACAAGCGCGCTCCT	ADI-26985 LAD5223_P05_D05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 94	1503	ALWYSDLWV	ADI-26985 LAD5223_P05_D05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 94	1504	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26985 LAD5223_P05_D05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 95	1505	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26986 LAD5223_P05_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 95	1506	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQGTLVTVSS	ADI-26986 LAD5223_P05_E04	Heavy chain variable region ("HC") amino acid sequence
Ab 95	1507	FTFDTYAMN	ADI-26986 LAD5223_P05_E04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 95	1508	TTCACCTTTGACACATATGCCATGAAC	ADI-26986 LAD5223_P05_E04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 95	1509	RIRSKYNNYATYYADSVKD	ADI-26986 LAD5223_P05_E04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 95	1510	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26986 LAD5223_P05_E04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 95	1511	VRHDNFGAGYVSWFAH	ADI-26986 LAD5223_P05_E04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 95	1512	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCAT	ADI-26986 LAD5223_P05_E04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 95	1513	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26986 LAD5223_P05_E04	Light chain variable region("LC") nucleic acid sequence
Ab 95	1514	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26986 LAD5223_P05_E04	Light chain variable region ("LC") amino acid sequence
Ab 95	1515	GSSTGAVTTSNYAN	ADI-26986 LAD5223_P05_E04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 95	1516	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26986 LAD5223_P05_E04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 95	1517	GTDKRAP	ADI-26986 LAD5223_P05_E04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 95	1518	GGCACAGACAAGCGCGCTCCT	ADI-26986 LAD5223_P05_E04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 95	1519	ALWYSDLWV	ADI-26986 LAD5223_P05_E04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 95	1520	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26986 LAD5223_P05_E04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 96	1521	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26987 LAD5223_P05_F05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 96	1522	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQGTLVTVSS	ADI-26987 LAD5223_P05_F05	Heavy chain variable region ("HC") amino acid sequence
Ab 96	1523	FTFDTYAMN	ADI-26987 LAD5223_P05_F05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 96	1524	TTCACCTTTGACACATATGCCATGAAC	ADI-26987 LAD5223_P05_F05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 96	1525	RIRSKYNNYATYYADSVKD	ADI-26987 LAD5223_P05_F05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 96	1526	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26987 LAD5223_P05_F05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 96	1527	VRHGNFGVGYVSWFAS	ADI-26987 LAD5223_P05_F05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 96	1528	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCT	ADI-26987 LAD5223_P05_F05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 96	1529	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26987 LAD5223_P05_F05	Light chain variable region("LC") nucleic acid sequence
Ab 96	1530	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26987 LAD5223_P05_F05	Light chain variable region ("LC") amino acid sequence
Ab 96	1531	GSSTGAVTTSNYAN	ADI-26987 LAD5223_P05_F05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 96	1532	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26987 LAD5223_P05_F05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 96	1533	GTDKRAP	ADI-26987 LAD5223_P05_F05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 96	1534	GGCACAGACAAGCGCGCTCCT	ADI-26987 LAD5223_P05_F05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 96	1535	ALWYSDLWV	ADI-26987 LAD5223_P05_F05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 96	1536	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26987 LAD5223_P05_F05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 97	1537	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26988 LAD5223_P05_B06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 97	1538	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQGTLVTVSS	ADI-26988 LAD5223_P05_B06	Heavy chain variable region ("HC") amino acid sequence
Ab 97	1539	FTFDTYAMN	ADI-26988 LAD5223_P05_B06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 97	1540	TTCACCTTTGACACATATGCCATGAAC	ADI-26988 LAD5223_P05_B06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 97	1541	RIRSKYNNYATYYADSVKD	ADI-26988 LAD5223_P05_B06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 97	1542	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26988 LAD5223_P05_B06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 97	1543	VRHGNFGGAYVSWFAH	ADI-26988 LAD5223_P05_B06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 97	1544	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCAT	ADI-26988 LAD5223_P05_B06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 97	1545	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26988 LAD5223_P05_B06	Light chain variable region("LC") nucleic acid sequence
Ab 97	1546	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26988 LAD5223_P05_B06	Light chain variable region ("LC") amino acid sequence
Ab 97	1547	GSSTGAVTTSNYAN	ADI-26988 LAD5223_P05_B06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 97	1548	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26988 LAD5223_P05_B06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 97	1549	GTDKRAP	ADI-26988 LAD5223_P05_B06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 97	1550	GGCACAGACAAGCGCGCTCCT	ADI-26988 LAD5223_P05_B06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 97	1551	ALWYSDLWV	ADI-26988 LAD5223_P05_B06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 97	1552	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26988 LAD5223_P05_B06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 98	1553	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26989 LAD5223_P05_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 98	1554	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQGTLVTVSS	ADI-26989 LAD5223_P05_F06	Heavy chain variable region ("HC") amino acid sequence
Ab 98	1555	FTFDTYAMN	ADI-26989 LAD5223_P05_F06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 98	1556	TTCACCTTTGACACATATGCCATGAAC	ADI-26989 LAD5223_P05_F06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 98	1557	RIRSKYNDYATYYADSVKD	ADI-26989 LAD5223_P05_F06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 98	1558	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26989 LAD5223_P05_F06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 98	1559	VRHGNFGEGYVSWFAH	ADI-26989 LAD5223_P05_F06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 98	1560	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTGGTTTGCTCAT	ADI-26989 LAD5223_P05_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 98	1561	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26989 LAD5223_P05_F06	Light chain variable region("LC") nucleic acid sequence
Ab 98	1562	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26989 LAD5223_P05_F06	Light chain variable region ("LC") amino acid sequence
Ab 98	1563	GSSTGAVTTSNYAN	ADI-26989 LAD5223_P05_F06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 98	1564	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26989 LAD5223_P05_F06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 98	1565	GTDKRAP	ADI-26989 LAD5223_P05_F06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 98	1566	GGCACAGACAAGCGCGCTCCT	ADI-26989 LAD5223_P05_F06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 98	1567	ALWYSDLWV	ADI-26989 LAD5223_P05_F06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 98	1568	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26989 LAD5223_P05_F06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 99	1569	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26990 LAD5223_P05_B07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 99	1570	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQGTLVTVSS	ADI-26990 LAD5223_P05_B07	Heavy chain variable region ("HC") amino acid sequence
Ab 99	1571	FTFDTYAMN	ADI-26990 LAD5223_P05_B07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 99	1572	TTCACCTTTGACACATATGCCATGAAC	ADI-26990 LAD5223_P05_B07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 99	1573	RIRSKYNDYATYYADSVKD	ADI-26990 LAD5223_P05_B07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 99	1574	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26990 LAD5223_P05_B07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 99	1575	VRHDNFGAGYVSWFAH	ADI-26990 LAD5223_P05_B07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 99	1576	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCAT	ADI-26990 LAD5223_P05_B07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 99	1577	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26990 LAD5223_P05_B07	Light chain variable region("LC") nucleic acid sequence
Ab 99	1578	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26990 LAD5223_P05_B07	Light chain variable region ("LC") amino acid sequence
Ab 99	1579	GSSTGAVTTSNYAN	ADI-26990 LAD5223_P05_B07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 99	1580	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26990 LAD5223_P05_B07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 99	1581	GTDKRAP	ADI-26990 LAD5223_P05_B07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 99	1582	GGCACAGACAAGCGCGCTCCT	ADI-26990 LAD5223_P05_B07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 99	1583	ALWYSDLWV	ADI-26990 LAD5223_P05_B07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 99	1584	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26990 LAD5223_P05_B07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 100	1585	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26991 LAD5223_P05_E07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 100	1586	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQGTLVTVSS	ADI-26991 LAD5223_P05_E07	Heavy chain variable region ("HC") amino acid sequence
Ab 100	1587	FTFDTYAMN	ADI-26991 LAD5223_P05_E07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 100	1588	TTCACCTTTGACACATATGCCATGAAC	ADI-26991 LAD5223_P05_E07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 100	1589	RIRSKYNDYATYYADSVKD	ADI-26991 LAD5223_P05_E07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 100	1590	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26991 LAD5223_P05_E07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 100	1591	VRHGNFGVGYVSWFAS	ADI-26991 LAD5223_P05_E07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 100	1592	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCT	ADI-26991 LAD5223_P05_E07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 100	1593	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26991 LAD5223_P05_E07	Light chain variable region("LC") nucleic acid sequence
Ab 100	1594	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26991 LAD5223_P05_E07	Light chain variable region ("LC") amino acid sequence
Ab 100	1595	GSSTGAVTTSNYAN	ADI-26991 LAD5223_P05_E07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 100	1596	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26991 LAD5223_P05_E07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 100	1597	GTDKRAP	ADI-26991 LAD5223_P05_E07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 100	1598	GGCACAGACAAGCGCGCTCCT	ADI-26991 LAD5223_P05_E07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 100	1599	ALWYSDLWV	ADI-26991 LAD5223_P05_E07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 100	1600	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26991 LAD5223_P05_E07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 101	1601	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26992 LAD5223_P05_D08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 101	1602	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQGTLVTVSS	ADI-26992 LAD5223_P05_D08	Heavy chain variable region ("HC") amino acid sequence
Ab 101	1603	FTFDTYAMN	ADI-26992 LAD5223_P05_D08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 101	1604	TTCACCTTTGACACATATGCCATGAAC	ADI-26992 LAD5223_P05_D08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 101	1605	RIRSKYNDYATYYADSVKD	ADI-26992 LAD5223_P05_D08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 101	1606	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26992 LAD5223_P05_D08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 101	1607	VRHGNFGGAYVSWFAH	ADI-26992 LAD5223_P05_D08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 101	1608	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTGGTTTGCTCAT	ADI-26992 LAD5223_P05_D08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 101	1609	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26992 LAD5223_P05_D08	Light chain variable region("LC") nucleic acid sequence
Ab 101	1610	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26992 LAD5223_P05_D08	Light chain variable region ("LC") amino acid sequence
Ab 101	1611	GSSTGAVTTSNYAN	ADI-26992 LAD5223_P05_D08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 101	1612	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26992 LAD5223_P05_D08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 101	1613	GTDKRAP	ADI-26992 LAD5223_P05_D08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 101	1614	GGCACAGACAAGCGCGCTCCT	ADI-26992 LAD5223_P05_D08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 101	1615	ALWYSDLWV	ADI-26992 LAD5223_P05_D08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 101	1616	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26992 LAD5223_P05_D08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 102	1617	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGGGCATTG	ADI-26993 LAD5223_P05_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 102	1618	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFGHWGQGTLVTVSS	ADI-26993 LAD5223_P05_F08	Heavy chain variable region ("HC") amino acid sequence
Ab 102	1619	FTFDAYAMN	ADI-26993 LAD5223_P05_F08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 102	1620	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26993 LAD5223_P05_F08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 102	1621	RIRSKYNDYATYYADSVKD	ADI-26993 LAD5223_P05_F08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 102	1622	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26993 LAD5223_P05_F08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 102	1623	VRHGNFGGGYVSWFGH	ADI-26993 LAD5223_P05_F08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 102	1624	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTGGTTTGGGCAT	ADI-26993 LAD5223_P05_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 102	1625	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26993 LAD5223_P05_F08	Light chain variable region("LC") nucleic acid sequence
Ab 102	1626	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26993 LAD5223_P05_F08	Light chain variable region ("LC") amino acid sequence
Ab 102	1627	GSSTGAVTTSNYAN	ADI-26993 LAD5223_P05_F08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 102	1628	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26993 LAD5223_P05_F08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 102	1629	GTDKRAP	ADI-26993 LAD5223_P05_F08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 102	1630	GGCACAGACAAGCGCGCTCCT	ADI-26993 LAD5223_P05_F08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 102	1631	ALWYSDLWV	ADI-26993 LAD5223_P05_F08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 102	1632	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26993 LAD5223_P05_F08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 103	1633	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTGGTTTGCTCATTG	ADI-26994 LAD5223_P05_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 103	1634	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNVGGGYVSWFAHWGQGTLVTVSS	ADI-26994 LAD5223_P05_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 103	1635	FTFDAYAMN	ADI-26994 LAD5223_P05_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 103	1636	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26994 LAD5223_P05_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 103	1637	RIRSKYNDYATYYADSVKD	ADI-26994 LAD5223_P05_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 103	1638	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26994 LAD5223_P05_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 103	1639	VRHGNVGGGYVSWFAH	ADI-26994 LAD5223_P05_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 103	1640	GTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-26994 LAD5223_P05_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 103	1641	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26994 LAD5223_P05_A09	Light chain variable region("LC") nucleic acid sequence
Ab 103	1642	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26994 LAD5223_P05_A09	Light chain variable region ("LC") amino acid sequence
Ab 103	1643	GSSTGAVTTSNYAN	ADI-26994 LAD5223_P05_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 103	1644	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26994 LAD5223_P05_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 103	1645	GTDKRAP	ADI-26994 LAD5223_P05_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 103	1646	GGCACAGACAAGCGCGCTCCT	ADI-26994 LAD5223_P05_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 103	1647	ALWYSDLWV	ADI-26994 LAD5223_P05_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 103	1648	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26994 LAD5223_P05_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 104	1649	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCATTGG	ADI-26995 LAD5223_P05_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 104	1650	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQGTLVTVSS	ADI-26995 LAD5223_P05_F09	Heavy chain variable region ("HC") amino acid sequence
Ab 104	1651	FTFDAYAMN	ADI-26995 LAD5223_P05_F09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 104	1652	TTCACCTTTGACGCTTATGCCATGAAC	ADI-26995 LAD5223_P05_F09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 104	1653	RIRSKYNDYATYYADSVKD	ADI-26995 LAD5223_P05_F09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 104	1654	AGGATTAGATCCAAGTATAACGATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-26995 LAD5223_P05_F09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 104	1655	VRHGNFGNYAVSWFAH	ADI-26995 LAD5223_P05_F09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 104	1656	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCAT	ADI-26995 LAD5223_P05_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 104	1657	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-26995 LAD5223_P05_F09	Light chain variable region("LC") nucleic acid sequence
Ab 104	1658	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGGGTKLTVL	ADI-26995 LAD5223_P05_F09	Light chain variable region ("LC") amino acid sequence
Ab 104	1659	GSSTGAVTTSNYAN	ADI-26995 LAD5223_P05_F09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 104	1660	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-26995 LAD5223_P05_F09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 104	1661	GTDKRAP	ADI-26995 LAD5223_P05_F09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 104	1662	GGCACAGACAAGCGCGCTCCT	ADI-26995 LAD5223_P05_F09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 104	1663	ALWYSDLWV	ADI-26995 LAD5223_P05_F09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 104	1664	GCGCTGTGGTACAGTGATCTGTGGGTG	ADI-26995 LAD5223_P05_F09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 105	1665	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28708 LAD4204_P01_B01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 105	1666	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28708 LAD4204_P01_B01	Heavy chain variable region ("HC") amino acid sequence
Ab 105	1667	FTFDTYAMN	ADI-28708 LAD4204_P01_B01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 105	1668	TTCACCTTTGACACATATGCCATGAAT	ADI-28708 LAD4204_P01_B01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 105	1669	RIRSKYNNYATYYADSVKD	ADI-28708 LAD4204_P01_B01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 105	1670	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28708 LAD4204_P01_B01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 105	1671	VRHGNFGNGYVSWFAH	ADI-28708 LAD4204_P01_B01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 105	1672	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28708 LAD4204_P01_B01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 105	1673	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28708 LAD4204_P01_B01	Light chain variable region("LC") nucleic acid sequence
Ab 105	1674	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28708 LAD4204_P01_B01	Light chain variable region ("LC") amino acid sequence
Ab 105	1675	GSSTGAVTTSNYAN	ADI-28708 LAD4204_P01_B01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 105	1676	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28708 LAD4204_P01_B01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 105	1677	GTDKRAP	ADI-28708 LAD4204_P01_B01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 105	1678	GGCACAGACAAGCGCGCTCCT	ADI-28708 LAD4204_P01_B01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 105	1679	ALWYSNLWV	ADI-28708 LAD4204_P01_B01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 105	1680	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28708 LAD4204_P01_B01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 106	1681	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28709 LAD4204_P01_E01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 106	1682	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28709 LAD4204_P01_E01	Heavy chain variable region ("HC") amino acid sequence
Ab 106	1683	FTFDTYAMN	ADI-28709 LAD4204_P01_E01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 106	1684	TTCACCTTTGACACATATGCCATGAAT	ADI-28709 LAD4204_P01_E01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 106	1685	RIRSKYNNYATYYADSVKD	ADI-28709 LAD4204_P01_E01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 106	1686	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28709 LAD4204_P01_E01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 106	1687	VRHGNFGNGYVSWFAH	ADI-28709 LAD4204_P01_E01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 106	1688	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28709 LAD4204_P01_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 106	1689	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28709 LAD4204_P01_E01	Light chain variable region("LC") nucleic acid sequence
Ab 106	1690	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28709 LAD4204_P01_E01	Light chain variable region ("LC") amino acid sequence
Ab 106	1691	GSSTGAVTTSNYAN	ADI-28709 LAD4204_P01_E01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 106	1692	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28709 LAD4204_P01_E01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 106	1693	GTDKRAP	ADI-28709 LAD4204_P01_E01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 106	1694	GGCACAGACAAGCGCGCTCCT	ADI-28709 LAD4204_P01_E01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 106	1695	ALWYSNLWV	ADI-28709 LAD4204_P01_E01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 106	1696	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28709 LAD4204_P01_E01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 107	1697	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28710 LAD4204_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 107	1698	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28710 LAD4204_P01_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 107	1699	FTFDTYAMN	ADI-28710 LAD4204_P01_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 107	1700	TTCACCTTTGACACATATGCCATGAAT	ADI-28710 LAD4204_P01_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 107	1701	RIRSKYNNYATYYADSVKD	ADI-28710 LAD4204_P01_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 107	1702	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28710 LAD4204_P01_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 107	1703	VRHGNFGNGYVSWFAH	ADI-28710 LAD4204_P01_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 107	1704	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28710 LAD4204_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 107	1705	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28710 LAD4204_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 107	1706	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28710 LAD4204_P01_A02	Light chain variable region ("LC") amino acid sequence
Ab 107	1707	GSSTGAVTTSNYAN	ADI-28710 LAD4204_P01_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 107	1708	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28710 LAD4204_P01_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 107	1709	GTDKRAP	ADI-28710 LAD4204_P01_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 107	1710	GGCACAGACAAGCGCGCTCCT	ADI-28710 LAD4204_P01_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 107	1711	VLWYSNLWV	ADI-28710 LAD4204_P01_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 107	1712	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28710 LAD4204_P01_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 108	1713	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28711 LAD4204_P01_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 108	1714	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28711 LAD4204_P01_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 108	1715	FTFDTYAMN	ADI-28711 LAD4204_P01_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 108	1716	TTCACCTTTGACACATATGCCATGAAT	ADI-28711 LAD4204_P01_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 108	1717	RIRSKYNNYATYYADSVKD	ADI-28711 LAD4204_P01_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 108	1718	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28711 LAD4204_P01_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 108	1719	VRHGNFGNGYVSWFAH	ADI-28711 LAD4204_P01_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 108	1720	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28711 LAD4204_P01_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 108	1721	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28711 LAD4204_P01_A03	Light chain variable region("LC") nucleic acid sequence
Ab 108	1722	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28711 LAD4204_P01_A03	Light chain variable region ("LC") amino acid sequence
Ab 108	1723	GSSTGAVTTSNYAN	ADI-28711 LAD4204_P01_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 108	1724	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28711 LAD4204_P01_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 108	1725	GTDKRAP	ADI-28711 LAD4204_P01_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 108	1726	GGCACAGACAAGCGCGCTCCT	ADI-28711 LAD4204_P01_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 108	1727	ALWYSNLWV	ADI-28711 LAD4204_P01_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 108	1728	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28711 LAD4204_P01_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 109	1729	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28712 LAD4204_P01_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 109	1730	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28712 LAD4204_P01_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 109	1731	FTFDTYAMN	ADI-28712 LAD4204_P01_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 109	1732	TTCACCTTTGACACATATGCCATGAAT	ADI-28712 LAD4204_P01_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 109	1733	RIRSKYNNYATYYADSVKD	ADI-28712 LAD4204_P01_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 109	1734	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28712 LAD4204_P01_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 109	1735	VRHGNFGNGYVSWFAH	ADI-28712 LAD4204_P01_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 109	1736	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28712 LAD4204_P01_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 109	1737	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28712 LAD4204_P01_E03	Light chain variable region("LC") nucleic acid sequence
Ab 109	1738	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28712 LAD4204_P01_E03	Light chain variable region ("LC") amino acid sequence
Ab 109	1739	GSSAGAVTTSNYAN	ADI-28712 LAD4204_P01_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 109	1740	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28712 LAD4204_P01_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 109	1741	GTDKRAP	ADI-28712 LAD4204_P01_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 109	1742	GGCACAGACAAGCGCGCTCCT	ADI-28712 LAD4204_P01_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 109	1743	ALWYSNLWV	ADI-28712 LAD4204_P01_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 109	1744	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28712 LAD4204_P01_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 110	1745	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28713 LAD4204_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 110	1746	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28713 LAD4204_P01_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 110	1747	FTFDTYAMN	ADI-28713 LAD4204_P01_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 110	1748	TTCACCTTTGACACATATGCCATGAAT	ADI-28713 LAD4204_P01_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 110	1749	RIRSKYNNYATYYADSVKD	ADI-28713 LAD4204_P01_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 110	1750	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28713 LAD4204_P01_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 110	1751	VRHGNFGNGYVSWFAH	ADI-28713 LAD4204_P01_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 110	1752	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28713 LAD4204_P01_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 110	1753	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28713 LAD4204_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 110	1754	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28713 LAD4204_P01_A04	Light chain variable region ("LC") amino acid sequence
Ab 110	1755	GSSTGAVTTSNYAN	ADI-28713 LAD4204_P01_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 110	1756	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28713 LAD4204_P01_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 110	1757	GTDKRAP	ADI-28713 LAD4204_P01_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 110	1758	GGCACAGACAAGCGCGCTCCT	ADI-28713 LAD4204_P01_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 110	1759	ALWYSNLWV	ADI-28713 LAD4204_P01_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 110	1760	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28713 LAD4204_P01_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 111	1761	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28714 LAD4204_P01_H04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 111	1762	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28714 LAD4204_P01_H04	Heavy chain variable region ("HC") amino acid sequence
Ab 111	1763	FTFDTYAMN	ADI-28714 LAD4204_P01_H04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 111	1764	TTCACCTTTGACACATATGCCATGAAT	ADI-28714 LAD4204_P01_H04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 111	1765	RIRSKYNNYATYYADSVKD	ADI-28714 LAD4204_P01_H04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 111	1766	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28714 LAD4204_P01_H04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 111	1767	VRHGNFGNGYVSWFAH	ADI-28714 LAD4204_P01_H04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 111	1768	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28714 LAD4204_P01_H04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 111	1769	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28714 LAD4204_P01_H04	Light chain variable region("LC") nucleic acid sequence
Ab 111	1770	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28714 LAD4204_P01_H04	Light chain variable region ("LC") amino acid sequence
Ab 111	1771	GSSTGAVTTSNYAN	ADI-28714 LAD4204_P01_H04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 111	1772	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28714 LAD4204_P01_H04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 111	1773	GTDKRAP	ADI-28714 LAD4204_P01_H04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 111	1774	GGCACAGACAAGCGCGCTCCT	ADI-28714 LAD4204_P01_H04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 111	1775	ALWYNNLWV	ADI-28714 LAD4204_P01_H04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 111	1776	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28714 LAD4204_P01_H04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 112	1777	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28715 LAD4204_P01_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 112	1778	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28715 LAD4204_P01_C05	Heavy chain variable region ("HC") amino acid sequence
Ab 112	1779	FTFDTYAMN	ADI-28715 LAD4204_P01_C05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 112	1780	TTCACCTTTGACACATATGCCATGAAT	ADI-28715 LAD4204_P01_C05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 112	1781	RIRSKYNNYATYYADSVKD	ADI-28715 LAD4204_P01_C05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 112	1782	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28715 LAD4204_P01_C05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 112	1783	VRHGNFGNGYVSWFAH	ADI-28715 LAD4204_P01_C05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 112	1784	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28715 LAD4204_P01_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 112	1785	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28715 LAD4204_P01_C05	Light chain variable region("LC") nucleic acid sequence
Ab 112	1786	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28715 LAD4204_P01_C05	Light chain variable region ("LC") amino acid sequence
Ab 112	1787	GSSTGAVTTSNYAN	ADI-28715 LAD4204_P01_C05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 112	1788	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28715 LAD4204_P01_C05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 112	1789	GTDKRAP	ADI-28715 LAD4204_P01_C05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 112	1790	GGCACAGACAAGCGCGCTCCT	ADI-28715 LAD4204_P01_C05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 112	1791	VLWYSNLWV	ADI-28715 LAD4204_P01_C05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 112	1792	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28715 LAD4204_P01_C05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 113	1793	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28716 LAD4204_P01_G05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 113	1794	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28716 LAD4204_P01_G05	Heavy chain variable region ("HC") amino acid sequence
Ab 113	1795	FTFDTYAMN	ADI-28716 LAD4204_P01_G05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 113	1796	TTCACCTTTGACACATATGCCATGAAT	ADI-28716 LAD4204_P01_G05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 113	1797	RIRSKYNNYATYYADSVKD	ADI-28716 LAD4204_P01_G05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 113	1798	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28716 LAD4204_P01_G05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 113	1799	VRHGNFGNGYVSWFAH	ADI-28716 LAD4204_P01_G05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 113	1800	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28716 LAD4204_P01_G05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 113	1801	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28716 LAD4204_P01_G05	Light chain variable region("LC") nucleic acid sequence
Ab 113	1802	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28716 LAD4204_P01_G05	Light chain variable region ("LC") amino acid sequence
Ab 113	1803	GSSAGAVTTSNYAN	ADI-28716 LAD4204_P01_G05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 113	1804	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28716 LAD4204_P01_G05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 113	1805	GTDKRAP	ADI-28716 LAD4204_P01_G05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 113	1806	GGCACAGACAAGCGCGCTCCT	ADI-28716 LAD4204_P01_G05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 113	1807	ALWYSNLWV	ADI-28716 LAD4204_P01_G05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 113	1808	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28716 LAD4204_P01_G05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 114	1809	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28717 LAD4204_P01_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 114	1810	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28717 LAD4204_P01_A07	Heavy chain variable region ("HC") amino acid sequence
Ab 114	1811	FTFDTYAMN	ADI-28717 LAD4204_P01_A07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 114	1812	TTCACCTTTGACACATATGCCATGAAT	ADI-28717 LAD4204_P01_A07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 114	1813	RIRSKYNNYATYYADSVKD	ADI-28717 LAD4204_P01_A07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 114	1814	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28717 LAD4204_P01_A07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 114	1815	VRHGNFGNGYVSWFAH	ADI-28717 LAD4204_P01_A07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 114	1816	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28717 LAD4204_P01_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 114	1817	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28717 LAD4204_P01_A07	Light chain variable region("LC") nucleic acid sequence
Ab 114	1818	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28717 LAD4204_P01_A07	Light chain variable region ("LC") amino acid sequence
Ab 114	1819	GSSTGAVTTSNYAN	ADI-28717 LAD4204_P01_A07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 114	1820	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28717 LAD4204_P01_A07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 114	1821	GTDKRAP	ADI-28717 LAD4204_P01_A07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 114	1822	GGCACAGACAAGCGCGCTCCT	ADI-28717 LAD4204_P01_A07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 114	1823	ALWYNNLWV	ADI-28717 LAD4204_P01_A07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 114	1824	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28717 LAD4204_P01_A07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 115	1825	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28718 LAD4204_P01_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 115	1826	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28718 LAD4204_P01_A08	Heavy chain variable region ("HC") amino acid sequence
Ab 115	1827	FTFDTYAMN	ADI-28718 LAD4204_P01_A08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 115	1828	TTCACCTTTGACACATATGCCATGAAT	ADI-28718 LAD4204_P01_A08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 115	1829	RIRSKYNNYATYYADSVKD	ADI-28718 LAD4204_P01_A08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 115	1830	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28718 LAD4204_P01_A08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 115	1831	VRHGNFGNGYVSWFAH	ADI-28718 LAD4204_P01_A08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 115	1832	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28718 LAD4204_P01_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 115	1833	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28718 LAD4204_P01_A08	Light chain variable region("LC") nucleic acid sequence
Ab 115	1834	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28718 LAD4204_P01_A08	Light chain variable region ("LC") amino acid sequence
Ab 115	1835	GSSTGAVTTSNYAN	ADI-28718 LAD4204_P01_A08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 115	1836	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28718 LAD4204_P01_A08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 115	1837	GTDKRAP	ADI-28718 LAD4204_P01_A08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 115	1838	GGCACAGACAAGCGCGCTCCT	ADI-28718 LAD4204_P01_A08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 115	1839	VLWYSNLWV	ADI-28718 LAD4204_P01_A08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 115	1840	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28718 LAD4204_P01_A08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 116	1841	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28719 LAD4205_P01_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 116	1842	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28719 LAD4205_P01_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 116	1843	FTFDTYAMN	ADI-28719 LAD4205_P01_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 116	1844	TTCACCTTTGACACATATGCCATGAAT	ADI-28719 LAD4205_P01_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 116	1845	RIRSKYNNYATYYADSVKG	ADI-28719 LAD4205_P01_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 116	1846	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28719 LAD4205_P01_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 116	1847	VRHGNFGNSYVSWFAH	ADI-28719 LAD4205_P01_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 116	1848	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28719 LAD4205_P01_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 116	1849	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28719 LAD4205_P01_A09	Light chain variable region("LC") nucleic acid sequence
Ab 116	1850	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28719 LAD4205_P01_A09	Light chain variable region ("LC") amino acid sequence
Ab 116	1851	GSSTGAVTTSNYAN	ADI-28719 LAD4205_P01_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 116	1852	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28719 LAD4205_P01_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 116	1853	GTDKRAP	ADI-28719 LAD4205_P01_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 116	1854	GGCACAGACAAGCGCGCTCCT	ADI-28719 LAD4205_P01_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 116	1855	ALWYSNLWV	ADI-28719 LAD4205_P01_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 116	1856	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28719 LAD4205_P01_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 117	1857	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28720 LAD4205_P01_G09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 117	1858	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28720 LAD4205_P01_G09	Heavy chain variable region ("HC") amino acid sequence
Ab 117	1859	FTFDTYAMN	ADI-28720 LAD4205_P01_G09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 117	1860	TTCACCTTTGACACATATGCCATGAAT	ADI-28720 LAD4205_P01_G09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 117	1861	RIRSKYNNYATYYADSVKG	ADI-28720 LAD4205_P01_G09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 117	1862	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28720 LAD4205_P01_G09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 117	1863	VRHGNFGNSYVSWFAH	ADI-28720 LAD4205_P01_G09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 117	1864	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28720 LAD4205_P01_G09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 117	1865	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28720 LAD4205_P01_G09	Light chain variable region("LC") nucleic acid sequence
Ab 117	1866	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28720 LAD4205_P01_G09	Light chain variable region ("LC") amino acid sequence
Ab 117	1867	GSSTGAVTTSNYAN	ADI-28720 LAD4205_P01_G09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 117	1868	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28720 LAD4205_P01_G09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 117	1869	GTDKRAP	ADI-28720 LAD4205_P01_G09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 117	1870	GGCACAGACAAGCGCGCTCCT	ADI-28720 LAD4205_P01_G09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 117	1871	ALWYSNLWV	ADI-28720 LAD4205_P01_G09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 117	1872	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28720 LAD4205_P01_G09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 118	1873	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28721 LAD4205_P01_A10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 118	1874	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28721 LAD4205_P01_A10	Heavy chain variable region ("HC") amino acid sequence
Ab 118	1875	FTFDTYAMN	ADI-28721 LAD4205_P01_A10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 118	1876	TTCACCTTTGACACATATGCCATGAAT	ADI-28721 LAD4205_P01_A10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 118	1877	RIRSKYNNYATYYADSVKG	ADI-28721 LAD4205_P01_A10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 118	1878	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28721 LAD4205_P01_A10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 118	1879	VRHGNFGNSYVSWFAH	ADI-28721 LAD4205_P01_A10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 118	1880	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28721 LAD4205_P01_A10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 118	1881	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28721 LAD4205_P01_A10	Light chain variable region("LC") nucleic acid sequence
Ab 118	1882	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28721 LAD4205_P01_A10	Light chain variable region ("LC") amino acid sequence
Ab 118	1883	GSSTGAVTTSNYAN	ADI-28721 LAD4205_P01_A10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 118	1884	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28721 LAD4205_P01_A10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 118	1885	GTDKRAP	ADI-28721 LAD4205_P01_A10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 118	1886	GGCACAGACAAGCGCGCTCCT	ADI-28721 LAD4205_P01_A10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 118	1887	VLWYSNLWV	ADI-28721 LAD4205_P01_A10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 118	1888	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28721 LAD4205_P01_A10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 119	1889	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28722 LAD4205_P01_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 119	1890	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28722 LAD4205_P01_E10	Heavy chain variable region ("HC") amino acid sequence
Ab 119	1891	FTFDTYAMN	ADI-28722 LAD4205_P01_E10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 119	1892	TTCACCTTTGACACATATGCCATGAAT	ADI-28722 LAD4205_P01_E10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 119	1893	RIRSKYNNYATYYADSVKG	ADI-28722 LAD4205_P01_E10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 119	1894	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28722 LAD4205_P01_E10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 119	1895	VRHGNFGNSYVSWFAH	ADI-28722 LAD4205_P01_E10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 119	1896	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28722 LAD4205_P01_E10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 119	1897	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28722 LAD4205_P01_E10	Light chain variable region("LC") nucleic acid sequence
Ab 119	1898	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28722 LAD4205_P01_E10	Light chain variable region ("LC") amino acid sequence
Ab 119	1899	GSSTGAVTTSNYAN	ADI-28722 LAD4205_P01_E10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 119	1900	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28722 LAD4205_P01_E10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 119	1901	GTDKRAP	ADI-28722 LAD4205_P01_E10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 119	1902	GGCACAGACAAGCGCGCTCCT	ADI-28722 LAD4205_P01_E10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 119	1903	ALWYSNHWV	ADI-28722 LAD4205_P01_E10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 119	1904	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28722 LAD4205_P01_E10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 120	1905	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28723 LAD4205_P01_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 120	1906	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28723 LAD4205_P01_A11	Heavy chain variable region ("HC") amino acid sequence
Ab 120	1907	FTFDTYAMN	ADI-28723 LAD4205_P01_A11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 120	1908	TTCACCTTTGACACATATGCCATGAAT	ADI-28723 LAD4205_P01_A11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 120	1909	RIRSKYNNYATYYADSVKG	ADI-28723 LAD4205_P01_A11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 120	1910	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28723 LAD4205_P01_A11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 120	1911	VRHGNFGNSYVSWFAH	ADI-28723 LAD4205_P01_A11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 120	1912	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28723 LAD4205_P01_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 120	1913	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28723 LAD4205_P01_A11	Light chain variable region("LC") nucleic acid sequence
Ab 120	1914	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28723 LAD4205_P01_A11	Light chain variable region ("LC") amino acid sequence
Ab 120	1915	GSSTGAVTTSNYAN	ADI-28723 LAD4205_P01_A11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 120	1916	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28723 LAD4205_P01_A11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 120	1917	GTDKRAP	ADI-28723 LAD4205_P01_A11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 120	1918	GGCACAGACAAGCGCGCTCCT	ADI-28723 LAD4205_P01_A11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 120	1919	ALWYSNLWV	ADI-28723 LAD4205_P01_A11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 120	1920	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28723 LAD4205_P01_A11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 121	1921	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28724 LAD4205_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 121	1922	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28724 LAD4205_P01_A12	Heavy chain variable region ("HC") amino acid sequence
Ab 121	1923	FTFDTYAMN	ADI-28724 LAD4205_P01_A12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 121	1924	TTCACCTTTGACACATATGCCATGAAT	ADI-28724 LAD4205_P01_A12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 121	1925	RIRSKYNNYATYYADSVKG	ADI-28724 LAD4205_P01_A12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 121	1926	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28724 LAD4205_P01_A12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 121	1927	VRHGNFGNSYVSWFAH	ADI-28724 LAD4205_P01_A12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 121	1928	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28724 LAD4205_P01_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 121	1929	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28724 LAD4205_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 121	1930	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28724 LAD4205_P01_A12	Light chain variable region ("LC") amino acid sequence
Ab 121	1931	GSSTGAVTTSNYAN	ADI-28724 LAD4205_P01_A12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 121	1932	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28724 LAD4205_P01_A12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 121	1933	GTDKRAP	ADI-28724 LAD4205_P01_A12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 121	1934	GGCACAGACAAGCGCGCTCCT	ADI-28724 LAD4205_P01_A12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 121	1935	ALWYSNLWV	ADI-28724 LAD4205_P01_A12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 121	1936	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28724 LAD4205_P01_A12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 122	1937	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28725 LAD4205_P01_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 122	1938	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28725 LAD4205_P01_F12	Heavy chain variable region ("HC") amino acid sequence
Ab 122	1939	FTFDTYAMN	ADI-28725 LAD4205_P01_F12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 122	1940	TTCACCTTTGACACATATGCCATGAAT	ADI-28725 LAD4205_P01_F12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 122	1941	RIRSKYNNYATYYADSVKG	ADI-28725 LAD4205_P01_F12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 122	1942	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28725 LAD4205_P01_F12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 122	1943	VRHGNFGNSYVSWFAH	ADI-28725 LAD4205_P01_F12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 122	1944	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28725 LAD4205_P01_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 122	1945	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28725 LAD4205_P01_F12	Light chain variable region("LC") nucleic acid sequence
Ab 122	1946	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28725 LAD4205_P01_F12	Light chain variable region ("LC") amino acid sequence
Ab 122	1947	GSSTGAVTTSNYAN	ADI-28725 LAD4205_P01_F12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 122	1948	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28725 LAD4205_P01_F12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 122	1949	GTDKRAP	ADI-28725 LAD4205_P01_F12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 122	1950	GGCACAGACAAGCGCGCTCCT	ADI-28725 LAD4205_P01_F12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 122	1951	ALWYNNLWV	ADI-28725 LAD4205_P01_F12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 122	1952	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28725 LAD4205_P01_F12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 123	1953	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28726 LAD4205_P02_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 123	1954	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28726 LAD4205_P02_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 123	1955	FTFDTYAMN	ADI-28726 LAD4205_P02_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 123	1956	TTCACCTTTGACACATATGCCATGAAT	ADI-28726 LAD4205_P02_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 123	1957	RIRSKYNNYATYYADSVKG	ADI-28726 LAD4205_P02_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 123	1958	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28726 LAD4205_P02_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 123	1959	VRHGNFGNSYVSWFAH	ADI-28726 LAD4205_P02_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 123	1960	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28726 LAD4205_P02_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 123	1961	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28726 LAD4205_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 123	1962	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28726 LAD4205_P02_A01	Light chain variable region ("LC") amino acid sequence
Ab 123	1963	GSSTGAVTTSNYAN	ADI-28726 LAD4205_P02_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 123	1964	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28726 LAD4205_P02_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 123	1965	GTDKRAP	ADI-28726 LAD4205_P02_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 123	1966	GGCACAGACAAGCGCGCTCCT	ADI-28726 LAD4205_P02_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 123	1967	VLWYSNLWV	ADI-28726 LAD4205_P02_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 123	1968	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28726 LAD4205_P02_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 124	1969	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28727 LAD4205_P02_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 124	1970	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28727 LAD4205_P02_F01	Heavy chain variable region ("HC") amino acid sequence
Ab 124	1971	FTFDTYAMN	ADI-28727 LAD4205_P02_F01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 124	1972	TTCACCTTTGACACATATGCCATGAAT	ADI-28727 LAD4205_P02_F01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 124	1973	RIRSKYNNYATYYADSVKG	ADI-28727 LAD4205_P02_F01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 124	1974	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28727 LAD4205_P02_F01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 124	1975	VRHGNFGNSYVSWFAH	ADI-28727 LAD4205_P02_F01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 124	1976	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28727 LAD4205_P02_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 124	1977	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28727 LAD4205_P02_F01	Light chain variable region("LC") nucleic acid sequence
Ab 124	1978	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28727 LAD4205_P02_F01	Light chain variable region ("LC") amino acid sequence
Ab 124	1979	GSSTGAVTTSNYAN	ADI-28727 LAD4205_P02_F01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 124	1980	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28727 LAD4205_P02_F01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 124	1981	GTDKRAP	ADI-28727 LAD4205_P02_F01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 124	1982	GGCACAGACAAGCGCGCTCCT	ADI-28727 LAD4205_P02_F01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 124	1983	ALWYSNHWV	ADI-28727 LAD4205_P02_F01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 124	1984	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28727 LAD4205_P02_F01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 125	1985	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28728 LAD4205_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 125	1986	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28728 LAD4205_P02_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 125	1987	FTFDTYAMN	ADI-28728 LAD4205_P02_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 125	1988	TTCACCTTTGACACATATGCCATGAAT	ADI-28728 LAD4205_P02_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 125	1989	RIRSKYNNYATYYADSVKG	ADI-28728 LAD4205_P02_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 125	1990	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28728 LAD4205_P02_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 125	1991	VRHGNFGNSYVSWFAH	ADI-28728 LAD4205_P02_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 125	1992	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28728 LAD4205_P02_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 125	1993	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28728 LAD4205_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 125	1994	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28728 LAD4205_P02_A02	Light chain variable region ("LC") amino acid sequence
Ab 125	1995	GSSAGAVTTSNYAN	ADI-28728 LAD4205_P02_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 125	1996	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28728 LAD4205_P02_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 125	1997	GTDKRAP	ADI-28728 LAD4205_P02_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 125	1998	GGCACAGACAAGCGCGCTCCT	ADI-28728 LAD4205_P02_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 125	1999	ALWYSNLWV	ADI-28728 LAD4205_P02_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 125	2000	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28728 LAD4205_P02_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 126	2001	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28729 LAD4205_P02_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 126	2002	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28729 LAD4205_P02_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 126	2003	FTFDTYAMN	ADI-28729 LAD4205_P02_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 126	2004	TTCACCTTTGACACATATGCCATGAAT	ADI-28729 LAD4205_P02_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 126	2005	RIRSKYNNYATYYADSVKG	ADI-28729 LAD4205_P02_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 126	2006	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28729 LAD4205_P02_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 126	2007	VRHGNFGNSYVSWFAH	ADI-28729 LAD4205_P02_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 126	2008	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28729 LAD4205_P02_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 126	2009	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28729 LAD4205_P02_E02	Light chain variable region("LC") nucleic acid sequence
Ab 126	2010	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28729 LAD4205_P02_E02	Light chain variable region ("LC") amino acid sequence
Ab 126	2011	GSSAGAVTTSNYAN	ADI-28729 LAD4205_P02_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 126	2012	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28729 LAD4205_P02_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 126	2013	GTDKRAP	ADI-28729 LAD4205_P02_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 126	2014	GGCACAGACAAGCGCGCTCCT	ADI-28729 LAD4205_P02_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 126	2015	VLWYSNLWV	ADI-28729 LAD4205_P02_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 126	2016	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28729 LAD4205_P02_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 127	2017	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28730 LAD4205_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 127	2018	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28730 LAD4205_P02_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 127	2019	FTFDTYAMN	ADI-28730 LAD4205_P02_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 127	2020	TTCACCTTTGACACATATGCCATGAAT	ADI-28730 LAD4205_P02_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 127	2021	RIRSKYNNYATYYADSVKG	ADI-28730 LAD4205_P02_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 127	2022	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28730 LAD4205_P02_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 127	2023	VRHGNFGNSYVSWFAH	ADI-28730 LAD4205_P02_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 127	2024	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28730 LAD4205_P02_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 127	2025	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28730 LAD4205_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 127	2026	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28730 LAD4205_P02_A03	Light chain variable region ("LC") amino acid sequence
Ab 127	2027	GSSAGAVTTSNYAN	ADI-28730 LAD4205_P02_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 127	2028	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28730 LAD4205_P02_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 127	2029	GTDKRAP	ADI-28730 LAD4205_P02_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 127	2030	GGCACAGACAAGCGCGCTCCT	ADI-28730 LAD4205_P02_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 127	2031	ALWYSNHWV	ADI-28730 LAD4205_P02_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 127	2032	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28730 LAD4205_P02_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 128	2033	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28731 LAD4205_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 128	2034	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28731 LAD4205_P02_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 128	2035	FTFDTYAMN	ADI-28731 LAD4205_P02_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 128	2036	TTCACCTTTGACACATATGCCATGAAT	ADI-28731 LAD4205_P02_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 128	2037	RIRSKYNNYATYYADSVKG	ADI-28731 LAD4205_P02_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 128	2038	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28731 LAD4205_P02_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 128	2039	VRHGNFGNSYVSWFAH	ADI-28731 LAD4205_P02_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 128	2040	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28731 LAD4205_P02_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 128	2041	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28731 LAD4205_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 128	2042	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28731 LAD4205_P02_E03	Light chain variable region ("LC") amino acid sequence
Ab 128	2043	GSSTGAVTTSNYAN	ADI-28731 LAD4205_P02_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 128	2044	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28731 LAD4205_P02_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 128	2045	GTDKRAP	ADI-28731 LAD4205_P02_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 128	2046	GGCACAGACAAGCGCGCTCCT	ADI-28731 LAD4205_P02_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 128	2047	ALWYNNLWV	ADI-28731 LAD4205_P02_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 128	2048	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28731 LAD4205_P02_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 129	2049	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28732 LAD4205_P02_C04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 129	2050	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28732 LAD4205_P02_C04	Heavy chain variable region ("HC") amino acid sequence
Ab 129	2051	FTFDTYAMN	ADI-28732 LAD4205_P02_C04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 129	2052	TTCACCTTTGACACATATGCCATGAAT	ADI-28732 LAD4205_P02_C04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 129	2053	RIRSKYNNYATYYADSVKG	ADI-28732 LAD4205_P02_C04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 129	2054	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28732 LAD4205_P02_C04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 129	2055	VRHGNFGNSYVSWFAH	ADI-28732 LAD4205_P02_C04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 129	2056	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28732 LAD4205_P02_C04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 129	2057	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28732 LAD4205_P02_C04	Light chain variable region("LC") nucleic acid sequence
Ab 129	2058	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28732 LAD4205_P02_C04	Light chain variable region ("LC") amino acid sequence
Ab 129	2059	GSSTGAVTTSNYAN	ADI-28732 LAD4205_P02_C04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 129	2060	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28732 LAD4205_P02_C04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 129	2061	GTDKRAP	ADI-28732 LAD4205_P02_C04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 129	2062	GGCACAGACAAGCGCGCTCCT	ADI-28732 LAD4205_P02_C04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 129	2063	VLWYSNLWV	ADI-28732 LAD4205_P02_C04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 129	2064	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28732 LAD4205_P02_C04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 130	2065	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28733 LAD4206_P01_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 130	2066	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28733 LAD4206_P01_D05	Heavy chain variable region ("HC") amino acid sequence
Ab 130	2067	FTFDTYAMN	ADI-28733 LAD4206_P01_D05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 130	2068	TTCACCTTTGACACATATGCCATGAAT	ADI-28733 LAD4206_P01_D05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 130	2069	RIRSKYNNYATYYADSVKD	ADI-28733 LAD4206_P01_D05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 130	2070	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28733 LAD4206_P01_D05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 130	2071	VRHSNFGNSYVSWFAH	ADI-28733 LAD4206_P01_D05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 130	2072	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28733 LAD4206_P01_D05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 130	2073	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28733 LAD4206_P01_D05	Light chain variable region("LC") nucleic acid sequence
Ab 130	2074	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28733 LAD4206_P01_D05	Light chain variable region ("LC") amino acid sequence
Ab 130	2075	GSSTGAVTTSNYAN	ADI-28733 LAD4206_P01_D05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 130	2076	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28733 LAD4206_P01_D05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 130	2077	GTDKRAP	ADI-28733 LAD4206_P01_D05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 130	2078	GGCACAGACAAGCGCGCTCCT	ADI-28733 LAD4206_P01_D05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 130	2079	ALWYSNLWV	ADI-28733 LAD4206_P01_D05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 130	2080	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28733 LAD4206_P01_D05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 131	2081	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28734 LAD4206_P01_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 131	2082	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28734 LAD4206_P01_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 131	2083	FTFDTYAMN	ADI-28734 LAD4206_P01_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 131	2084	TTCACCTTTGACACATATGCCATGAAT	ADI-28734 LAD4206_P01_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 131	2085	RIRSKYNNYATYYADSVKD	ADI-28734 LAD4206_P01_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 131	2086	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28734 LAD4206_P01_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 131	2087	VRHSNFGNSYVSWFAH	ADI-28734 LAD4206_P01_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 131	2088	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28734 LAD4206_P01_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 131	2089	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28734 LAD4206_P01_E05	Light chain variable region("LC") nucleic acid sequence
Ab 131	2090	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28734 LAD4206_P01_E05	Light chain variable region ("LC") amino acid sequence
Ab 131	2091	GSSTGAVTTSNYAN	ADI-28734 LAD4206_P01_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 131	2092	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28734 LAD4206_P01_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 131	2093	GTDKRAP	ADI-28734 LAD4206_P01_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 131	2094	GGCACAGACAAGCGCGCTCCT	ADI-28734 LAD4206_P01_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 131	2095	ALWYSNLWV	ADI-28734 LAD4206_P01_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 131	2096	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28734 LAD4206_P01_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 132	2097	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28735 LAD4206_P01_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 132	2098	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28735 LAD4206_P01_D06	Heavy chain variable region ("HC") amino acid sequence
Ab 132	2099	FTFDTYAMN	ADI-28735 LAD4206_P01_D06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 132	2100	TTCACCTTTGACACATATGCCATGAAT	ADI-28735 LAD4206_P01_D06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 132	2101	RIRSKYNNYATYYADSVKD	ADI-28735 LAD4206_P01_D06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 132	2102	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28735 LAD4206_P01_D06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 132	2103	VRHSNFGNSYVSWFAH	ADI-28735 LAD4206_P01_D06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 132	2104	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28735 LAD4206_P01_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 132	2105	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28735 LAD4206_P01_D06	Light chain variable region("LC") nucleic acid sequence
Ab 132	2106	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28735 LAD4206_P01_D06	Light chain variable region ("LC") amino acid sequence
Ab 132	2107	GSSTGAVTTSNYAN	ADI-28735 LAD4206_P01_D06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 132	2108	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28735 LAD4206_P01_D06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 132	2109	GTDKRAP	ADI-28735 LAD4206_P01_D06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 132	2110	GGCACAGACAAGCGCGCTCCT	ADI-28735 LAD4206_P01_D06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 132	2111	VLWYSNLWV	ADI-28735 LAD4206_P01_D06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 132	2112	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28735 LAD4206_P01_D06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 133	2113	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28736 LAD4206_P01_E06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 133	2114	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28736 LAD4206_P01_E06	Heavy chain variable region ("HC") amino acid sequence
Ab 133	2115	FTFDTYAMN	ADI-28736 LAD4206_P01_E06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 133	2116	TTCACCTTTGACACATATGCCATGAAT	ADI-28736 LAD4206_P01_E06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 133	2117	RIRSKYNNYATYYADSVKD	ADI-28736 LAD4206_P01_E06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 133	2118	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28736 LAD4206_P01_E06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 133	2119	VRHSNFGNSYVSWFAH	ADI-28736 LAD4206_P01_E06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 133	2120	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28736 LAD4206_P01_E06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 133	2121	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28736 LAD4206_P01_E06	Light chain variable region("LC") nucleic acid sequence
Ab 133	2122	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28736 LAD4206_P01_E06	Light chain variable region ("LC") amino acid sequence
Ab 133	2123	GSSTGAVTTSNYAN	ADI-28736 LAD4206_P01_E06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 133	2124	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28736 LAD4206_P01_E06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 133	2125	GTDKRAP	ADI-28736 LAD4206_P01_E06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 133	2126	GGCACAGACAAGCGCGCTCCT	ADI-28736 LAD4206_P01_E06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 133	2127	ALWYSNHWV	ADI-28736 LAD4206_P01_E06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 133	2128	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28736 LAD4206_P01_E06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 134	2129	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28737 LAD4206_P01_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 134	2130	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28737 LAD4206_P01_A07	Heavy chain variable region ("HC") amino acid sequence
Ab 134	2131	FTFDTYAMN	ADI-28737 LAD4206_P01_A07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 134	2132	TTCACCTTTGACACATATGCCATGAAT	ADI-28737 LAD4206_P01_A07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 134	2133	RIRSKYNNYATYYADSVKD	ADI-28737 LAD4206_P01_A07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 134	2134	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28737 LAD4206_P01_A07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 134	2135	VRHSNFGNSYVSWFAH	ADI-28737 LAD4206_P01_A07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 134	2136	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28737 LAD4206_P01_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 134	2137	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28737 LAD4206_P01_A07	Light chain variable region("LC") nucleic acid sequence
Ab 134	2138	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28737 LAD4206_P01_A07	Light chain variable region ("LC") amino acid sequence
Ab 134	2139	GSSTGAVTTSNYAN	ADI-28737 LAD4206_P01_A07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 134	2140	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28737 LAD4206_P01_A07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 134	2141	GTDKRAP	ADI-28737 LAD4206_P01_A07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 134	2142	GGCACAGACAAGCGCGCTCCT	ADI-28737 LAD4206_P01_A07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 134	2143	ALWYSNLWV	ADI-28737 LAD4206_P01_A07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 134	2144	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28737 LAD4206_P01_A07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 135	2145	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28738 LAD4206_P01_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 135	2146	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28738 LAD4206_P01_F07	Heavy chain variable region ("HC") amino acid sequence
Ab 135	2147	FTFDTYAMN	ADI-28738 LAD4206_P01_F07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 135	2148	TTCACCTTTGACACATATGCCATGAAT	ADI-28738 LAD4206_P01_F07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 135	2149	RIRSKYNNYATYYADSVKD	ADI-28738 LAD4206_P01_F07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 135	2150	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28738 LAD4206_P01_F07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 135	2151	VRHSNFGNSYVSWFAH	ADI-28738 LAD4206_P01_F07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 135	2152	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28738 LAD4206_P01_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 135	2153	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28738 LAD4206_P01_F07	Light chain variable region("LC") nucleic acid sequence
Ab 135	2154	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28738 LAD4206_P01_F07	Light chain variable region ("LC") amino acid sequence
Ab 135	2155	GSSAGAVTTSNYAN	ADI-28738 LAD4206_P01_F07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 135	2156	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28738 LAD4206_P01_F07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 135	2157	GTDKRAP	ADI-28738 LAD4206_P01_F07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 135	2158	GGCACAGACAAGCGCGCTCCT	ADI-28738 LAD4206_P01_F07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 135	2159	ALWYSNLWV	ADI-28738 LAD4206_P01_F07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 135	2160	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28738 LAD4206_P01_F07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 136	2161	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28739 LAD4206_P01_D08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 136	2162	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28739 LAD4206_P01_D08	Heavy chain variable region ("HC") amino acid sequence
Ab 136	2163	FTFDTYAMN	ADI-28739 LAD4206_P01_D08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 136	2164	TTCACCTTTGACACATATGCCATGAAT	ADI-28739 LAD4206_P01_D08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 136	2165	RIRSKYNNYATYYADSVKD	ADI-28739 LAD4206_P01_D08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 136	2166	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28739 LAD4206_P01_D08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 136	2167	VRHSNFGNSYVSWFAH	ADI-28739 LAD4206_P01_D08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 136	2168	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28739 LAD4206_P01_D08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 136	2169	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28739 LAD4206_P01_D08	Light chain variable region("LC") nucleic acid sequence
Ab 136	2170	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28739 LAD4206_P01_D08	Light chain variable region ("LC") amino acid sequence
Ab 136	2171	GSSTGAVTTSNYAN	ADI-28739 LAD4206_P01_D08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 136	2172	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28739 LAD4206_P01_D08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 136	2173	GTDKRAP	ADI-28739 LAD4206_P01_D08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 136	2174	GGCACAGACAAGCGCGCTCCT	ADI-28739 LAD4206_P01_D08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 136	2175	ALWYSNLWV	ADI-28739 LAD4206_P01_D08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 136	2176	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28739 LAD4206_P01_D08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 137	2177	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28740 LAD4206_P01_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 137	2178	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28740 LAD4206_P01_F08	Heavy chain variable region ("HC") amino acid sequence
Ab 137	2179	FTFDTYAMN	ADI-28740 LAD4206_P01_F08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 137	2180	TTCACCTTTGACACATATGCCATGAAT	ADI-28740 LAD4206_P01_F08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 137	2181	RIRSKYNNYATYYADSVKD	ADI-28740 LAD4206_P01_F08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 137	2182	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28740 LAD4206_P01_F08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 137	2183	VRHSNFGNSYVSWFAH	ADI-28740 LAD4206_P01_F08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 137	2184	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28740 LAD4206_P01_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 137	2185	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28740 LAD4206_P01_F08	Light chain variable region("LC") nucleic acid sequence
Ab 137	2186	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28740 LAD4206_P01_F08	Light chain variable region ("LC") amino acid sequence
Ab 137	2187	GSSTGAVTTSNYAN	ADI-28740 LAD4206_P01_F08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 137	2188	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28740 LAD4206_P01_F08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 137	2189	GTDKRAP	ADI-28740 LAD4206_P01_F08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 137	2190	GGCACAGACAAGCGCGCTCCT	ADI-28740 LAD4206_P01_F08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 137	2191	ALWYNNLWV	ADI-28740 LAD4206_P01_F08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 137	2192	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28740 LAD4206_P01_F08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 138	2193	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28741 LAD4206_P01_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 138	2194	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28741 LAD4206_P01_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 138	2195	FTFDTYAMN	ADI-28741 LAD4206_P01_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 138	2196	TTCACCTTTGACACATATGCCATGAAT	ADI-28741 LAD4206_P01_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 138	2197	RIRSKYNNYATYYADSVKD	ADI-28741 LAD4206_P01_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 138	2198	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28741 LAD4206_P01_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 138	2199	VRHSNFGNSYVSWFAH	ADI-28741 LAD4206_P01_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 138	2200	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28741 LAD4206_P01_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 138	2201	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28741 LAD4206_P01_A09	Light chain variable region("LC") nucleic acid sequence
Ab 138	2202	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28741 LAD4206_P01_A09	Light chain variable region ("LC") amino acid sequence
Ab 138	2203	GSSTGAVTTSNYAN	ADI-28741 LAD4206_P01_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 138	2204	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28741 LAD4206_P01_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 138	2205	GTDKRAP	ADI-28741 LAD4206_P01_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 138	2206	GGCACAGACAAGCGCGCTCCT	ADI-28741 LAD4206_P01_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 138	2207	VLWYSNLWV	ADI-28741 LAD4206_P01_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 138	2208	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28741 LAD4206_P01_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 139	2209	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28742 LAD4206_P01_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 139	2210	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28742 LAD4206_P01_E09	Heavy chain variable region ("HC") amino acid sequence
Ab 139	2211	FTFDTYAMN	ADI-28742 LAD4206_P01_E09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 139	2212	TTCACCTTTGACACATATGCCATGAAT	ADI-28742 LAD4206_P01_E09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 139	2213	RIRSKYNNYATYYADSVKD	ADI-28742 LAD4206_P01_E09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 139	2214	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28742 LAD4206_P01_E09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 139	2215	VRHSNFGNSYVSWFAH	ADI-28742 LAD4206_P01_E09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 139	2216	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28742 LAD4206_P01_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 139	2217	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28742 LAD4206_P01_E09	Light chain variable region("LC") nucleic acid sequence
Ab 139	2218	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28742 LAD4206_P01_E09	Light chain variable region ("LC") amino acid sequence
Ab 139	2219	GSSTGAVTTSNYAN	ADI-28742 LAD4206_P01_E09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 139	2220	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28742 LAD4206_P01_E09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 139	2221	GTDKRAP	ADI-28742 LAD4206_P01_E09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 139	2222	GGCACAGACAAGCGCGCTCCT	ADI-28742 LAD4206_P01_E09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 139	2223	ALWYSNHWV	ADI-28742 LAD4206_P01_E09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 139	2224	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28742 LAD4206_P01_E09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 140	2225	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28743 LAD4206_P01_B10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 140	2226	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28743 LAD4206_P01_B10	Heavy chain variable region ("HC") amino acid sequence
Ab 140	2227	FTFDTYAMN	ADI-28743 LAD4206_P01_B10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 140	2228	TTCACCTTTGACACATATGCCATGAAT	ADI-28743 LAD4206_P01_B10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 140	2229	RIRSKYNNYATYYADSVKD	ADI-28743 LAD4206_P01_B10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 140	2230	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28743 LAD4206_P01_B10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 140	2231	VRHSNFGNSYVSWFAH	ADI-28743 LAD4206_P01_B10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 140	2232	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28743 LAD4206_P01_B10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 140	2233	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28743 LAD4206_P01_B10	Light chain variable region("LC") nucleic acid sequence
Ab 140	2234	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28743 LAD4206_P01_B10	Light chain variable region ("LC") amino acid sequence
Ab 140	2235	GSSAGAVTTSNYAN	ADI-28743 LAD4206_P01_B10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 140	2236	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28743 LAD4206_P01_B10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 140	2237	GTDKRAP	ADI-28743 LAD4206_P01_B10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 140	2238	GGCACAGACAAGCGCGCTCCT	ADI-28743 LAD4206_P01_B10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 140	2239	ALWYSNLWV	ADI-28743 LAD4206_P01_B10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 140	2240	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28743 LAD4206_P01_B10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 141	2241	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28744 LAD4206_P01_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 141	2242	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28744 LAD4206_P01_A11	Heavy chain variable region ("HC") amino acid sequence
Ab 141	2243	FTFDTYAMN	ADI-28744 LAD4206_P01_A11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 141	2244	TTCACCTTTGACACATATGCCATGAAT	ADI-28744 LAD4206_P01_A11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 141	2245	RIRSKYNNYATYYADSVKD	ADI-28744 LAD4206_P01_A11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 141	2246	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28744 LAD4206_P01_A11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 141	2247	VRHSNFGNSYVSWFAH	ADI-28744 LAD4206_P01_A11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 141	2248	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28744 LAD4206_P01_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 141	2249	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28744 LAD4206_P01_A11	Light chain variable region("LC") nucleic acid sequence
Ab 141	2250	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28744 LAD4206_P01_A11	Light chain variable region ("LC") amino acid sequence
Ab 141	2251	GSSTGAVTTSNYAN	ADI-28744 LAD4206_P01_A11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 141	2252	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28744 LAD4206_P01_A11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 141	2253	GTDKRAP	ADI-28744 LAD4206_P01_A11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 141	2254	GGCACAGACAAGCGCGCTCCT	ADI-28744 LAD4206_P01_A11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 141	2255	ALWYNNLWV	ADI-28744 LAD4206_P01_A11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 141	2256	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28744 LAD4206_P01_A11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 142	2257	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28745 LAD4206_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 142	2258	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28745 LAD4206_P01_A12	Heavy chain variable region ("HC") amino acid sequence
Ab 142	2259	FTFDTYAMN	ADI-28745 LAD4206_P01_A12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 142	2260	TTCACCTTTGACACATATGCCATGAAT	ADI-28745 LAD4206_P01_A12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 142	2261	RIRSKYNNYATYYADSVKD	ADI-28745 LAD4206_P01_A12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 142	2262	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28745 LAD4206_P01_A12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 142	2263	VRHSNFGNSYVSWFAH	ADI-28745 LAD4206_P01_A12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 142	2264	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28745 LAD4206_P01_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 142	2265	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28745 LAD4206_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 142	2266	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28745 LAD4206_P01_A12	Light chain variable region ("LC") amino acid sequence
Ab 142	2267	GSSTGAVTTSNYAN	ADI-28745 LAD4206_P01_A12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 142	2268	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28745 LAD4206_P01_A12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 142	2269	GTDKRAP	ADI-28745 LAD4206_P01_A12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 142	2270	GGCACAGACAAGCGCGCTCCT	ADI-28745 LAD4206_P01_A12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 142	2271	VLWYSNLWV	ADI-28745 LAD4206_P01_A12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 142	2272	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28745 LAD4206_P01_A12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 143	2273	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28746 LAD4206_P01_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 143	2274	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28746 LAD4206_P01_F12	Heavy chain variable region ("HC") amino acid sequence
Ab 143	2275	FTFDTYAMN	ADI-28746 LAD4206_P01_F12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 143	2276	TTCACCTTTGACACATATGCCATGAAT	ADI-28746 LAD4206_P01_F12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 143	2277	RIRSKYNNYATYYADSVKD	ADI-28746 LAD4206_P01_F12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 143	2278	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28746 LAD4206_P01_F12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 143	2279	VRHSNFGNSYVSWFAH	ADI-28746 LAD4206_P01_F12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 143	2280	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28746 LAD4206_P01_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 143	2281	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28746 LAD4206_P01_F12	Light chain variable region("LC") nucleic acid sequence
Ab 143	2282	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28746 LAD4206_P01_F12	Light chain variable region ("LC") amino acid sequence
Ab 143	2283	GSSTGAVTTSNYAN	ADI-28746 LAD4206_P01_F12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 143	2284	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28746 LAD4206_P01_F12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 143	2285	GTDKRAP	ADI-28746 LAD4206_P01_F12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 143	2286	GGCACAGACAAGCGCGCTCCT	ADI-28746 LAD4206_P01_F12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 143	2287	ALWYSNHWV	ADI-28746 LAD4206_P01_F12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 143	2288	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28746 LAD4206_P01_F12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 144	2289	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28747 LAD4204_P02_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 144	2290	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28747 LAD4204_P02_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 144	2291	FTFDTYAMN	ADI-28747 LAD4204_P02_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 144	2292	TTCACCTTTGACACATATGCCATGAAT	ADI-28747 LAD4204_P02_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 144	2293	RIRSKYNNYATYYADSVKD	ADI-28747 LAD4204_P02_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 144	2294	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28747 LAD4204_P02_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 144	2295	VRHGNFGNGYVSWFAH	ADI-28747 LAD4204_P02_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 144	2296	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28747 LAD4204_P02_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 144	2297	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28747 LAD4204_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 144	2298	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28747 LAD4204_P02_A01	Light chain variable region ("LC") amino acid sequence
Ab 144	2299	GSSTGAVTTSNYAN	ADI-28747 LAD4204_P02_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 144	2300	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28747 LAD4204_P02_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 144	2301	GTDKRAP	ADI-28747 LAD4204_P02_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 144	2302	GGCACAGACAAGCGCGCTCCT	ADI-28747 LAD4204_P02_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 144	2303	ALWYSNLWV	ADI-28747 LAD4204_P02_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 144	2304	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28747 LAD4204_P02_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 145	2305	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28748 LAD4204_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 145	2306	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28748 LAD4204_P02_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 145	2307	FTFDTYAMN	ADI-28748 LAD4204_P02_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 145	2308	TTCACCTTTGACACATATGCCATGAAT	ADI-28748 LAD4204_P02_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 145	2309	RIRSKYNNYATYYADSVKD	ADI-28748 LAD4204_P02_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 145	2310	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28748 LAD4204_P02_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 145	2311	VRHGNFGNGYVSWFAH	ADI-28748 LAD4204_P02_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 145	2312	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28748 LAD4204_P02_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 145	2313	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28748 LAD4204_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 145	2314	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28748 LAD4204_P02_A02	Light chain variable region ("LC") amino acid sequence
Ab 145	2315	GSSTGAVTTSNYAN	ADI-28748 LAD4204_P02_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 145	2316	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28748 LAD4204_P02_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 145	2317	GTDKRAP	ADI-28748 LAD4204_P02_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 145	2318	GGCACAGACAAGCGCGCTCCT	ADI-28748 LAD4204_P02_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 145	2319	ALWYNNLWV	ADI-28748 LAD4204_P02_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 145	2320	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28748 LAD4204_P02_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 146	2321	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28749 LAD4204_P02_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 146	2322	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28749 LAD4204_P02_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 146	2323	FTFDTYAMN	ADI-28749 LAD4204_P02_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 146	2324	TTCACCTTTGACACATATGCCATGAAT	ADI-28749 LAD4204_P02_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 146	2325	RIRSKYNNYATYYADSVKD	ADI-28749 LAD4204_P02_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 146	2326	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28749 LAD4204_P02_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 146	2327	VRHGNFGNGYVSWFAH	ADI-28749 LAD4204_P02_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 146	2328	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28749 LAD4204_P02_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 146	2329	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28749 LAD4204_P02_E05	Light chain variable region("LC") nucleic acid sequence
Ab 146	2330	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYNNLWVFGGGTKLTVL	ADI-28749 LAD4204_P02_E05	Light chain variable region ("LC") amino acid sequence
Ab 146	2331	GSSTGAVTTSNYAN	ADI-28749 LAD4204_P02_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 146	2332	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28749 LAD4204_P02_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 146	2333	GTDKRAP	ADI-28749 LAD4204_P02_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 146	2334	GGCACAGACAAGCGCGCTCCT	ADI-28749 LAD4204_P02_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 146	2335	VLWYNNLWV	ADI-28749 LAD4204_P02_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 146	2336	GTGCTGTGGTACAATAACCTTTGGGTG	ADI-28749 LAD4204_P02_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 147	2337	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28750 LAD4205_P03_B07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 147	2338	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28750 LAD4205_P03_B07	Heavy chain variable region ("HC") amino acid sequence
Ab 147	2339	FTFDTYAMN	ADI-28750 LAD4205_P03_B07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 147	2340	TTCACCTTTGACACATATGCCATGAAT	ADI-28750 LAD4205_P03_B07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 147	2341	RIRSKYNNYATYYADSVKG	ADI-28750 LAD4205_P03_B07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 147	2342	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28750 LAD4205_P03_B07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 147	2343	VRHGNFGNSYVSWFAH	ADI-28750 LAD4205_P03_B07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 147	2344	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28750 LAD4205_P03_B07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 147	2345	AGACATGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCCCAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28750 LAD4205_P03_B07	Light chain variable region("LC") nucleic acid sequence
Ab 147	2346	RHVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGPDKRAPGVPDRFSGSLLGDKAALIITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28750 LAD4205_P03_B07	Light chain variable region ("LC") amino acid sequence
Ab 147	2347	GSSTGAVTTSNYAN	ADI-28750 LAD4205_P03_B07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 147	2348	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28750 LAD4205_P03_B07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 147	2349	GPDKRAP	ADI-28750 LAD4205_P03_B07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 147	2350	GGCCCAGACAAGCGCGCTCCT	ADI-28750 LAD4205_P03_B07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 147	2351	ALWYSNLWV	ADI-28750 LAD4205_P03_B07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 147	2352	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28750 LAD4205_P03_B07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 148	2353	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28751 LAD4206_P02_H05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 148	2354	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28751 LAD4206_P02_H05	Heavy chain variable region ("HC") amino acid sequence
Ab 148	2355	FTFDTYAMN	ADI-28751 LAD4206_P02_H05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 148	2356	TTCACCTTTGACACATATGCCATGAAT	ADI-28751 LAD4206_P02_H05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 148	2357	RIRSKYNNYATYYADSVKD	ADI-28751 LAD4206_P02_H05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 148	2358	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28751 LAD4206_P02_H05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 148	2359	VRHSNFGNSYVSWFAH	ADI-28751 LAD4206_P02_H05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 148	2360	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28751 LAD4206_P02_H05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 148	2361	AGAACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28751 LAD4206_P02_H05	Light chain variable region("LC") nucleic acid sequence
Ab 148	2362	RTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYNNLWVFGGGTKLTVL	ADI-28751 LAD4206_P02_H05	Light chain variable region ("LC") amino acid sequence
Ab 148	2363	GSSTGAVTTSNYAN	ADI-28751 LAD4206_P02_H05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 148	2364	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28751 LAD4206_P02_H05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 148	2365	GTDKRAP	ADI-28751 LAD4206_P02_H05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 148	2366	GGCACAGACAAGCGCGCTCCT	ADI-28751 LAD4206_P02_H05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 148	2367	VLWYNNLWV	ADI-28751 LAD4206_P02_H05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 148	2368	GTGCTGTGGTACAATAACCTTTGGGTG	ADI-28751 LAD4206_P02_H05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 149	2369	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28752 LAD4204_P02_G02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 149	2370	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28752 LAD4204_P02_G02	Heavy chain variable region ("HC") amino acid sequence
Ab 149	2371	FTFDTYAMN	ADI-28752 LAD4204_P02_G02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 149	2372	TTCACCTTTGACACATATGCCATGAAT	ADI-28752 LAD4204_P02_G02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 149	2373	RIRSKYNNYATYYADSVKG	ADI-28752 LAD4204_P02_G02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 149	2374	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28752 LAD4204_P02_G02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 149	2375	VRHGNFGNSYVSWFAH	ADI-28752 LAD4204_P02_G02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 149	2376	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28752 LAD4204_P02_G02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 149	2377	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28752 LAD4204_P02_G02	Light chain variable region("LC") nucleic acid sequence
Ab 149	2378	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28752 LAD4204_P02_G02	Light chain variable region ("LC") amino acid sequence
Ab 149	2379	GSSAGAVTTSNYAN	ADI-28752 LAD4204_P02_G02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 149	2380	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28752 LAD4204_P02_G02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 149	2381	GTDKRAP	ADI-28752 LAD4204_P02_G02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 149	2382	GGCACAGACAAGCGCGCTCCT	ADI-28752 LAD4204_P02_G02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 149	2383	ALWYSNLWV	ADI-28752 LAD4204_P02_G02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 149	2384	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28752 LAD4204_P02_G02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 150	2385	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28753 LAD4204_P02_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 150	2386	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28753 LAD4204_P02_H03	Heavy chain variable region ("HC") amino acid sequence
Ab 150	2387	FTFDTYAMN	ADI-28753 LAD4204_P02_H03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 150	2388	TTCACCTTTGACACATATGCCATGAAT	ADI-28753 LAD4204_P02_H03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 150	2389	RIRSKYNNYATYYADSVKD	ADI-28753 LAD4204_P02_H03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 150	2390	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28753 LAD4204_P02_H03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 150	2391	VRHGNFGNGYVSWFAH	ADI-28753 LAD4204_P02_H03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 150	2392	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28753 LAD4204_P02_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 150	2393	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28753 LAD4204_P02_H03	Light chain variable region("LC") nucleic acid sequence
Ab 150	2394	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28753 LAD4204_P02_H03	Light chain variable region ("LC") amino acid sequence
Ab 150	2395	GSSTGAVTTSNYAN	ADI-28753 LAD4204_P02_H03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 150	2396	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28753 LAD4204_P02_H03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 150	2397	GTDKRAP	ADI-28753 LAD4204_P02_H03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 150	2398	GGCACAGACAAGCGCGCTCCT	ADI-28753 LAD4204_P02_H03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 150	2399	ALWYSNLWV	ADI-28753 LAD4204_P02_H03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 150	2400	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28753 LAD4204_P02_H03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 151	2401	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28754 LAD4204_P02_B04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 151	2402	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28754 LAD4204_P02_B04	Heavy chain variable region ("HC") amino acid sequence
Ab 151	2403	FTFDTYAMN	ADI-28754 LAD4204_P02_B04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 151	2404	TTCACCTTTGACACATATGCCATGAAT	ADI-28754 LAD4204_P02_B04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 151	2405	RIRSKYNNYATYYADSVKD	ADI-28754 LAD4204_P02_B04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 151	2406	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28754 LAD4204_P02_B04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 151	2407	VRHGNFGNGYVSWFAH	ADI-28754 LAD4204_P02_B04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 151	2408	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28754 LAD4204_P02_B04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 151	2409	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28754 LAD4204_P02_B04	Light chain variable region("LC") nucleic acid sequence
Ab 151	2410	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28754 LAD4204_P02_B04	Light chain variable region ("LC") amino acid sequence
Ab 151	2411	GSSTGAVTTSNYAN	ADI-28754 LAD4204_P02_B04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 151	2412	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28754 LAD4204_P02_B04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 151	2413	GTDKRAP	ADI-28754 LAD4204_P02_B04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 151	2414	GGCACAGACAAGCGCGCTCCT	ADI-28754 LAD4204_P02_B04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 151	2415	ALWYNNLWV	ADI-28754 LAD4204_P02_B04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 151	2416	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28754 LAD4204_P02_B04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 152	2417	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28755 LAD4204_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 152	2418	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28755 LAD4204_P02_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 152	2419	FTFDTYAMN	ADI-28755 LAD4204_P02_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 152	2420	TTCACCTTTGACACATATGCCATGAAT	ADI-28755 LAD4204_P02_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 152	2421	RIRSKYNNYATYYADSVKD	ADI-28755 LAD4204_P02_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 152	2422	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28755 LAD4204_P02_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 152	2423	VRHGNFGNGYVSWFAH	ADI-28755 LAD4204_P02_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 152	2424	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28755 LAD4204_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 152	2425	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28755 LAD4204_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 152	2426	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNHWVFGGGTKLTVL	ADI-28755 LAD4204_P02_A06	Light chain variable region ("LC") amino acid sequence
Ab 152	2427	GSSTGAVTTSNYAN	ADI-28755 LAD4204_P02_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 152	2428	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28755 LAD4204_P02_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 152	2429	GTDKRAP	ADI-28755 LAD4204_P02_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 152	2430	GGCACAGACAAGCGCGCTCCT	ADI-28755 LAD4204_P02_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 152	2431	VLWYSNHWV	ADI-28755 LAD4204_P02_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 152	2432	GTGCTGTGGTACAGTAACCATTGGGTG	ADI-28755 LAD4204_P02_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 153	2433	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28756 LAD4204_P02_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 153	2434	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQGTLVTVSS	ADI-28756 LAD4204_P02_F06	Heavy chain variable region ("HC") amino acid sequence
Ab 153	2435	FTFDTYAMN	ADI-28756 LAD4204_P02_F06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 153	2436	TTCACCTTTGACACATATGCCATGAAT	ADI-28756 LAD4204_P02_F06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 153	2437	RIRSKYNNYATYYADSVKD	ADI-28756 LAD4204_P02_F06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 153	2438	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28756 LAD4204_P02_F06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 153	2439	VRHGNFGNGYVSWFAH	ADI-28756 LAD4204_P02_F06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 153	2440	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTGGTTTGCTCAT	ADI-28756 LAD4204_P02_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 153	2441	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28756 LAD4204_P02_F06	Light chain variable region("LC") nucleic acid sequence
Ab 153	2442	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28756 LAD4204_P02_F06	Light chain variable region ("LC") amino acid sequence
Ab 153	2443	GSSTGAVTTSNYAN	ADI-28756 LAD4204_P02_F06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 153	2444	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28756 LAD4204_P02_F06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 153	2445	GTDKRAP	ADI-28756 LAD4204_P02_F06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 153	2446	GGCACAGACAAGCGCGCTCCT	ADI-28756 LAD4204_P02_F06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 153	2447	ALWYSNHWV	ADI-28756 LAD4204_P02_F06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 153	2448	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28756 LAD4204_P02_F06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 154	2449	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28757 LAD4205_P03_C07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 154	2450	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28757 LAD4205_P03_C07	Heavy chain variable region ("HC") amino acid sequence
Ab 154	2451	FTFDTYAMN	ADI-28757 LAD4205_P03_C07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 154	2452	TTCACCTTTGACACATATGCCATGAAT	ADI-28757 LAD4205_P03_C07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 154	2453	RIRSKYNNYATYYADSVKG	ADI-28757 LAD4205_P03_C07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 154	2454	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28757 LAD4205_P03_C07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 154	2455	VRHGNFGNSYVSWFAH	ADI-28757 LAD4205_P03_C07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 154	2456	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28757 LAD4205_P03_C07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 154	2457	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28757 LAD4205_P03_C07	Light chain variable region("LC") nucleic acid sequence
Ab 154	2458	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNHWVFGGGTKLTVL	ADI-28757 LAD4205_P03_C07	Light chain variable region ("LC") amino acid sequence
Ab 154	2459	GSSTGAVTTSNYAN	ADI-28757 LAD4205_P03_C07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 154	2460	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28757 LAD4205_P03_C07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 154	2461	GTDKRAP	ADI-28757 LAD4205_P03_C07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 154	2462	GGCACAGACAAGCGCGCTCCT	ADI-28757 LAD4205_P03_C07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 154	2463	ALWYNNHWV	ADI-28757 LAD4205_P03_C07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 154	2464	GCGCTGTGGTACAATAACCATTGGGTG	ADI-28757 LAD4205_P03_C07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 155	2465	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28758 LAD4205_P03_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 155	2466	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28758 LAD4205_P03_F07	Heavy chain variable region ("HC") amino acid sequence
Ab 155	2467	FTFDTYAMN	ADI-28758 LAD4205_P03_F07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 155	2468	TTCACCTTTGACACATATGCCATGAAT	ADI-28758 LAD4205_P03_F07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 155	2469	RIRSKYNNYATYYADSVKG	ADI-28758 LAD4205_P03_F07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 155	2470	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28758 LAD4205_P03_F07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 155	2471	VRHGNFGNSYVSWFAH	ADI-28758 LAD4205_P03_F07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 155	2472	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28758 LAD4205_P03_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 155	2473	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28758 LAD4205_P03_F07	Light chain variable region("LC") nucleic acid sequence
Ab 155	2474	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28758 LAD4205_P03_F07	Light chain variable region ("LC") amino acid sequence
Ab 155	2475	GSSAGAVTTSNYAN	ADI-28758 LAD4205_P03_F07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 155	2476	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28758 LAD4205_P03_F07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 155	2477	GTDKRAP	ADI-28758 LAD4205_P03_F07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 155	2478	GGCACAGACAAGCGCGCTCCT	ADI-28758 LAD4205_P03_F07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 155	2479	ALWYSNLWV	ADI-28758 LAD4205_P03_F07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 155	2480	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28758 LAD4205_P03_F07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 156	2481	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28759 LAD4205_P03_B08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 156	2482	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28759 LAD4205_P03_B08	Heavy chain variable region ("HC") amino acid sequence
Ab 156	2483	FTFDTYAMN	ADI-28759 LAD4205_P03_B08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 156	2484	TTCACCTTTGACACATATGCCATGAAT	ADI-28759 LAD4205_P03_B08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 156	2485	RIRSKYNNYATYYADSVKG	ADI-28759 LAD4205_P03_B08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 156	2486	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28759 LAD4205_P03_B08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 156	2487	VRHGNFGNSYVSWFAH	ADI-28759 LAD4205_P03_B08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 156	2488	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28759 LAD4205_P03_B08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 156	2489	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28759 LAD4205_P03_B08	Light chain variable region("LC") nucleic acid sequence
Ab 156	2490	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28759 LAD4205_P03_B08	Light chain variable region ("LC") amino acid sequence
Ab 156	2491	GSSTGAVTTSNYAN	ADI-28759 LAD4205_P03_B08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 156	2492	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28759 LAD4205_P03_B08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 156	2493	GTDKRAP	ADI-28759 LAD4205_P03_B08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 156	2494	GGCACAGACAAGCGCGCTCCT	ADI-28759 LAD4205_P03_B08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 156	2495	ALWYNNLWV	ADI-28759 LAD4205_P03_B08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 156	2496	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28759 LAD4205_P03_B08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 157	2497	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28760 LAD4205_P03_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 157	2498	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28760 LAD4205_P03_F08	Heavy chain variable region ("HC") amino acid sequence
Ab 157	2499	FTFDTYAMN	ADI-28760 LAD4205_P03_F08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 157	2500	TTCACCTTTGACACATATGCCATGAAT	ADI-28760 LAD4205_P03_F08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 157	2501	RIRSKYNNYATYYADSVKG	ADI-28760 LAD4205_P03_F08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 157	2502	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28760 LAD4205_P03_F08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 157	2503	VRHGNFGNSYVSWFAH	ADI-28760 LAD4205_P03_F08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 157	2504	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28760 LAD4205_P03_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 157	2505	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28760 LAD4205_P03_F08	Light chain variable region("LC") nucleic acid sequence
Ab 157	2506	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28760 LAD4205_P03_F08	Light chain variable region ("LC") amino acid sequence
Ab 157	2507	GSSAGAVTTSNYAN	ADI-28760 LAD4205_P03_F08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 157	2508	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28760 LAD4205_P03_F08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 157	2509	GTDKRAP	ADI-28760 LAD4205_P03_F08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 157	2510	GGCACAGACAAGCGCGCTCCT	ADI-28760 LAD4205_P03_F08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 157	2511	ALWYSNLWV	ADI-28760 LAD4205_P03_F08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 157	2512	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28760 LAD4205_P03_F08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 158	2513	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28761 LAD4205_P03_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 158	2514	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28761 LAD4205_P03_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 158	2515	FTFDTYAMN	ADI-28761 LAD4205_P03_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 158	2516	TTCACCTTTGACACATATGCCATGAAT	ADI-28761 LAD4205_P03_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 158	2517	RIRSKYNNYATYYADSVKG	ADI-28761 LAD4205_P03_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 158	2518	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28761 LAD4205_P03_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 158	2519	VRHGNFGNSYVSWFAH	ADI-28761 LAD4205_P03_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 158	2520	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28761 LAD4205_P03_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 158	2521	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28761 LAD4205_P03_A09	Light chain variable region("LC") nucleic acid sequence
Ab 158	2522	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28761 LAD4205_P03_A09	Light chain variable region ("LC") amino acid sequence
Ab 158	2523	GSSAGAVTTSNYAN	ADI-28761 LAD4205_P03_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 158	2524	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28761 LAD4205_P03_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 158	2525	GTDKRAP	ADI-28761 LAD4205_P03_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 158	2526	GGCACAGACAAGCGCGCTCCT	ADI-28761 LAD4205_P03_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 158	2527	ALWYNNLWV	ADI-28761 LAD4205_P03_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 158	2528	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28761 LAD4205_P03_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 159	2529	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28762 LAD4205_P03_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 159	2530	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28762 LAD4205_P03_E09	Heavy chain variable region ("HC") amino acid sequence
Ab 159	2531	FTFDTYAMN	ADI-28762 LAD4205_P03_E09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 159	2532	TTCACCTTTGACACATATGCCATGAAT	ADI-28762 LAD4205_P03_E09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 159	2533	RIRSKYNNYATYYADSVKG	ADI-28762 LAD4205_P03_E09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 159	2534	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28762 LAD4205_P03_E09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 159	2535	VRHGNFGNSYVSWFAH	ADI-28762 LAD4205_P03_E09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 159	2536	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28762 LAD4205_P03_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 159	2537	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28762 LAD4205_P03_E09	Light chain variable region("LC") nucleic acid sequence
Ab 159	2538	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28762 LAD4205_P03_E09	Light chain variable region ("LC") amino acid sequence
Ab 159	2539	GSSTGAVTTSNYAN	ADI-28762 LAD4205_P03_E09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 159	2540	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28762 LAD4205_P03_E09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 159	2541	GTDKRAP	ADI-28762 LAD4205_P03_E09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 159	2542	GGCACAGACAAGCGCGCTCCT	ADI-28762 LAD4205_P03_E09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 159	2543	ALWYSNLWV	ADI-28762 LAD4205_P03_E09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 159	2544	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28762 LAD4205_P03_E09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 160	2545	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28763 LAD4205_P03_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 160	2546	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28763 LAD4205_P03_E10	Heavy chain variable region ("HC") amino acid sequence
Ab 160	2547	FTFDTYAMN	ADI-28763 LAD4205_P03_E10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 160	2548	TTCACCTTTGACACATATGCCATGAAT	ADI-28763 LAD4205_P03_E10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 160	2549	RIRSKYNNYATYYADSVKG	ADI-28763 LAD4205_P03_E10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 160	2550	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28763 LAD4205_P03_E10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 160	2551	VRHGNFGNSYVSWFAH	ADI-28763 LAD4205_P03_E10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 160	2552	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28763 LAD4205_P03_E10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 160	2553	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28763 LAD4205_P03_E10	Light chain variable region("LC") nucleic acid sequence
Ab 160	2554	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28763 LAD4205_P03_E10	Light chain variable region ("LC") amino acid sequence
Ab 160	2555	GSSTGAVTTSNYAN	ADI-28763 LAD4205_P03_E10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 160	2556	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28763 LAD4205_P03_E10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 160	2557	GTDKRAP	ADI-28763 LAD4205_P03_E10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 160	2558	GGCACAGACAAGCGCGCTCCT	ADI-28763 LAD4205_P03_E10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 160	2559	VLWYSNLWV	ADI-28763 LAD4205_P03_E10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 160	2560	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28763 LAD4205_P03_E10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 161	2561	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28764 LAD4205_P03_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 161	2562	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28764 LAD4205_P03_A11	Heavy chain variable region ("HC") amino acid sequence
Ab 161	2563	FTFDTYAMN	ADI-28764 LAD4205_P03_A11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 161	2564	TTCACCTTTGACACATATGCCATGAAT	ADI-28764 LAD4205_P03_A11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 161	2565	RIRSKYNNYATYYADSVKG	ADI-28764 LAD4205_P03_A11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 161	2566	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28764 LAD4205_P03_A11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 161	2567	VRHGNFGNSYVSWFAH	ADI-28764 LAD4205_P03_A11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 161	2568	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28764 LAD4205_P03_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 161	2569	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28764 LAD4205_P03_A11	Light chain variable region("LC") nucleic acid sequence
Ab 161	2570	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28764 LAD4205_P03_A11	Light chain variable region ("LC") amino acid sequence
Ab 161	2571	GSSTGAVTTSNYAN	ADI-28764 LAD4205_P03_A11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 161	2572	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28764 LAD4205_P03_A11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 161	2573	GTDKRAP	ADI-28764 LAD4205_P03_A11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 161	2574	GGCACAGACAAGCGCGCTCCT	ADI-28764 LAD4205_P03_A11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 161	2575	ALWYSNHWV	ADI-28764 LAD4205_P03_A11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 161	2576	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28764 LAD4205_P03_A11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 162	2577	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28765 LAD4205_P03_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 162	2578	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28765 LAD4205_P03_F11	Heavy chain variable region ("HC") amino acid sequence
Ab 162	2579	FTFDTYAMN	ADI-28765 LAD4205_P03_F11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 162	2580	TTCACCTTTGACACATATGCCATGAAT	ADI-28765 LAD4205_P03_F11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 162	2581	RIRSKYNNYATYYADSVKG	ADI-28765 LAD4205_P03_F11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 162	2582	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28765 LAD4205_P03_F11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 162	2583	VRHGNFGNSYVSWFAH	ADI-28765 LAD4205_P03_F11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 162	2584	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28765 LAD4205_P03_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 162	2585	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28765 LAD4205_P03_F11	Light chain variable region("LC") nucleic acid sequence
Ab 162	2586	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYNNLWVFGGGTKLTVL	ADI-28765 LAD4205_P03_F11	Light chain variable region ("LC") amino acid sequence
Ab 162	2587	GSSTGAVTTSNYAN	ADI-28765 LAD4205_P03_F11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 162	2588	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28765 LAD4205_P03_F11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 162	2589	GTDKRAP	ADI-28765 LAD4205_P03_F11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 162	2590	GGCACAGACAAGCGCGCTCCT	ADI-28765 LAD4205_P03_F11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 162	2591	VLWYNNLWV	ADI-28765 LAD4205_P03_F11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 162	2592	GTGCTGTGGTACAATAACCTTTGGGTG	ADI-28765 LAD4205_P03_F11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 163	2593	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28766 LAD4205_P03_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 163	2594	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28766 LAD4205_P03_A12	Heavy chain variable region ("HC") amino acid sequence
Ab 163	2595	FTFDTYAMN	ADI-28766 LAD4205_P03_A12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 163	2596	TTCACCTTTGACACATATGCCATGAAT	ADI-28766 LAD4205_P03_A12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 163	2597	RIRSKYNNYATYYADSVKG	ADI-28766 LAD4205_P03_A12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 163	2598	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28766 LAD4205_P03_A12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 163	2599	VRHGNFGNSYVSWFAH	ADI-28766 LAD4205_P03_A12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 163	2600	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28766 LAD4205_P03_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 163	2601	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28766 LAD4205_P03_A12	Light chain variable region("LC") nucleic acid sequence
Ab 163	2602	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNHWVFGGGTKLTVL	ADI-28766 LAD4205_P03_A12	Light chain variable region ("LC") amino acid sequence
Ab 163	2603	GSSTGAVTTSNYAN	ADI-28766 LAD4205_P03_A12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 163	2604	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28766 LAD4205_P03_A12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 163	2605	GTDKRAP	ADI-28766 LAD4205_P03_A12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 163	2606	GGCACAGACAAGCGCGCTCCT	ADI-28766 LAD4205_P03_A12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 163	2607	VLWYSNHWV	ADI-28766 LAD4205_P03_A12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 163	2608	GTGCTGTGGTACAGTAACCATTGGGTG	ADI-28766 LAD4205_P03_A12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 164	2609	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28767 LAD4205_P03_E12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 164	2610	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKSTLYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-28767 LAD4205_P03_E12	Heavy chain variable region ("HC") amino acid sequence
Ab 164	2611	FTFDTYAMN	ADI-28767 LAD4205_P03_E12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 164	2612	TTCACCTTTGACACATATGCCATGAAT	ADI-28767 LAD4205_P03_E12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 164	2613	RIRSKYNNYATYYADSVKG	ADI-28767 LAD4205_P03_E12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 164	2614	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGGT	ADI-28767 LAD4205_P03_E12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 164	2615	VRHGNFGNSYVSWFAH	ADI-28767 LAD4205_P03_E12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 164	2616	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28767 LAD4205_P03_E12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 164	2617	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28767 LAD4205_P03_E12	Light chain variable region("LC") nucleic acid sequence
Ab 164	2618	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28767 LAD4205_P03_E12	Light chain variable region ("LC") amino acid sequence
Ab 164	2619	GSSTGAVTTSNYAN	ADI-28767 LAD4205_P03_E12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 164	2620	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28767 LAD4205_P03_E12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 164	2621	GTDKRAP	ADI-28767 LAD4205_P03_E12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 164	2622	GGCACAGACAAGCGCGCTCCT	ADI-28767 LAD4205_P03_E12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 164	2623	ALWYSNHWV	ADI-28767 LAD4205_P03_E12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 164	2624	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28767 LAD4205_P03_E12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 165	2625	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28768 LAD4206_P02_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 165	2626	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28768 LAD4206_P02_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 165	2627	FTFDTYAMN	ADI-28768 LAD4206_P02_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 165	2628	TTCACCTTTGACACATATGCCATGAAT	ADI-28768 LAD4206_P02_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 165	2629	RIRSKYNNYATYYADSVKD	ADI-28768 LAD4206_P02_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 165	2630	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28768 LAD4206_P02_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 165	2631	VRHSNFGNSYVSWFAH	ADI-28768 LAD4206_P02_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 165	2632	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28768 LAD4206_P02_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 165	2633	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28768 LAD4206_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 165	2634	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28768 LAD4206_P02_A01	Light chain variable region ("LC") amino acid sequence
Ab 165	2635	GSSTGAVTTSNYAN	ADI-28768 LAD4206_P02_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 165	2636	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28768 LAD4206_P02_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 165	2637	GTDKRAP	ADI-28768 LAD4206_P02_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 165	2638	GGCACAGACAAGCGCGCTCCT	ADI-28768 LAD4206_P02_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 165	2639	ALWYSNLWV	ADI-28768 LAD4206_P02_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 165	2640	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28768 LAD4206_P02_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 166	2641	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28769 LAD4206_P02_H01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 166	2642	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28769 LAD4206_P02_H01	Heavy chain variable region ("HC") amino acid sequence
Ab 166	2643	FTFDTYAMN	ADI-28769 LAD4206_P02_H01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 166	2644	TTCACCTTTGACACATATGCCATGAAT	ADI-28769 LAD4206_P02_H01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 166	2645	RIRSKYNNYATYYADSVKD	ADI-28769 LAD4206_P02_H01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 166	2646	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28769 LAD4206_P02_H01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 166	2647	VRHSNFGNSYVSWFAH	ADI-28769 LAD4206_P02_H01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 166	2648	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28769 LAD4206_P02_H01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 166	2649	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28769 LAD4206_P02_H01	Light chain variable region("LC") nucleic acid sequence
Ab 166	2650	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28769 LAD4206_P02_H01	Light chain variable region ("LC") amino acid sequence
Ab 166	2651	GSSTGAVTTSNYAN	ADI-28769 LAD4206_P02_H01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 166	2652	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28769 LAD4206_P02_H01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 166	2653	GTDKRAP	ADI-28769 LAD4206_P02_H01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 166	2654	GGCACAGACAAGCGCGCTCCT	ADI-28769 LAD4206_P02_H01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 166	2655	ALWYNNLWV	ADI-28769 LAD4206_P02_H01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 166	2656	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28769 LAD4206_P02_H01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 167	2657	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28770 LAD4206_P02_F02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 167	2658	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28770 LAD4206_P02_F02	Heavy chain variable region ("HC") amino acid sequence
Ab 167	2659	FTFDTYAMN	ADI-28770 LAD4206_P02_F02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 167	2660	TTCACCTTTGACACATATGCCATGAAT	ADI-28770 LAD4206_P02_F02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 167	2661	RIRSKYNNYATYYADSVKD	ADI-28770 LAD4206_P02_F02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 167	2662	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28770 LAD4206_P02_F02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 167	2663	VRHSNFGNSYVSWFAH	ADI-28770 LAD4206_P02_F02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 167	2664	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28770 LAD4206_P02_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 167	2665	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28770 LAD4206_P02_F02	Light chain variable region("LC") nucleic acid sequence
Ab 167	2666	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28770 LAD4206_P02_F02	Light chain variable region ("LC") amino acid sequence
Ab 167	2667	GSSAGAVTTSNYAN	ADI-28770 LAD4206_P02_F02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 167	2668	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28770 LAD4206_P02_F02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 167	2669	GTDKRAP	ADI-28770 LAD4206_P02_F02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 167	2670	GGCACAGACAAGCGCGCTCCT	ADI-28770 LAD4206_P02_F02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 167	2671	ALWYSNLWV	ADI-28770 LAD4206_P02_F02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 167	2672	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28770 LAD4206_P02_F02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 168	2673	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28771 LAD4206_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 168	2674	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28771 LAD4206_P02_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 168	2675	FTFDTYAMN	ADI-28771 LAD4206_P02_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 168	2676	TTCACCTTTGACACATATGCCATGAAT	ADI-28771 LAD4206_P02_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 168	2677	RIRSKYNNYATYYADSVKD	ADI-28771 LAD4206_P02_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 168	2678	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28771 LAD4206_P02_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 168	2679	VRHSNFGNSYVSWFAH	ADI-28771 LAD4206_P02_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 168	2680	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28771 LAD4206_P02_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 168	2681	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28771 LAD4206_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 168	2682	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	ADI-28771 LAD4206_P02_E03	Light chain variable region ("LC") amino acid sequence
Ab 168	2683	GSSTGAVTTSNYAN	ADI-28771 LAD4206_P02_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 168	2684	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28771 LAD4206_P02_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 168	2685	GTDKRAP	ADI-28771 LAD4206_P02_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 168	2686	GGCACAGACAAGCGCGCTCCT	ADI-28771 LAD4206_P02_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 168	2687	ALWYSNLWV	ADI-28771 LAD4206_P02_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 168	2688	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-28771 LAD4206_P02_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 169	2689	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28772 LAD4206_P02_D04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 169	2690	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28772 LAD4206_P02_D04	Heavy chain variable region ("HC") amino acid sequence
Ab 169	2691	FTFDTYAMN	ADI-28772 LAD4206_P02_D04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 169	2692	TTCACCTTTGACACATATGCCATGAAT	ADI-28772 LAD4206_P02_D04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 169	2693	RIRSKYNNYATYYADSVKD	ADI-28772 LAD4206_P02_D04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 169	2694	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28772 LAD4206_P02_D04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 169	2695	VRHSNFGNSYVSWFAH	ADI-28772 LAD4206_P02_D04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 169	2696	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28772 LAD4206_P02_D04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 169	2697	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28772 LAD4206_P02_D04	Light chain variable region("LC") nucleic acid sequence
Ab 169	2698	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYNNLWVFGGGTKLTVL	ADI-28772 LAD4206_P02_D04	Light chain variable region ("LC") amino acid sequence
Ab 169	2699	GSSTGAVTTSNYAN	ADI-28772 LAD4206_P02_D04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 169	2700	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28772 LAD4206_P02_D04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 169	2701	GTDKRAP	ADI-28772 LAD4206_P02_D04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 169	2702	GGCACAGACAAGCGCGCTCCT	ADI-28772 LAD4206_P02_D04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 169	2703	ALWYNNLWV	ADI-28772 LAD4206_P02_D04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 169	2704	GCGCTGTGGTACAATAACCTTTGGGTG	ADI-28772 LAD4206_P02_D04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 170	2705	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28773 LAD4206_P02_H04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 170	2706	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28773 LAD4206_P02_H04	Heavy chain variable region ("HC") amino acid sequence
Ab 170	2707	FTFDTYAMN	ADI-28773 LAD4206_P02_H04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 170	2708	TTCACCTTTGACACATATGCCATGAAT	ADI-28773 LAD4206_P02_H04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 170	2709	RIRSKYNNYATYYADSVKD	ADI-28773 LAD4206_P02_H04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 170	2710	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28773 LAD4206_P02_H04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 170	2711	VRHSNFGNSYVSWFAH	ADI-28773 LAD4206_P02_H04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 170	2712	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28773 LAD4206_P02_H04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 170	2713	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28773 LAD4206_P02_H04	Light chain variable region("LC") nucleic acid sequence
Ab 170	2714	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCVLWYSNLWVFGGGTKLTVL	ADI-28773 LAD4206_P02_H04	Light chain variable region ("LC") amino acid sequence
Ab 170	2715	GSSTGAVTTSNYAN	ADI-28773 LAD4206_P02_H04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 170	2716	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28773 LAD4206_P02_H04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 170	2717	GTDKRAP	ADI-28773 LAD4206_P02_H04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 170	2718	GGCACAGACAAGCGCGCTCCT	ADI-28773 LAD4206_P02_H04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 170	2719	VLWYSNLWV	ADI-28773 LAD4206_P02_H04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 170	2720	GTGCTGTGGTACAGTAACCTTTGGGTG	ADI-28773 LAD4206_P02_H04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 171	2721	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28774 LAD4206_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 171	2722	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28774 LAD4206_P02_A05	Heavy chain variable region ("HC") amino acid sequence
Ab 171	2723	FTFDTYAMN	ADI-28774 LAD4206_P02_A05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 171	2724	TTCACCTTTGACACATATGCCATGAAT	ADI-28774 LAD4206_P02_A05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 171	2725	RIRSKYNNYATYYADSVKD	ADI-28774 LAD4206_P02_A05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 171	2726	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28774 LAD4206_P02_A05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 171	2727	VRHSNFGNSYVSWFAH	ADI-28774 LAD4206_P02_A05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 171	2728	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28774 LAD4206_P02_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 171	2729	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28774 LAD4206_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 171	2730	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-28774 LAD4206_P02_A05	Light chain variable region ("LC") amino acid sequence
Ab 171	2731	GSSTGAVTTSNYAN	ADI-28774 LAD4206_P02_A05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 171	2732	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28774 LAD4206_P02_A05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 171	2733	GTDKRAP	ADI-28774 LAD4206_P02_A05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 171	2734	GGCACAGACAAGCGCGCTCCT	ADI-28774 LAD4206_P02_A05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 171	2735	ALWYSNHWV	ADI-28774 LAD4206_P02_A05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 171	2736	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-28774 LAD4206_P02_A05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 172	2737	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28775 LAD4206_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 172	2738	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKSTLYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQGTLVTVSS	ADI-28775 LAD4206_P02_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 172	2739	FTFDTYAMN	ADI-28775 LAD4206_P02_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 172	2740	TTCACCTTTGACACATATGCCATGAAT	ADI-28775 LAD4206_P02_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 172	2741	RIRSKYNNYATYYADSVKD	ADI-28775 LAD4206_P02_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 172	2742	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-28775 LAD4206_P02_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 172	2743	VRHSNFGNSYVSWFAH	ADI-28775 LAD4206_P02_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 172	2744	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-28775 LAD4206_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 172	2745	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGTGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-28775 LAD4206_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 172	2746	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNHWVFGGGTKLTVL	ADI-28775 LAD4206_P02_A06	Light chain variable region ("LC") amino acid sequence
Ab 172	2747	GSSTGAVTTSNYAN	ADI-28775 LAD4206_P02_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 172	2748	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-28775 LAD4206_P02_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 172	2749	GTDKRAP	ADI-28775 LAD4206_P02_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 172	2750	GGCACAGACAAGCGCGCTCCT	ADI-28775 LAD4206_P02_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 172	2751	VLWYSNHWV	ADI-28775 LAD4206_P02_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 172	2752	GTGCTGTGGTACAGTAACCATTGGGTG	ADI-28775 LAD4206_P02_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 173	2753	CAGGTACAGCTGCAGCAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCATAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGCCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGTCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGATAACTACTCCTTTGCTTACTGGGGCCAAGGCAACCACGGTCACCGTCT	ADI-15505 SAD4961_P03_F02	Heavy chain variable region ("HC") nucleic acid sequence

		CCTC		
Ab 173	2754	QVQLQQSGPELVKPGASVRISCKASGYTFISYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKAKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDDNYSFAYWGQGNHGHRLL	ADI-15505 SAD4961_P03_F02	Heavy chain variable region ("HC") amino acid sequence
Ab 173	2755	YTFISYYIH	ADI-15505 SAD4961_P03_F02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 173	2756	TACACCTTCATAAGCTACTATATACAC	ADI-15505 SAD4961_P03_F02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 173	2757	WIYPGNVNTKYNEKFKA	ADI-15505 SAD4961_P03_F02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 173	2758	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGCC	ADI-15505 SAD4961_P03_F02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 173	2759	ARDDNYSFAY	ADI-15505 SAD4961_P03_F02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 173	2760	GCAAGAGATGATAACTACTCCTTTGCTTAC	ADI-15505 SAD4961_P03_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 173	2761	GACATCGTGATGATCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAAATAAAA	ADI-15505 SAD4961_P03_F02	Light chain variable region("LC") nucleic acid sequence
Ab 173	2762	DIVMIQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	ADI-15505 SAD4961_P03_F02	Light chain variable region ("LC") amino acid sequence
Ab 173	2763	KSSQSLLNSRTRKNYLA	ADI-15505 SAD4961_P03_F02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 173	2764	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15505 SAD4961_P03_F02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 173	2765	WASTRES	ADI-15505 SAD4961_P03_F02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 173	2766	TGGGCATCCACTAGGGAATCT	ADI-15505 SAD4961_P03_F02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 173	2767	KQSYNLRT	ADI-15505 SAD4961_P03_F02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 173	2768	AAGCAATCTTATAATCTTCGGACG	ADI-15505 SAD4961_P03_F02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 174	2769	GAAGTACAGCTGCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACGCCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCTTGGAGATGGTAGTACTAACTACAATGAGAAGTTCAAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGACTCTGCGACCTATTTCTGTGCAAGGGATGATTCGTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-15506 SAD4961_P03_B03	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 174	2770	EVQLQQSGPDLVKPGASVKMSCKASGYAFTSYYIHWVKQRPGQGLEWIGWIYLGDGSTNYNEKFKGKTTLTADKSSSTAYMLLSSLTSEDSATYFCARDDSYYFDYWGQGTTVTVSS	ADI-15506 SAD4961_P03_B03	Heavy chain variable region ("HC") amino acid sequence
Ab 174	2771	YAFTSYYIH	ADI-15506 SAD4961_P03_B03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 174	2772	TACGCCTTCACAAGCTACTATATACAC	ADI-15506 SAD4961_P03_B03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 174	2773	WIYLGDGSTNYNEKFKG	ADI-15506 SAD4961_P03_B03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 174	2774	TGGATTTATCTTGGAGATGGTAGTACTAACTACAATGAGAAGTTCAAGGGC	ADI-15506 SAD4961_P03_B03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 174	2775	ARDDSYYFDY	ADI-15506 SAD4961_P03_B03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 174	2776	GCAAGGGATGATTCGTACTACTTTGACTAC	ADI-15506 SAD4961_P03_B03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 174	2777	GACATTCAGCTCACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAACAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAGTCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAAATCAAA	ADI-15506 SAD4961_P03_B03	Light chain variable region("LC") nucleic acid sequence
Ab 174	2778	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYSLRTFGGGTKLEIK	ADI-15506 SAD4961_P03_B03	Light chain variable region ("LC") amino acid sequence
Ab 174	2779	KSSQSLLNSRTRKNYLA	ADI-15506 SAD4961_P03_B03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 174	2780	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15506 SAD4961_P03_B03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 174	2781	WASTRES	ADI-15506 SAD4961_P03_B03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 174	2782	TGGGCATCCACTAGGGAATCT	ADI-15506 SAD4961_P03_B03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 174	2783	KQSYSLRT	ADI-15506 SAD4961_P03_B03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 174	2784	AAGCAATCTTATAGTCTTCGGACG	ADI-15506 SAD4961_P03_B03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 175	2785	CAGGTGAAGCTGGAGGAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACACGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAATACAATGAGAAGTTCAAGGGCAAGGCCACACTGTCTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15507 SAD4961_P03_G05	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 175	2786	QVKLEESGPELVKPGASVRISCKASGYTFTRYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLSADKSSSTAYMQLSSLTSEDSAVYFCARDGDYYFDYWGQGTTVTVSS	ADI-15507 SAD4961_P03_G05	Heavy chain variable region ("HC") amino acid sequence
Ab 175	2787	YTFTRYYIH	ADI-15507 SAD4961_P03_G05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 175	2788	TACACCTTCACACGCTACTATATACAC	ADI-15507 SAD4961_P03_G05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 175	2789	WIYPGNVNTKYNEKFKG	ADI-15507 SAD4961_P03_G05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 175	2790	TGGATTTATCCTGGAAATGTTAATACTAAATACAATGAGAAGTTCAAGGGC	ADI-15507 SAD4961_P03_G05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 175	2791	ARDGDYYFDY	ADI-15507 SAD4961_P03_G05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 175	2792	GCAAGAGATGGTGATTACTACTTTGACTAC	ADI-15507 SAD4961_P03_G05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 175	2793	GACATTCAGCTCACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA	ADI-15507 SAD4961_P03_G05	Light chain variable region("LC") nucleic acid sequence
Ab 175	2794	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	ADI-15507 SAD4961_P03_G05	Light chain variable region ("LC") amino acid sequence
Ab 175	2795	KSSQSLLNSRTRKNYLA	ADI-15507 SAD4961_P03_G05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 175	2796	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15507 SAD4961_P03_G05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 175	2797	WASTRES	ADI-15507 SAD4961_P03_G05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 175	2798	TGGGCATCCACTAGGGAATCT	ADI-15507 SAD4961_P03_G05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 175	2799	KQSYNLRT	ADI-15507 SAD4961_P03_G05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 175	2800	AAGCAATCTTATAATCTTCGGACG	ADI-15507 SAD4961_P03_G05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 176	2801	GAGGTGCAGCTGCAGGAGTCTGGACCTGAGCTGGTGAAACCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15508 SAD4961_P03_H08	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 176	2802	EVQLQESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDGDYYFDYWGQGTTVTVSS	ADI-15508 SAD4961_P03_H08	Heavy chain variable region ("HC") amino acid sequence
Ab 176	2803	YTFTSYYIH	ADI-15508 SAD4961_P03_H08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 176	2804	TACACCTTCACAAGCTACTATATACAC	ADI-15508 SAD4961_P03_H08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 176	2805	WIYPGNVNTKYNEKFKG	ADI-15508 SAD4961_P03_H08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 176	2806	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15508 SAD4961_P03_H08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 176	2807	ARDGDYYFDY	ADI-15508 SAD4961_P03_H08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 176	2808	GCAAGAGATGGTGATTACTACTTTGACTAC	ADI-15508 SAD4961_P03_H08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 176	2809	GACATTCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15508 SAD4961_P03_H08	Light chain variable region("LC") nucleic acid sequence
Ab 176	2810	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-15508 SAD4961_P03_H08	Light chain variable region ("LC") amino acid sequence
Ab 176	2811	KSSQSLLNSRTRKNYLA	ADI-15508 SAD4961_P03_H08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 176	2812	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15508 SAD4961_P03_H08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 176	2813	WASTRES	ADI-15508 SAD4961_P03_H08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 176	2814	TGGGCATCCACTAGGGAATCT	ADI-15508 SAD4961_P03_H08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 176	2815	KQSYNLRT	ADI-15508 SAD4961_P03_H08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 176	2816	AAGCAATCTTATAATCTTCGGACG	ADI-15508 SAD4961_P03_H08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 177	2817	GAGGTCAAGCTGGAGGAGTCAGGACCTGAGCTGGCGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGGTAACTACTTCTTCGATGTCTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15509 SAD4961_P03_D01	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 177	2818	EVKLEESGPELAKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARDGNYFFDVWGQGTTVTVSS	ADI-15509 SAD4961_P03_D01	Heavy chain variable region ("HC") amino acid sequence
Ab 177	2819	YTFTSYYIH	ADI-15509 SAD4961_P03_D01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 177	2820	TACACCTTCACAAGCTACTATATACAC	ADI-15509 SAD4961_P03_D01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 177	2821	WIYPGNVNTKYNEKFKG	ADI-15509 SAD4961_P03_D01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 177	2822	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15509 SAD4961_P03_D01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 177	2823	ARDGNYFFDV	ADI-15509 SAD4961_P03_D01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 177	2824	GCAAGAGATGGTAACTACTTCTTCGATGTC	ADI-15509 SAD4961_P03_D01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 177	2825	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACCTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAACCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15509 SAD4961_P03_D01	Light chain variable region("LC") nucleic acid sequence
Ab 177	2826	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-15509 SAD4961_P03_D01	Light chain variable region ("LC") amino acid sequence
Ab 177	2827	KSSQSLLNSRTRKNYLA	ADI-15509 SAD4961_P03_D01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 177	2828	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACCTGGCT	ADI-15509 SAD4961_P03_D01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 177	2829	WASTRES	ADI-15509 SAD4961_P03_D01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 177	2830	TGGGCATCCACTAGGGAATCT	ADI-15509 SAD4961_P03_D01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 177	2831	KQSYNLRT	ADI-15509 SAD4961_P03_D01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 177	2832	AAGCAATCTTATAACCTTCGGACG	ADI-15509 SAD4961_P03_D01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 178	2833	GAGGTTCAGCTGGAGGAGTCTGGACCTGAACTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCAATCTATTTCTGTGCAAGAGATGGTAACTACTTCTTCGATGTCTGGGGCCAAGGCACCACGGTCACCGTCTCC	ADI-15510 SAD4961_P03_H06	Heavy chain variable region ("HC") nucleic acid sequence

		TCA		
Ab 178	2834	EVQLEESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAIYFCARDGNYFFDVWGQGTTVTVSS	ADI-15510 SAD4961_P03_H06	Heavy chain variable region ("HC") amino acid sequence
Ab 178	2835	YTFTSYYIH	ADI-15510 SAD4961_P03_H06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 178	2836	TACACCTTCACAAGCTACTATATACAC	ADI-15510 SAD4961_P03_H06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 178	2837	WIYPGNVNTKYNEKFKG	ADI-15510 SAD4961_P03_H06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 178	2838	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15510 SAD4961_P03_H06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 178	2839	ARDGNYFFDV	ADI-15510 SAD4961_P03_H06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 178	2840	GCAAGAGATGGTAACTACTTCTTCGATGTC	ADI-15510 SAD4961_P03_H06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 178	2841	GATATCGAGCTGATTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAATCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCGGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTATATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15510 SAD4961_P03_H06	Light chain variable region("LC") nucleic acid sequence
Ab 178	2842	DIELIQSPSSLAVSAGEKVTMSCKSSQNLLNSRTRKNYLAWYRQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-15510 SAD4961_P03_H06	Light chain variable region ("LC") amino acid sequence
Ab 178	2843	KSSQNLLNSRTRKNYLA	ADI-15510 SAD4961_P03_H06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 178	2844	AAATCCAGTCAGAATCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15510 SAD4961_P03_H06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 178	2845	WASTRES	ADI-15510 SAD4961_P03_H06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 178	2846	TGGGCATCCACTAGGGAATCT	ADI-15510 SAD4961_P03_H06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 178	2847	KQSYNLRT	ADI-15510 SAD4961_P03_H06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 178	2848	AAGCAATCTTATAATCTTCGGACG	ADI-15510 SAD4961_P03_H06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 179	2849	CAGGTAAAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCAACACCTTCACAAGCTCCTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGTCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGACGGTAGTAGCTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGT	ADI-15511 SAD4961_P03_D09	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 179	2850	QVKLQQSGPELVKPGASVRISCKASGNTFTSSYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTVYMQLSSLTSEDSAVYFCARDGSSYYFDYWGQGTTVTVSS	ADI-15511 SAD4961_P03_D09	Heavy chain variable region ("HC") amino acid sequence
Ab 179	2851	NTFTSSYIH	ADI-15511 SAD4961_P03_D09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 179	2852	AACACCTTCACAAGCTCCTATATACAC	ADI-15511 SAD4961_P03_D09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 179	2853	WIYPGNVNTKYNEKFKG	ADI-15511 SAD4961_P03_D09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 179	2854	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15511 SAD4961_P03_D09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 179	2855	ARDGSSYYFDY	ADI-15511 SAD4961_P03_D09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 179	2856	GCAAGAGACGGTAGTAGCTACTACTTTGACTAC	ADI-15511 SAD4961_P03_D09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 179	2857	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15511 SAD4961_P03_D09	Light chain variable region("LC") nucleic acid sequence
Ab 179	2858	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-15511 SAD4961_P03_D09	Light chain variable region ("LC") amino acid sequence
Ab 179	2859	KSSQSLLNSRTRKNYLA	ADI-15511 SAD4961_P03_D09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 179	2860	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15511 SAD4961_P03_D09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 179	2861	WASTRES	ADI-15511 SAD4961_P03_D09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 179	2862	TGGGCATCCACTAGGGAATCT	ADI-15511 SAD4961_P03_D09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 179	2863	KQSYNLRT	ADI-15511 SAD4961_P03_D09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 179	2864	AAGCAATCTTATAATCTTCGGACG	ADI-15511 SAD4961_P03_D09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 180	2865	GAAGTGCAGCTGGAGCAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGTTCAAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGACTCTGCGATCTATTTCTGTGCAAGGGATGGTTCGTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15512 SAD4961_P03_F09	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 180	2866	EVQLEQSGPELVKPGASVKMSCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGDGSTKYNEKFKGKTTLTADKSSSTAYMLLSSLTSEDSAIYFCARDGSYYFDYWGQGTTVTVSS	ADI-15512 SAD4961_P03_F09	Heavy chain variable region ("HC") amino acid sequence
Ab 180	2867	YTFTSYYIH	ADI-15512 SAD4961_P03_F09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 180	2868	TACACCTTCACAAGCTACTATATACAC	ADI-15512 SAD4961_P03_F09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 180	2869	WIYPGDGSTKYNEKFKG	ADI-15512 SAD4961_P03_F09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 180	2870	TGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15512 SAD4961_P03_F09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 180	2871	ARDGSYYFDY	ADI-15512 SAD4961_P03_F09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 180	2872	GCAAGGGATGGTTCGTACTACTTTGACTAC	ADI-15512 SAD4961_P03_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 180	2873	GACATTCAGCTCACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAACAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAGTCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15512 SAD4961_P03_F09	Light chain variable region("LC") nucleic acid sequence

Ab 180	2874	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYSLRTFGGGTKLELK	ADI-15512 SAD4961_P03_F09	Light chain variable region ("LC") amino acid sequence
Ab 180	2875	KSSQSLLNSRTRKNYLA	ADI-15512 SAD4961_P03_F09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 180	2876	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15512 SAD4961_P03_F09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 180	2877	WASTRES	ADI-15512 SAD4961_P03_F09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 180	2878	TGGGCATCCACTAGGGAATCT	ADI-15512 SAD4961_P03_F09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 180	2879	KQSYSLRT	ADI-15512 SAD4961_P03_F09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 180	2880	AAGCAATCTTATAGTCTTCGGACG	ADI-15512 SAD4961_P03_F09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 181	2881	GAGGTGAAGCTGGAGGAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGTTCAAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGACTCTGCGATCTATTTCTGTGCAAGGGATGGTTCGTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTCCTCA	ADI-15513 SAD4961_P03_H11	Heavy chain variable region ("HC") nucleic acid sequence
Ab 181	2882	EVKLEESGPELVKPGASVKMSCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGDGSTKYNEKFKGKTTLTADKSSSTAYMLLSSLTSEDSAIYFCARDGSYYFDYWGQGTTVTVSS	ADI-15513 SAD4961_P03_H11	Heavy chain variable region ("HC") amino acid sequence
Ab 181	2883	YTFTSYYIH	ADI-15513 SAD4961_P03_H11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 181	2884	TACACCTTCACAAGCTACTATATACAC	ADI-15513 SAD4961_P03_H11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 181	2885	WIYPGDGSTKYNEKFKG	ADI-15513	Heavy chain variable region CDR H2 ("H2")

			SAD4961_P03_H11	amino acid sequence
Ab 181	2886	TGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15513 SAD4961_P03_H11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 181	2887	ARDGSYYFDY	ADI-15513 SAD4961_P03_H11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 181	2888	GCAAGGGATGGTTCGTACTACTTTGACTAC	ADI-15513 SAD4961_P03_H11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 181	2889	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAACAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAGTCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15513 SAD4961_P03_H11	Light chain variable region("LC") nucleic acid sequence
Ab 181	2890	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYSLRTFGGGTKLELK	ADI-15513 SAD4961_P03_H11	Light chain variable region ("LC") amino acid sequence
Ab 181	2891	KSSQSLLNSRTRKNYLA	ADI-15513 SAD4961_P03_H11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 181	2892	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15513 SAD4961_P03_H11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 181	2893	WASTRES	ADI-15513 SAD4961_P03_H11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 181	2894	TGGGCATCCACTAGGGAATCT	ADI-15513 SAD4961_P03_H11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 181	2895	KQSYSLRT	ADI-15513 SAD4961_P03_H11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 181	2896	AAGCAATCTTATAGTCTTCGGACG	ADI-15513 SAD4961_P03_H11	Light chain variable region CDR L3 ("L3") nucleic acid sequence

Ab 182	2897	GAAGTCAAGCTGCAGGAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGTTCAAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGACTCTGCGATCTATTTCTGTGCAAGGGACTACGGGTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTCCTCA	ADI-15514 SAD4961_P03_C02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 182	2898	EVKLQESGPELVKPGASVKMSCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGDGSTKYNEKFKGKTTLTADKSSSTAYMLLSSLTSEDSAIYFCARDYGYYFDYWGQGTTVTVSS	ADI-15514 SAD4961_P03_C02	Heavy chain variable region ("HC") amino acid sequence
Ab 182	2899	YTFTSYYIH	ADI-15514 SAD4961_P03_C02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 182	2900	TACACCTTCACAAGCTACTATATACAC	ADI-15514 SAD4961_P03_C02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 182	2901	WIYPGDGSTKYNEKFKG	ADI-15514 SAD4961_P03_C02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 182	2902	TGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15514 SAD4961_P03_C02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 182	2903	ARDYGYYFDY	ADI-15514 SAD4961_P03_C02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 182	2904	GCAAGGGACTACGGGTACTACTTTGACTAC	ADI-15514 SAD4961_P03_C02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 182	2905	GACATTCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15514 SAD4961_P03_C02	Light chain variable region("LC") nucleic acid sequence
Ab 182	2906	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-15514 SAD4961_P03_C02	Light chain variable region ("LC") amino acid sequence
Ab 182	2907	KSSQSLLNSRTRKNYLA	ADI-15514 SAD4961_P03_C02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 182	2908	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15514 SAD4961_P03_C02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 182	2909	WASTRES	ADI-15514 SAD4961_P03_C02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 182	2910	TGGGCATCCACTAGGGAATCT	ADI-15514 SAD4961_P03_C02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 182	2911	KQSYNLRT	ADI-15514 SAD4961_P03_C02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 182	2912	AAGCAATCTTATAATCTTCGGACG	ADI-15514 SAD4961_P03_C02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 183	2913	GAGGTTAAGCTGGAGGAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGTTTATATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGACTATGGTTACTACTTTGACTATTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15515 SAD4961_P03_H03	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 183	2914	EVKLEESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTVYMQLSSLTSEDSAVYFCARDYGYYFDYWGQGTTVTVSS	ADI-15515 SAD4961_P03_H03	Heavy chain variable region ("HC") amino acid sequence
Ab 183	2915	YTFTSYYIH	ADI-15515 SAD4961_P03_H03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 183	2916	TACACCTTCACAAGCTACTATATACAC	ADI-15515 SAD4961_P03_H03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 183	2917	WIYPGNVNTKYNEKFKG	ADI-15515 SAD4961_P03_H03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 183	2918	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15515 SAD4961_P03_H03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 183	2919	ARDYGYYFDY	ADI-15515 SAD4961_P03_H03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 183	2920	GCAAGAGACTATGGTTACTACTTTGACTAT	ADI-15515 SAD4961_P03_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 183	2921	GACATTGTGCTGACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACCATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15515 SAD4961_P03_H03	Light chain variable region("LC") nucleic acid sequence
Ab 183	2922	DIVLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-15515 SAD4961_P03_H03	Light chain variable region ("LC") amino acid sequence
Ab 183	2923	KSSQSLLNSRTRKNYLA	ADI-15515 SAD4961_P03_H03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 183	2924	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15515 SAD4961_P03_H03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 183	2925	WASTRES	ADI-15515 SAD4961_P03_H03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 183	2926	TGGGCATCCACTAGGGAATCT	ADI-15515 SAD4961_P03_H03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 183	2927	KQSYNLRT	ADI-15515 SAD4961_P03_H03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 183	2928	AAGCAATCTTATAATCTTCGGACG	ADI-15515 SAD4961_P03_H03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 184	2929	GAGGTGCAGCTGGAGGAGTCAGGACCTGAGCTGGTGAGGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTCCTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCACCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGACTATGGTTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15516 SAD4961_P03_C11	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 184	2930	EVQLEESGPELVRPGASVRISCKASGYTFTSSYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAYMHLSSLTSEDSAVYFCARDYGYYFDYWGQGTTVTVSS	ADI-15516 SAD4961_P03_C11	Heavy chain variable region ("HC") amino acid sequence
Ab 184	2931	YTFTSSYIH	ADI-15516 SAD4961_P03_C11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 184	2932	TACACCTTCACAAGCTCCTATATACAC	ADI-15516 SAD4961_P03_C11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 184	2933	WIYPGNVNTKYNEKFKG	ADI-15516 SAD4961_P03_C11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 184	2934	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15516 SAD4961_P03_C11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 184	2935	ARDYGYYFDY	ADI-15516 SAD4961_P03_C11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 184	2936	GCAAGAGACTATGGTTACTACTTTGACTAC	ADI-15516 SAD4961_P03_C11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 184	2937	GACATTGTGCTGACCCAATCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAAGCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15516 SAD4961_P03_C11	Light chain variable region("LC") nucleic acid sequence
Ab 184	2938	DIVLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKAGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-15516 SAD4961_P03_C11	Light chain variable region ("LC") amino acid sequence
Ab 184	2939	KSSQSLLNSRTRKNYLA	ADI-15516 SAD4961_P03_C11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 184	2940	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15516 SAD4961_P03_C11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 184	2941	WASTRES	ADI-15516 SAD4961_P03_C11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 184	2942	TGGGCATCCACTAGGGAATCT	ADI-15516 SAD4961_P03_C11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 184	2943	KQSYNLRT	ADI-15516 SAD4961_P03_C11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 184	2944	AAGCAATCTTATAATCTTCGGACG	ADI-15516 SAD4961_P03_C11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 185	2945	GAGGTTCAGCTGGAGCAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGTCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAATACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGACTATGGTTACTACTTTGGCTCCTGGGGCCAAGGCACCACGGTCACCGTCTCC	ADI-15517 SAD4961_P03_H10	Heavy chain variable region ("HC") nucleic acid sequence

		TCA		
Ab 185	2946	EVQLEQSGPELVKPGASVRISCKSSGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDYGYYFGSWGQGTTVTVSS	ADI-15517 SAD4961_P03_H10	Heavy chain variable region ("HC") amino acid sequence
Ab 185	2947	YTFTSYYIH	ADI-15517 SAD4961_P03_H10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 185	2948	TACACCTTCACAAGCTACTATATACAC	ADI-15517 SAD4961_P03_H10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 185	2949	WIYPGNVNTKYNEKFKG	ADI-15517 SAD4961_P03_H10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 185	2950	TGGATTTATCCTGGAAATGTTAATACTAAATACAATGAGAAGTTCAAGGGC	ADI-15517 SAD4961_P03_H10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 185	2951	ARDYGYYFGS	ADI-15517 SAD4961_P03_H10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 185	2952	GCAAGAGACTATGGTTACTACTTTGGCTCC	ADI-15517 SAD4961_P03_H10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 185	2953	GACATCCAGCTCACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAACTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAATTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGCACAAAGCTGGAAATCAAA	ADI-15517 SAD4961_P03_H10	Light chain variable region("LC") nucleic acid sequence
Ab 185	2954	DIQLTQSPSSLAVSAGEKVTMNCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	ADI-15517 SAD4961_P03_H10	Light chain variable region ("LC") amino acid sequence
Ab 185	2955	KSSQSLLNSRTRKNYLA	ADI-15517 SAD4961_P03_H10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 185	2956	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-15517 SAD4961_P03_H10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 185	2957	WASTRES	ADI-15517 SAD4961_P03_H10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 185	2958	TGGGCATCCACTAGGGAATCT	ADI-15517 SAD4961_P03_H10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 185	2959	KQSYNLRT	ADI-15517 SAD4961_P03_H10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 185	2960	AAGCAATCTTATAATCTTCGGACG	ADI-15517 SAD4961_P03_H10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 186	2961	GAAGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGTTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGTCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGGAAGAGATTACTACGGCTCGTACTACTTTGACAACTGGGGCCAAGGCACCACGGTCA	ADI-15518 SAD4961_P03_C07	Heavy chain variable region ("HC") nucleic acid sequence

		CCGTCTCCTCA		
Ab 186	2962	EVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTVYMQLSSLTSEDSAVYFCGRDYYGSYYFDNWGQGTTVTVSS	ADI-15518 SAD4961_P03_C07	Heavy chain variable region ("HC") amino acid sequence
Ab 186	2963	YTFTSYYIH	ADI-15518 SAD4961_P03_C07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 186	2964	TACACCTTCACAAGCTACTATATACAC	ADI-15518 SAD4961_P03_C07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 186	2965	WIYPGNVNTKYNEKFKG	ADI-15518 SAD4961_P03_C07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 186	2966	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-15518 SAD4961_P03_C07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 186	2967	GRDYYGSYYFDN	ADI-15518 SAD4961_P03_C07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 186	2968	GGAAGAGATTACTACGGCTCGTACTACTTTGACAAC	ADI-15518 SAD4961_P03_C07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 186	2969	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAGGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGCACAAAGTTGGAAATAAAA	ADI-15518 SAD4961_P03_C07	Light chain variable region("LC") nucleic acid sequence
Ab 186	2970	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	ADI-15518 SAD4961_P03_C07	Light chain variable region ("LC") amino acid sequence
Ab 186	2971	KSSQSLLNSRTRKNYLA	ADI-15518 SAD4961_P03_C07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 186	2972	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	ADI-15518 SAD4961_P03_C07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 186	2973	WASTRES	ADI-15518 SAD4961_P03_C07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 186	2974	TGGGCATCCACTAGGGAATCT	ADI-15518 SAD4961_P03_C07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 186	2975	KQSYNLRT	ADI-15518 SAD4961_P03_C07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 186	2976	AAGCAATCTTATAATCTTCGGACG	ADI-15518 SAD4961_P03_C07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 187	2977	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGA TCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAG TTCAAGGGCAGAGTCACCATGACCAGGGACACGTCCAC GAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTG AGGACACGGCGGTGTACTACTGCGCTAGGGATGGCTCC TACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18562 LAD3451_P02_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 187	2978	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18562 LAD3451_P02_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 187	2979	YTFTSYYIH	ADI-18562 LAD3451_P02_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 187	2980	TACACCTTCACCAGCTACTATATACAC	ADI-18562 LAD3451_P02_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 187	2981	WIYPGDGSTKYNEKFKG	ADI-18562 LAD3451_P02_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 187	2982	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18562 LAD3451_P02_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 187	2983	ARDGSYYFDY	ADI-18562 LAD3451_P02_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 187	2984	GCTAGGGATGGCTCCTACTACTTTGACTAC	ADI-18562 LAD3451_P02_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 187	2985	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18562 LAD3451_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 187	2986	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18562 LAD3451_P02_A01	Light chain variable region ("LC") amino acid sequence
Ab 187	2987	KSSQSLLNSRTRKNYLA	ADI-18562 LAD3451_P02_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 187	2988	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18562 LAD3451_P02_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 187	2989	WASTRES	ADI-18562 LAD3451_P02_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 187	2990	TGGGCATCTACCCGGGAATCC	ADI-18562 LAD3451_P02_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 187	2991	KQSYSLRT	ADI-18562 LAD3451_P02_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 187	2992	AAGCAATCTTATTCTCTGAGAACT	ADI-18562 LAD3451_P02_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 188	2993	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATAACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGATGGAAGCTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18563 LAD3451_P02_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 188	2994	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGWIYPGDGSTKYNEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18563 LAD3451_P02_F01	Heavy chain variable region ("HC") amino acid sequence
Ab 188	2995	YTFTSYYIH	ADI-18563 LAD3451_P02_F01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 188	2996	TACACCTTCACCAGCTACTATATACAC	ADI-18563 LAD3451_P02_F01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 188	2997	WIYPGDGSTKYNEKFKG	ADI-18563 LAD3451_P02_F01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 188	2998	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18563 LAD3451_P02_F01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 188	2999	ARDGSYYFDY	ADI-18563 LAD3451_P02_F01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 188	3000	GCGAGGGATGGAAGCTATTACTTTGACTAC	ADI-18563 LAD3451_P02_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 188	3001	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18563 LAD3451_P02_F01	Light chain variable region("LC") nucleic acid sequence
Ab 188	3002	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18563 LAD3451_P02_F01	Light chain variable region ("LC") amino acid sequence
Ab 188	3003	KSSQSLLNSRTRKNYLA	ADI-18563 LAD3451_P02_F01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 188	3004	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18563 LAD3451_P02_F01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 188	3005	WASTRES	ADI-18563 LAD3451_P02_F01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 188	3006	TGGGCATCTACCCGGGAATCC	ADI-18563 LAD3451_P02_F01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 188	3007	KQSYSLRT	ADI-18563 LAD3451_P02_F01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 188	3008	AAGCAATCTTATTCTCTGAGAACT	ADI-18563 LAD3451_P02_F01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 189	3009	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGGGATGGTTCCTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18564 LAD3451_P03_A01	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 189	3010	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGWIYPGDGSTKYNEKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18564 LAD3451_P03_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 189	3011	YTFTSYYIH	ADI-18564 LAD3451_P03_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 189	3012	TACACCTTCACCAGCTACTATATACAC	ADI-18564 LAD3451_P03_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 189	3013	WIYPGDGSTKYNEKFKG	ADI-18564 LAD3451_P03_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 189	3014	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18564 LAD3451_P03_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 189	3015	ARDGSYYFDY	ADI-18564 LAD3451_P03_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 189	3016	GCCAGGGATGGTTCCTATTACTTTGACTAC	ADI-18564 LAD3451_P03_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 189	3017	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18564 LAD3451_P03_A01	Light chain variable region("LC") nucleic acid sequence
Ab 189	3018	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18564 LAD3451_P03_A01	Light chain variable region ("LC") amino acid sequence
Ab 189	3019	KSSQSLLNSRTRKNYLA	ADI-18564 LAD3451_P03_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 189	3020	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18564 LAD3451_P03_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 189	3021	WASTRES	ADI-18564 LAD3451_P03_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 189	3022	TGGGCATCTACCCGGGAATCC	ADI-18564 LAD3451_P03_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 189	3023	KQSYSLRT	ADI-18564 LAD3451_P03_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 189	3024	AAGCAATCTTATTCTCTGAGAACT	ADI-18564 LAD3451_P03_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 190	3025	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGAGATGGCTCATATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18565 LAD3451_P03_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 190	3026	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18565 LAD3451_P03_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 190	3027	YTFTSYYIH	ADI-18565 LAD3451_P03_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 190	3028	TACACCTTCACCAGCTACTATATACAC	ADI-18565 LAD3451_P03_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 190	3029	WIYPGDGSTKYNEKFKG	ADI-18565 LAD3451_P03_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 190	3030	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18565 LAD3451_P03_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 190	3031	ARDGSYYFDY	ADI-18565 LAD3451_P03_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 190	3032	GCTAGAGATGGCTCATATTACTTTGACTAC	ADI-18565 LAD3451_P03_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 190	3033	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18565 LAD3451_P03_A02	Light chain variable region("LC") nucleic acid sequence
Ab 190	3034	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18565 LAD3451_P03_A02	Light chain variable region ("LC") amino acid sequence
Ab 190	3035	KSSQSLLNSRTRKNYLA	ADI-18565 LAD3451_P03_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 190	3036	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18565 LAD3451_P03_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 190	3037	WASTRES	ADI-18565 LAD3451_P03_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 190	3038	TGGGCATCTACCCGGGAATCC	ADI-18565 LAD3451_P03_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 190	3039	KQSYSLRT	ADI-18565 LAD3451_P03_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 190	3040	AAGCAATCTTATTCTCTGAGAACT	ADI-18565 LAD3451_P03_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 191	3041	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGAGACGGATCTTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18566 LAD3451_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 191	3042	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18566 LAD3451_P02_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 191	3043	YTFTSYYIH	ADI-18566 LAD3451_P02_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 191	3044	TACACCTTCACCAGCTACTATATACAC	ADI-18566 LAD3451_P02_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 191	3045	WIYPGDGSTKYNEKFKG	ADI-18566 LAD3451_P02_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 191	3046	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18566 LAD3451_P02_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 191	3047	ARDGSYYFDY	ADI-18566 LAD3451_P02_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 191	3048	GCTAGAGACGGATCTTATTACTTTGACTAC	ADI-18566 LAD3451_P02_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 191	3049	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18566 LAD3451_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 191	3050	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18566 LAD3451_P02_A03	Light chain variable region ("LC") amino acid sequence
Ab 191	3051	KSSQSLLNSRTRKNYLA	ADI-18566 LAD3451_P02_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 191	3052	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18566 LAD3451_P02_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 191	3053	WASTRES	ADI-18566 LAD3451_P02_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 191	3054	TGGGCATCTACCCGGGAATCC	ADI-18566 LAD3451_P02_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 191	3055	KQSYSLRT	ADI-18566 LAD3451_P02_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 191	3056	AAGCAATCTTATTCTCTGAGAACT	ADI-18566 LAD3451_P02_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 192	3057	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGAGATGGTAGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18567 LAD3451_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 192	3058	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18567 LAD3451_P02_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 192	3059	YTFTSYYIH	ADI-18567 LAD3451_P02_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 192	3060	TACACCTTCACCAGCTACTATATACAC	ADI-18567 LAD3451_P02_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 192	3061	WIYPGDGSTKYNEKFKG	ADI-18567 LAD3451_P02_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 192	3062	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18567 LAD3451_P02_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 192	3063	ARDGSYYFDY	ADI-18567 LAD3451_P02_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 192	3064	GCGAGAGATGGTAGCTACTACTTTGACTAC	ADI-18567 LAD3451_P02_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 192	3065	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTTAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18567 LAD3451_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 192	3066	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18567 LAD3451_P02_E03	Light chain variable region ("LC") amino acid sequence
Ab 192	3067	KSSQSLLNSRTRKNYLA	ADI-18567 LAD3451_P02_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 192	3068	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18567 LAD3451_P02_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 192	3069	WASTRES	ADI-18567 LAD3451_P02_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 192	3070	TGGGCATCTACCCGGGAATCC	ADI-18567 LAD3451_P02_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 192	3071	KQSYSLRT	ADI-18567 LAD3451_P02_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 192	3072	AAGCAATCTTATTCTCTTAGAACT	ADI-18567 LAD3451_P02_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 193	3073	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGGGATGGCTCCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18568 LAD3451_P02_B04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 193	3074	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18568 LAD3451_P02_B04	Heavy chain variable region ("HC") amino acid sequence
Ab 193	3075	YTFTSYYIH	ADI-18568 LAD3451_P02_B04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 193	3076	TACACCTTCACCAGCTACTATATACAC	ADI-18568 LAD3451_P02_B04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 193	3077	WIYPGDGSTKYNEKFKG	ADI-18568 LAD3451_P02_B04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 193	3078	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18568 LAD3451_P02_B04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 193	3079	ARDGSYYFDY	ADI-18568 LAD3451_P02_B04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 193	3080	GCTAGGGATGGCTCCTACTACTTTGACTAC	ADI-18568 LAD3451_P02_B04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 193	3081	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18568 LAD3451_P02_B04	Light chain variable region("LC") nucleic acid sequence
Ab 193	3082	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18568 LAD3451_P02_B04	Light chain variable region ("LC") amino acid sequence
Ab 193	3083	KSSQSLLNSRTRKNYLA	ADI-18568 LAD3451_P02_B04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 193	3084	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18568 LAD3451_P02_B04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 193	3085	WASTRES	ADI-18568 LAD3451_P02_B04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 193	3086	TGGGCATCTACCCGGGAATCC	ADI-18568 LAD3451_P02_B04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 193	3087	KQSYNLRT	ADI-18568 LAD3451_P02_B04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 193	3088	AAGCAGAGTTACAATTTGAGAACT	ADI-18568 LAD3451_P02_B04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 194	3089	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATAACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGATGGAAGCTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18569 LAD3451_P02_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 194	3090	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGWIYPGDGSTKYNEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18569 LAD3451_P02_E04	Heavy chain variable region ("HC") amino acid sequence
Ab 194	3091	YTFTSYYIH	ADI-18569 LAD3451_P02_E04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 194	3092	TACACCTTCACCAGCTACTATATACAC	ADI-18569 LAD3451_P02_E04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 194	3093	WIYPGDGSTKYNEKFKG	ADI-18569 LAD3451_P02_E04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 194	3094	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18569 LAD3451_P02_E04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 194	3095	ARDGSYYFDY	ADI-18569 LAD3451_P02_E04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 194	3096	GCGAGGGATGGAAGCTATTACTTTGACTAC	ADI-18569 LAD3451_P02_E04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 194	3097	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18569 LAD3451_P02_E04	Light chain variable region("LC") nucleic acid sequence
Ab 194	3098	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18569 LAD3451_P02_E04	Light chain variable region ("LC") amino acid sequence
Ab 194	3099	KSSQSLLNSRTRKNYLA	ADI-18569 LAD3451_P02_E04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 194	3100	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18569 LAD3451_P02_E04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 194	3101	WASTRES	ADI-18569 LAD3451_P02_E04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 194	3102	TGGGCATCTACCCGGGAATCC	ADI-18569 LAD3451_P02_E04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 194	3103	KQSYNLRT	ADI-18569 LAD3451_P02_E04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 194	3104	AAGCAGAGTTACAATTTGAGAACT	ADI-18569 LAD3451_P02_E04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 195	3105	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGGGATGGTTCCTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18570 LAD3451_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 195	3106	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGWIYPGDGSTKYNEKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18570 LAD3451_P02_A05	Heavy chain variable region ("HC") amino acid sequence
Ab 195	3107	YTFTSYYIH	ADI-18570 LAD3451_P02_A05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 195	3108	TACACCTTCACCAGCTACTATATACAC	ADI-18570 LAD3451_P02_A05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 195	3109	WIYPGDGSTKYNEKFKG	ADI-18570 LAD3451_P02_A05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 195	3110	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18570 LAD3451_P02_A05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 195	3111	ARDGSYYFDY	ADI-18570 LAD3451_P02_A05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 195	3112	GCCAGGGATGGTTCCTATTACTTTGACTAC	ADI-18570 LAD3451_P02_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 195	3113	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18570 LAD3451_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 195	3114	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18570 LAD3451_P02_A05	Light chain variable region ("LC") amino acid sequence
Ab 195	3115	KSSQSLLNSRTRKNYLA	ADI-18570 LAD3451_P02_A05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 195	3116	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18570 LAD3451_P02_A05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 195	3117	WASTRES	ADI-18570 LAD3451_P02_A05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 195	3118	TGGGCATCTACCCGGGAATCC	ADI-18570 LAD3451_P02_A05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 195	3119	KQSYNLRT	ADI-18570 LAD3451_P02_A05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 195	3120	AAGCAGAGTTACAATTTGAGAACT	ADI-18570 LAD3451_P02_A05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 196	3121	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGAGATGGCTCATATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18571 LAD3451_P02_H05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 196	3122	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18571 LAD3451_P02_H05	Heavy chain variable region ("HC") amino acid sequence
Ab 196	3123	YTFTSYYIH	ADI-18571 LAD3451_P02_H05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 196	3124	TACACCTTCACCAGCTACTATATACAC	ADI-18571 LAD3451_P02_H05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 196	3125	WIYPGDGSTKYNEKFKG	ADI-18571 LAD3451_P02_H05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 196	3126	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18571 LAD3451_P02_H05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 196	3127	ARDGSYYFDY	ADI-18571 LAD3451_P02_H05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 196	3128	GCTAGAGATGGCTCATATTACTTTGACTAC	ADI-18571 LAD3451_P02_H05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 196	3129	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18571 LAD3451_P02_H05	Light chain variable region("LC") nucleic acid sequence
Ab 196	3130	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18571 LAD3451_P02_H05	Light chain variable region ("LC") amino acid sequence
Ab 196	3131	KSSQSLLNSRTRKNYLA	ADI-18571 LAD3451_P02_H05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 196	3132	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18571 LAD3451_P02_H05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 196	3133	WASTRES	ADI-18571 LAD3451_P02_H05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 196	3134	TGGGCATCTACCCGGGAATCC	ADI-18571 LAD3451_P02_H05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 196	3135	KQSYNLRT	ADI-18571 LAD3451_P02_H05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 196	3136	AAGCAGAGTTACAATTTGAGAACT	ADI-18571 LAD3451_P02_H05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 197	3137	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGAGACGGATCTTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18572 LAD3451_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 197	3138	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18572 LAD3451_P02_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 197	3139	YTFTSYYIH	ADI-18572 LAD3451_P02_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 197	3140	TACACCTTCACCAGCTACTATATACAC	ADI-18572 LAD3451_P02_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 197	3141	WIYPGDGSTKYNEKFKG	ADI-18572 LAD3451_P02_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 197	3142	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18572 LAD3451_P02_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 197	3143	ARDGSYYFDY	ADI-18572 LAD3451_P02_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 197	3144	GCTAGAGACGGATCTTATTACTTTGACTAC	ADI-18572 LAD3451_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 197	3145	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18572 LAD3451_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 197	3146	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18572 LAD3451_P02_A06	Light chain variable region ("LC") amino acid sequence
Ab 197	3147	KSSQSLLNSRTRKNYLA	ADI-18572 LAD3451_P02_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 197	3148	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18572 LAD3451_P02_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 197	3149	WASTRES	ADI-18572 LAD3451_P02_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 197	3150	TGGGCATCTACCCGGGAATCC	ADI-18572 LAD3451_P02_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 197	3151	KQSYNLRT	ADI-18572 LAD3451_P02_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 197	3152	AAGCAGAGTTACAATTTGAGAACT	ADI-18572 LAD3451_P02_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 198	3153	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGAGATGGTAGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18573 LAD3451_P02_G06	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 198	3154	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-18573 LAD3451_P02_G06	Heavy chain variable region ("HC") amino acid sequence
Ab 198	3155	YTFTSYYIH	ADI-18573 LAD3451_P02_G06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 198	3156	TACACCTTCACCAGCTACTATATACAC	ADI-18573 LAD3451_P02_G06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 198	3157	WIYPGDGSTKYNEKFKG	ADI-18573 LAD3451_P02_G06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 198	3158	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18573 LAD3451_P02_G06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 198	3159	ARDGSYYFDY	ADI-18573 LAD3451_P02_G06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 198	3160	GCGAGAGATGGTAGCTACTACTTTGACTAC	ADI-18573 LAD3451_P02_G06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 198	3161	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGCTGGAGATCAAA	ADI-18573 LAD3451_P02_G06	Light chain variable region("LC") nucleic acid sequence
Ab 198	3162	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKLEIK	ADI-18573 LAD3451_P02_G06	Light chain variable region ("LC") amino acid sequence
Ab 198	3163	KSSQSLLNSRTRKNYLA	ADI-18573 LAD3451_P02_G06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 198	3164	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18573 LAD3451_P02_G06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 198	3165	WASTRES	ADI-18573 LAD3451_P02_G06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 198	3166	TGGGCATCTACCCGGGAATCC	ADI-18573 LAD3451_P02_G06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 198	3167	KQSYNLRT	ADI-18573 LAD3451_P02_G06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 198	3168	AAGCAGAGTTACAATTTGAGAACT	ADI-18573 LAD3451_P02_G06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 199	3169	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATAACCAGGGACACGTCCGCGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGGGATTATGGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18574 LAD3452_P02_A07	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 199	3170	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQRLEWMGWIYPGNVNTKYNEKFKGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18574 LAD3452_P02_A07	Heavy chain variable region ("HC") amino acid sequence
Ab 199	3171	YTFTSSYIH	ADI-18574 LAD3452_P02_A07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 199	3172	TACACCTTCACCAGCTCCTATATACAC	ADI-18574 LAD3452_P02_A07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 199	3173	WIYPGNVNTKYNEKFKG	ADI-18574 LAD3452_P02_A07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 199	3174	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18574 LAD3452_P02_A07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 199	3175	ARDYGYYFDY	ADI-18574 LAD3452_P02_A07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 199	3176	GCTAGGGATTATGGCTACTACTTTGACTAC	ADI-18574 LAD3452_P02_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 199	3177	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18574 LAD3452_P02_A07	Light chain variable region("LC") nucleic acid sequence
Ab 199	3178	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18574 LAD3452_P02_A07	Light chain variable region ("LC") amino acid sequence
Ab 199	3179	KSSQSLLNSRTRKNYLA	ADI-18574 LAD3452_P02_A07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 199	3180	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18574 LAD3452_P02_A07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 199	3181	WASTRES	ADI-18574 LAD3452_P02_A07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 199	3182	TGGGCATCTACCCGGGAATCC	ADI-18574 LAD3452_P02_A07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 199	3183	KQSYSLRT	ADI-18574 LAD3452_P02_A07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 199	3184	AAGCAATCTTATTCTCTGAGAACT	ADI-18574 LAD3452_P02_A07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 200	3185	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCGCGAGCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGAGACTACGGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18575 LAD3452_P02_E07	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 200	3186	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSASTAYMHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18575 LAD3452_P02_E07	Heavy chain variable region ("HC") amino acid sequence
Ab 200	3187	YTFTSSYIH	ADI-18575 LAD3452_P02_E07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 200	3188	TACACCTTCACCAGCTCCTATATACAC	ADI-18575 LAD3452_P02_E07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 200	3189	WIYPGNVNTKYNEKFKG	ADI-18575 LAD3452_P02_E07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 200	3190	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18575 LAD3452_P02_E07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 200	3191	ARDYGYYFDY	ADI-18575 LAD3452_P02_E07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 200	3192	GCGAGAGACTACGGCTACTACTTTGACTAC	ADI-18575 LAD3452_P02_E07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 200	3193	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18575 LAD3452_P02_E07	Light chain variable region("LC") nucleic acid sequence
Ab 200	3194	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18575 LAD3452_P02_E07	Light chain variable region ("LC") amino acid sequence
Ab 200	3195	KSSQSLLNSRTRKNYLA	ADI-18575 LAD3452_P02_E07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 200	3196	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18575 LAD3452_P02_E07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 200	3197	WASTRES	ADI-18575 LAD3452_P02_E07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 200	3198	TGGGCATCTACCCGGGAATCC	ADI-18575 LAD3452_P02_E07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 200	3199	KQSYSLRT	ADI-18575 LAD3452_P02_E07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 200	3200	AAGCAATCTTATTCTCTGAGAACT	ADI-18575 LAD3452_P02_E07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 201	3201	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATAACCGCGGACAAGTCCGCGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGATTACGGATACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18576 LAD3452_P02_A08	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 201	3202	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQRLEWIGWIYPGNVNTKYNEKFKGRVTITADKSASTAYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18576 LAD3452_P02_A08	Heavy chain variable region ("HC") amino acid sequence
Ab 201	3203	YTFTSSYIH	ADI-18576 LAD3452_P02_A08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 201	3204	TACACCTTCACCAGCTCCTATATACAC	ADI-18576 LAD3452_P02_A08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 201	3205	WIYPGNVNTKYNEKFKG	ADI-18576 LAD3452_P02_A08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 201	3206	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18576 LAD3452_P02_A08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 201	3207	ARDYGYYFDY	ADI-18576 LAD3452_P02_A08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 201	3208	GCGAGGGATTACGGATACTACTTTGACTAC	ADI-18576 LAD3452_P02_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 201	3209	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18576 LAD3452_P02_A08	Light chain variable region("LC") nucleic acid sequence
Ab 201	3210	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18576 LAD3452_P02_A08	Light chain variable region ("LC") amino acid sequence
Ab 201	3211	KSSQSLLNSRTRKNYLA	ADI-18576 LAD3452_P02_A08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 201	3212	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18576 LAD3452_P02_A08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 201	3213	WASTRES	ADI-18576 LAD3452_P02_A08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 201	3214	TGGGCATCTACCCGGGAATCC	ADI-18576 LAD3452_P02_A08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 201	3215	KQSYSLRT	ADI-18576 LAD3452_P02_A08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 201	3216	AAGCAATCTTATTCTCTGAGAACT	ADI-18576 LAD3452_P02_A08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 202	3217	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGGGACTATGGTTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18577 LAD3452_P02_G08	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 202	3218	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWMGWIYPGNVNTKYNEKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18577 LAD3452_P02_G08	Heavy chain variable region ("HC") amino acid sequence
Ab 202	3219	YTFTSSYIH	ADI-18577 LAD3452_P02_G08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 202	3220	TACACCTTCACCAGCTCCTATATACAC	ADI-18577 LAD3452_P02_G08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 202	3221	WIYPGNVNTKYNEKFKG	ADI-18577 LAD3452_P02_G08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 202	3222	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18577 LAD3452_P02_G08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 202	3223	ARDYGYYFDY	ADI-18577 LAD3452_P02_G08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 202	3224	GCTAGGGACTATGGTTACTACTTTGACTAC	ADI-18577 LAD3452_P02_G08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 202	3225	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18577 LAD3452_P02_G08	Light chain variable region("LC") nucleic acid sequence
Ab 202	3226	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18577 LAD3452_P02_G08	Light chain variable region ("LC") amino acid sequence
Ab 202	3227	KSSQSLLNSRTRKNYLA	ADI-18577 LAD3452_P02_G08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 202	3228	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18577 LAD3452_P02_G08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 202	3229	WASTRES	ADI-18577 LAD3452_P02_G08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 202	3230	TGGGCATCTACCCGGGAATCC	ADI-18577 LAD3452_P02_G08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 202	3231	KQSYSLRT	ADI-18577 LAD3452_P02_G08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 202	3232	AAGCAATCTTATTCTCTGAGAACT	ADI-18577 LAD3452_P02_G08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 203	3233	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGGGACTACGGTTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18578 LAD3452_P02_C09	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 203	3234	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWIGWIYPGNVNTKYNEKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18578 LAD3452_P02_C09	Heavy chain variable region ("HC") amino acid sequence
Ab 203	3235	YTFTSSYIH	ADI-18578 LAD3452_P02_C09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 203	3236	TACACCTTCACCAGCTCCTATATACAC	ADI-18578 LAD3452_P02_C09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 203	3237	WIYPGNVNTKYNEKFKG	ADI-18578 LAD3452_P02_C09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 203	3238	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18578 LAD3452_P02_C09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 203	3239	ARDYGYYFDY	ADI-18578 LAD3452_P02_C09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 203	3240	GCTAGGGACTACGGTTATTACTTTGACTAC	ADI-18578 LAD3452_P02_C09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 203	3241	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18578 LAD3452_P02_C09	Light chain variable region("LC") nucleic acid sequence
Ab 203	3242	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18578 LAD3452_P02_C09	Light chain variable region ("LC") amino acid sequence
Ab 203	3243	KSSQSLLNSRTRKNYLA	ADI-18578 LAD3452_P02_C09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 203	3244	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18578 LAD3452_P02_C09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 203	3245	WASTRES	ADI-18578 LAD3452_P02_C09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 203	3246	TGGGCATCTACCCGGGAATCC	ADI-18578 LAD3452_P02_C09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 203	3247	KQSYSLRT	ADI-18578 LAD3452_P02_C09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 203	3248	AAGCAATCTTATTCTCTGAGAACT	ADI-18578 LAD3452_P02_C09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 204	3249	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCACGAGCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGACTATGGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18579 LAD3452_P02_E09	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 204	3250	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSTSTAYMHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18579 LAD3452_P02_E09	Heavy chain variable region ("HC") amino acid sequence
Ab 204	3251	YTFTSSYIH	ADI-18579 LAD3452_P02_E09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 204	3252	TACACCTTCACCAGCTCCTATATACAC	ADI-18579 LAD3452_P02_E09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 204	3253	WIYPGNVNTKYNEKFKG	ADI-18579 LAD3452_P02_E09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 204	3254	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18579 LAD3452_P02_E09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 204	3255	ARDYGYYFDY	ADI-18579 LAD3452_P02_E09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 204	3256	GCGAGGGACTATGGCTACTACTTTGACTAC	ADI-18579 LAD3452_P02_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 204	3257	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18579 LAD3452_P02_E09	Light chain variable region("LC") nucleic acid sequence
Ab 204	3258	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18579 LAD3452_P02_E09	Light chain variable region ("LC") amino acid sequence
Ab 204	3259	KSSQSLLNSRTRKNYLA	ADI-18579 LAD3452_P02_E09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 204	3260	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18579 LAD3452_P02_E09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 204	3261	WASTRES	ADI-18579 LAD3452_P02_E09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 204	3262	TGGGCATCTACCCGGGAATCC	ADI-18579 LAD3452_P02_E09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 204	3263	KQSYSLRT	ADI-18579 LAD3452_P02_E09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 204	3264	AAGCAATCTTATTCTCTGAGAACT	ADI-18579 LAD3452_P02_E09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 205	3265	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATAACCAGGGACACGTCCGCGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGGGATTATGGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18580 LAD3452_P02_B10	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 205	3266	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQRLEWMGWIYPGNVNTKYNEKFKGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18580 LAD3452_P02_B10	Heavy chain variable region ("HC") amino acid sequence
Ab 205	3267	YTFTSSYIH	ADI-18580 LAD3452_P02_B10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 205	3268	TACACCTTCACCAGCTCCTATATACAC	ADI-18580 LAD3452_P02_B10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 205	3269	WIYPGNVNTKYNEKFKG	ADI-18580 LAD3452_P02_B10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 205	3270	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18580 LAD3452_P02_B10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 205	3271	ARDYGYYFDY	ADI-18580 LAD3452_P02_B10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 205	3272	GCTAGGGATTATGGCTACTACTTTGACTAC	ADI-18580 LAD3452_P02_B10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 205	3273	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18580 LAD3452_P02_B10	Light chain variable region("LC") nucleic acid sequence
Ab 205	3274	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18580 LAD3452_P02_B10	Light chain variable region ("LC") amino acid sequence
Ab 205	3275	KSSQSLLNSRTRKNYLA	ADI-18580 LAD3452_P02_B10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 205	3276	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18580 LAD3452_P02_B10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 205	3277	WASTRES	ADI-18580 LAD3452_P02_B10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 205	3278	TGGGCATCTACCCGGGAATCC	ADI-18580 LAD3452_P02_B10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 205	3279	KQSYNLRT	ADI-18580 LAD3452_P02_B10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 205	3280	AAGCAGAGTTACAATTTGAGAACT	ADI-18580 LAD3452_P02_B10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 206	3281	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCGCGAGCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGAGACTACGGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18581 LAD3452_P02_F10	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 206	3282	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSASTAYMHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18581 LAD3452_P02_F10	Heavy chain variable region ("HC") amino acid sequence
Ab 206	3283	YTFTSSYIH	ADI-18581 LAD3452_P02_F10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 206	3284	TACACCTTCACCAGCTCCTATATACAC	ADI-18581 LAD3452_P02_F10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 206	3285	WIYPGNVNTKYNEKFKG	ADI-18581 LAD3452_P02_F10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 206	3286	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18581 LAD3452_P02_F10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 206	3287	ARDYGYYFDY	ADI-18581 LAD3452_P02_F10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 206	3288	GCGAGAGACTACGGCTACTACTTTGACTAC	ADI-18581 LAD3452_P02_F10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 206	3289	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18581 LAD3452_P02_F10	Light chain variable region("LC") nucleic acid sequence
Ab 206	3290	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18581 LAD3452_P02_F10	Light chain variable region ("LC") amino acid sequence
Ab 206	3291	KSSQSLLNSRTRKNYLA	ADI-18581 LAD3452_P02_F10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 206	3292	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18581 LAD3452_P02_F10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 206	3293	WASTRES	ADI-18581 LAD3452_P02_F10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 206	3294	TGGGCATCTACCCGGGAATCC	ADI-18581 LAD3452_P02_F10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 206	3295	KQSYNLRT	ADI-18581 LAD3452_P02_F10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 206	3296	AAGCAGAGTTACAATTTGAGAACT	ADI-18581 LAD3452_P02_F10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 207	3297	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATAACCGCGGACAAGTCCGCGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGATTACGGATACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18582 LAD3452_P02_B11	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 207	3298	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQRLEWIGWIYPGNVNTKYNEKFKGRVTITADKSASTAYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18582 LAD3452_P02_B11	Heavy chain variable region ("HC") amino acid sequence
Ab 207	3299	YTFTSSYIH	ADI-18582 LAD3452_P02_B11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 207	3300	TACACCTTCACCAGCTCCTATATACAC	ADI-18582 LAD3452_P02_B11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 207	3301	WIYPGNVNTKYNEKFKG	ADI-18582 LAD3452_P02_B11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 207	3302	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18582 LAD3452_P02_B11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 207	3303	ARDYGYYFDY	ADI-18582 LAD3452_P02_B11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 207	3304	GCGAGGGATTACGGATACTACTTTGACTAC	ADI-18582 LAD3452_P02_B11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 207	3305	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18582 LAD3452_P02_B11	Light chain variable region("LC") nucleic acid sequence
Ab 207	3306	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18582 LAD3452_P02_B11	Light chain variable region ("LC") amino acid sequence
Ab 207	3307	KSSQSLLNSRTRKNYLA	ADI-18582 LAD3452_P02_B11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 207	3308	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18582 LAD3452_P02_B11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 207	3309	WASTRES	ADI-18582 LAD3452_P02_B11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 207	3310	TGGGCATCTACCCGGGAATCC	ADI-18582 LAD3452_P02_B11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 207	3311	KQSYNLRT	ADI-18582 LAD3452_P02_B11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 207	3312	AAGCAGAGTTACAATTTGAGAACT	ADI-18582 LAD3452_P02_B11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 208	3313	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGGGACTATGGTTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18583 LAD3452_P02_E11	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 208	3314	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWMGWIYPGNVNTKYNEKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18583 LAD3452_P02_E11	Heavy chain variable region ("HC") amino acid sequence
Ab 208	3315	YTFTSSYIH	ADI-18583 LAD3452_P02_E11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 208	3316	TACACCTTCACCAGCTCCTATATACAC	ADI-18583 LAD3452_P02_E11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 208	3317	WIYPGNVNTKYNEKFKG	ADI-18583 LAD3452_P02_E11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 208	3318	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18583 LAD3452_P02_E11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 208	3319	ARDYGYYFDY	ADI-18583 LAD3452_P02_E11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 208	3320	GCTAGGGACTATGGTTACTACTTTGACTAC	ADI-18583 LAD3452_P02_E11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 208	3321	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18583 LAD3452_P02_E11	Light chain variable region("LC") nucleic acid sequence
Ab 208	3322	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18583 LAD3452_P02_E11	Light chain variable region ("LC") amino acid sequence
Ab 208	3323	KSSQSLLNSRTRKNYLA	ADI-18583 LAD3452_P02_E11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 208	3324	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18583 LAD3452_P02_E11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 208	3325	WASTRES	ADI-18583 LAD3452_P02_E11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 208	3326	TGGGCATCTACCCGGGAATCC	ADI-18583 LAD3452_P02_E11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 208	3327	KQSYNLRT	ADI-18583 LAD3452_P02_E11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 208	3328	AAGCAGAGTTACAATTTGAGAACT	ADI-18583 LAD3452_P02_E11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 209	3329	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGGGACTACGGTTATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18584 LAD3452_P02_C12	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 209	3330	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWIGWIYPGNVNTKYNEKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18584 LAD3452_P02_C12	Heavy chain variable region ("HC") amino acid sequence
Ab 209	3331	YTFTSSYIH	ADI-18584 LAD3452_P02_C12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 209	3332	TACACCTTCACCAGCTCCTATATACAC	ADI-18584 LAD3452_P02_C12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 209	3333	WIYPGNVNTKYNEKFKG	ADI-18584 LAD3452_P02_C12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 209	3334	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18584 LAD3452_P02_C12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 209	3335	ARDYGYYFDY	ADI-18584 LAD3452_P02_C12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 209	3336	GCTAGGGACTACGGTTATTACTTTGACTAC	ADI-18584 LAD3452_P02_C12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 209	3337	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTAGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18584 LAD3452_P02_C12	Light chain variable region("LC") nucleic acid sequence
Ab 209	3338	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18584 LAD3452_P02_C12	Light chain variable region ("LC") amino acid sequence
Ab 209	3339	KSSQSLLNSRTRKNYLA	ADI-18584 LAD3452_P02_C12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 209	3340	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18584 LAD3452_P02_C12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 209	3341	WASTRES	ADI-18584 LAD3452_P02_C12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 209	3342	TGGGCATCTACCCGGGAATCC	ADI-18584 LAD3452_P02_C12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 209	3343	KQSYNLRT	ADI-18584 LAD3452_P02_C12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 209	3344	AAGCAGAGTTACAATTTGAGAACT	ADI-18584 LAD3452_P02_C12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 210	3345	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCACGAGCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGACTATGGCTACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18585 LAD3452_P02_H12	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 210	3346	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSTSTAYMHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-18585 LAD3452_P02_H12	Heavy chain variable region ("HC") amino acid sequence
Ab 210	3347	YTFTSSYIH	ADI-18585 LAD3452_P02_H12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 210	3348	TACACCTTCACCAGCTCCTATATACAC	ADI-18585 LAD3452_P02_H12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 210	3349	WIYPGNVNTKYNEKFKG	ADI-18585 LAD3452_P02_H12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 210	3350	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTTCAAGGGC	ADI-18585 LAD3452_P02_H12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 210	3351	ARDYGYYFDY	ADI-18585 LAD3452_P02_H12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 210	3352	GCGAGGGACTATGGCTACTACTTTGACTAC	ADI-18585 LAD3452_P02_H12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 210	3353	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18585 LAD3452_P02_H12	Light chain variable region("LC") nucleic acid sequence
Ab 210	3354	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18585 LAD3452_P02_H12	Light chain variable region ("LC") amino acid sequence
Ab 210	3355	KSSQSLLNSRTRKNYLA	ADI-18585 LAD3452_P02_H12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 210	3356	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18585 LAD3452_P02_H12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 210	3357	WASTRES	ADI-18585 LAD3452_P02_H12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 210	3358	TGGGCATCTACCCGGGAATCC	ADI-18585 LAD3452_P02_H12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 210	3359	KQSYNLRT	ADI-18585 LAD3452_P02_H12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 210	3360	AAGCAGAGTTACAATTTGAGAACT	ADI-18585 LAD3452_P02_H12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 211	3361	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGAGACGGATATGCAAGGTATTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18586 LAD3453_P02_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 211	3362	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWMGWIDPENGNTIYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18586 LAD3453_P02_D01	Heavy chain variable region ("HC") amino acid sequence
Ab 211	3363	FNIKDYYMH	ADI-18586 LAD3453_P02_D01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 211	3364	TTCAACATCAAGGACTACTATATGCAC	ADI-18586 LAD3453_P02_D01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 211	3365	WIDPENGNTIYDPKFQG	ADI-18586 LAD3453_P02_D01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 211	3366	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGC	ADI-18586 LAD3453_P02_D01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 211	3367	ARDGYARYYFDY	ADI-18586 LAD3453_P02_D01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 211	3368	GCTAGAGACGGATATGCAAGGTATTACTTTGACTAC	ADI-18586 LAD3453_P02_D01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 211	3369	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18586 LAD3453_P02_D01	Light chain variable region("LC") nucleic acid sequence
Ab 211	3370	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18586 LAD3453_P02_D01	Light chain variable region ("LC") amino acid sequence
Ab 211	3371	KSSQSLLNSRTRKNYLA	ADI-18586 LAD3453_P02_D01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 211	3372	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18586 LAD3453_P02_D01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 211	3373	WASTRES	ADI-18586 LAD3453_P02_D01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 211	3374	TGGGCATCTACCCGGGAATCC	ADI-18586 LAD3453_P02_D01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 211	3375	KQSYSLRT	ADI-18586 LAD3453_P02_D01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 211	3376	AAGCAATCTTATTCTCTGAGAACT	ADI-18586 LAD3453_P02_D01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 212	3377	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGCAGAGTCACCATGACCGCGGACACGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGACGGTTATGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-18587 LAD3453_P02_E01	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 212	3378	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWIGWIDPENGNTIYDPKFQGRVTMTADTSTSTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18587 LAD3453_P02_E01	Heavy chain variable region ("HC") amino acid sequence
Ab 212	3379	FNIKDYYMH	ADI-18587 LAD3453_P02_E01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 212	3380	TTCAACATCAAGGACTACTATATGCAC	ADI-18587 LAD3453_P02_E01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 212	3381	WIDPENGNTIYDPKFQG	ADI-18587 LAD3453_P02_E01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 212	3382	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGC	ADI-18587 LAD3453_P02_E01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 212	3383	ARDGYARYYFDY	ADI-18587 LAD3453_P02_E01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 212	3384	GCGAGGGACGGTTATGCTAGATATTACTTTGACTAC	ADI-18587 LAD3453_P02_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 212	3385	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18587 LAD3453_P02_E01	Light chain variable region("LC") nucleic acid sequence
Ab 212	3386	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18587 LAD3453_P02_E01	Light chain variable region ("LC") amino acid sequence
Ab 212	3387	KSSQSLLNSRTRKNYLA	ADI-18587 LAD3453_P02_E01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 212	3388	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18587 LAD3453_P02_E01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 212	3389	WASTRES	ADI-18587 LAD3453_P02_E01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 212	3390	TGGGCATCTACCCGGGAATCC	ADI-18587 LAD3453_P02_E01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 212	3391	KQSYSLRT	ADI-18587 LAD3453_P02_E01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 212	3392	AAGCAATCTTATTCTCTGAGAACT	ADI-18587 LAD3453_P02_E01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 213	3393	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGCAGAGCCACCATAACCGCGGACACGTCCACGAACACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGATGGTTATGCCAGATACTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18588 LAD3453_P02_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 213	3394	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWIGWIDPENGNTIYDPKFQGRATITADTSTNTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18588 LAD3453_P02_B02	Heavy chain variable region ("HC") amino acid sequence
Ab 213	3395	FNIKDYYMH	ADI-18588 LAD3453_P02_B02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 213	3396	TTCAACATCAAGGACTACTATATGCAC	ADI-18588 LAD3453_P02_B02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 213	3397	WIDPENGNTIYDPKFQG	ADI-18588 LAD3453_P02_B02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 213	3398	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGC	ADI-18588 LAD3453_P02_B02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 213	3399	ARDGYARYYFDY	ADI-18588 LAD3453_P02_B02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 213	3400	GCCAGAGATGGTTATGCCAGATACTACTTTGACTAC	ADI-18588 LAD3453_P02_B02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 213	3401	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18588 LAD3453_P02_B02	Light chain variable region("LC") nucleic acid sequence
Ab 213	3402	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18588 LAD3453_P02_B02	Light chain variable region ("LC") amino acid sequence
Ab 213	3403	KSSQSLLNSRTRKNYLA	ADI-18588 LAD3453_P02_B02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 213	3404	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18588 LAD3453_P02_B02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 213	3405	WASTRES	ADI-18588 LAD3453_P02_B02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 213	3406	TGGGCATCTACCCGGGAATCC	ADI-18588 LAD3453_P02_B02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 213	3407	KQSYSLRT	ADI-18588 LAD3453_P02_B02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 213	3408	AAGCAATCTTATTCTCTGAGAACT	ADI-18588 LAD3453_P02_B02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 214	3409	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18589 LAD3453_P02_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 214	3410	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18589 LAD3453_P02_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 214	3411	FNIKDYYMH	ADI-18589 LAD3453_P02_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 214	3412	TTCAACATCAAGGACTACTATATGCAC	ADI-18589 LAD3453_P02_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 214	3413	WIDPENGNTIYDPKFQG	ADI-18589 LAD3453_P02_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 214	3414	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-18589 LAD3453_P02_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 214	3415	ARDGYARYYFDY	ADI-18589 LAD3453_P02_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 214	3416	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-18589 LAD3453_P02_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 214	3417	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18589 LAD3453_P02_E02	Light chain variable region("LC") nucleic acid sequence
Ab 214	3418	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18589 LAD3453_P02_E02	Light chain variable region ("LC") amino acid sequence
Ab 214	3419	KSSQSLLNSRTRKNYLA	ADI-18589 LAD3453_P02_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 214	3420	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18589 LAD3453_P02_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 214	3421	WASTRES	ADI-18589 LAD3453_P02_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 214	3422	TGGGCATCTACCCGGGAATCC	ADI-18589 LAD3453_P02_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 214	3423	KQSYSLRT	ADI-18589 LAD3453_P02_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 214	3424	AAGCAATCTTATTCTCTGAGAACT	ADI-18589 LAD3453_P02_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 215	3425	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCGCGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACGCCAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-18590 LAD3453_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 215	3426	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18590 LAD3453_P02_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 215	3427	FNIKDYYMH	ADI-18590 LAD3453_P02_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 215	3428	TTCAACATCAAGGACTACTATATGCAC	ADI-18590 LAD3453_P02_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 215	3429	WIDPENGNTIYDPKFQG	ADI-18590 LAD3453_P02_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 215	3430	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-18590 LAD3453_P02_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 215	3431	ARDGYARYYFDY	ADI-18590 LAD3453_P02_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 215	3432	GCTAGAGACGGTTACGCCAGATATTACTTTGACTAC	ADI-18590 LAD3453_P02_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 215	3433	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18590 LAD3453_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 215	3434	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18590 LAD3453_P02_A03	Light chain variable region ("LC") amino acid sequence
Ab 215	3435	KSSQSLLNSRTRKNYLA	ADI-18590 LAD3453_P02_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 215	3436	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18590 LAD3453_P02_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 215	3437	WASTRES	ADI-18590 LAD3453_P02_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 215	3438	TGGGCATCTACCCGGGAATCC	ADI-18590 LAD3453_P02_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 215	3439	KQSYSLRT	ADI-18590 LAD3453_P02_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 215	3440	AAGCAATCTTATTCTCTGAGAACT	ADI-18590 LAD3453_P02_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 216	3441	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGCCACCATAACCGCGGACACGTCCGCCAACACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGACGGATACGCGAGATACTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18591 LAD3453_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 216	3442	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDPENGNTIYDPKFQGRATITADTSANTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18591 LAD3453_P02_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 216	3443	FNIKDYYMH	ADI-18591 LAD3453_P02_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 216	3444	TTCAACATCAAGGACTACTATATGCAC	ADI-18591 LAD3453_P02_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 216	3445	WIDPENGNTIYDPKFQG	ADI-18591 LAD3453_P02_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 216	3446	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-18591 LAD3453_P02_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 216	3447	ARDGYARYYFDY	ADI-18591 LAD3453_P02_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 216	3448	GCGAGAGACGGATACGCGAGATACTACTTTGACTAC	ADI-18591 LAD3453_P02_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 216	3449	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18591 LAD3453_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 216	3450	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-18591 LAD3453_P02_E03	Light chain variable region ("LC") amino acid sequence
Ab 216	3451	KSSQSLLNSRTRKNYLA	ADI-18591 LAD3453_P02_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 216	3452	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18591 LAD3453_P02_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 216	3453	WASTRES	ADI-18591 LAD3453_P02_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 216	3454	TGGGCATCTACCCGGGAATCC	ADI-18591 LAD3453_P02_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 216	3455	KQSYSLRT	ADI-18591 LAD3453_P02_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 216	3456	AAGCAATCTTATTCTCTGAGAACT	ADI-18591 LAD3453_P02_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 217	3457	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGAGACGGATATGCAAGGTATTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18592 LAD3453_P02_B04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 217	3458	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWMGWIDPENGNTIYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18592 LAD3453_P02_B04	Heavy chain variable region ("HC") amino acid sequence
Ab 217	3459	FNIKDYYMH	ADI-18592 LAD3453_P02_B04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 217	3460	TTCAACATCAAGGACTACTATATGCAC	ADI-18592 LAD3453_P02_B04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 217	3461	WIDPENGNTIYDPKFQG	ADI-18592 LAD3453_P02_B04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 217	3462	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGC	ADI-18592 LAD3453_P02_B04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 217	3463	ARDGYARYYFDY	ADI-18592 LAD3453_P02_B04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 217	3464	GCTAGAGACGGATATGCAAGGTATTACTTTGACTAC	ADI-18592 LAD3453_P02_B04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 217	3465	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18592 LAD3453_P02_B04	Light chain variable region("LC") nucleic acid sequence
Ab 217	3466	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18592 LAD3453_P02_B04	Light chain variable region ("LC") amino acid sequence
Ab 217	3467	KSSQSLLNSRTRKNYLA	ADI-18592 LAD3453_P02_B04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 217	3468	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18592 LAD3453_P02_B04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 217	3469	WASTRES	ADI-18592 LAD3453_P02_B04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 217	3470	TGGGCATCTACCCGGGAATCC	ADI-18592 LAD3453_P02_B04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 217	3471	KQSYNLRT	ADI-18592 LAD3453_P02_B04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 217	3472	AAGCAGAGTTACAATTTGAGAACT	ADI-18592 LAD3453_P02_B04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 218	3473	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGCAGAGCCACCATAACCGCGGACACGTCCACGAACACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGATGGTTATGCCAGATACTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18593 LAD3453_P02_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 218	3474	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWIGWIDPENGNTIYDPKFQGRATITADTSTNTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18593 LAD3453_P02_C05	Heavy chain variable region ("HC") amino acid sequence
Ab 218	3475	FNIKDYYMH	ADI-18593 LAD3453_P02_C05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 218	3476	TTCAACATCAAGGACTACTATATGCAC	ADI-18593 LAD3453_P02_C05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 218	3477	WIDPENGNTIYDPKFQG	ADI-18593 LAD3453_P02_C05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 218	3478	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGC	ADI-18593 LAD3453_P02_C05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 218	3479	ARDGYARYYFDY	ADI-18593 LAD3453_P02_C05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 218	3480	GCCAGAGATGGTTATGCCAGATACTACTTTGACTAC	ADI-18593 LAD3453_P02_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 218	3481	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18593 LAD3453_P02_C05	Light chain variable region("LC") nucleic acid sequence
Ab 218	3482	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18593 LAD3453_P02_C05	Light chain variable region ("LC") amino acid sequence
Ab 218	3483	KSSQSLLNSRTRKNYLA	ADI-18593 LAD3453_P02_C05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 218	3484	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18593 LAD3453_P02_C05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 218	3485	WASTRES	ADI-18593 LAD3453_P02_C05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 218	3486	TGGGCATCTACCCGGGAATCC	ADI-18593 LAD3453_P02_C05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 218	3487	KQSYNLRT	ADI-18593 LAD3453_P02_C05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 218	3488	AAGCAGAGTTACAATTTGAGAACT	ADI-18593 LAD3453_P02_C05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 219	3489	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18594 LAD3453_P02_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 219	3490	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18594 LAD3453_P02_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 219	3491	FNIKDYYMH	ADI-18594 LAD3453_P02_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 219	3492	TTCAACATCAAGGACTACTATATGCAC	ADI-18594 LAD3453_P02_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 219	3493	WIDPENGNTIYDPKFQG	ADI-18594 LAD3453_P02_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 219	3494	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-18594 LAD3453_P02_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 219	3495	ARDGYARYYFDY	ADI-18594 LAD3453_P02_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 219	3496	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-18594 LAD3453_P02_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 219	3497	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18594 LAD3453_P02_E05	Light chain variable region("LC") nucleic acid sequence
Ab 219	3498	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18594 LAD3453_P02_E05	Light chain variable region ("LC") amino acid sequence
Ab 219	3499	KSSQSLLNSRTRKNYLA	ADI-18594 LAD3453_P02_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 219	3500	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18594 LAD3453_P02_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 219	3501	WASTRES	ADI-18594 LAD3453_P02_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 219	3502	TGGGCATCTACCCGGGAATCC	ADI-18594 LAD3453_P02_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 219	3503	KQSYNLRT	ADI-18594 LAD3453_P02_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 219	3504	AAGCAGAGTTACAATTTGAGAACT	ADI-18594 LAD3453_P02_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 220	3505	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCGCGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACGCCAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-18595 LAD3453_P02_D06	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 220	3506	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18595 LAD3453_P02_D06	Heavy chain variable region ("HC") amino acid sequence
Ab 220	3507	FNIKDYYMH	ADI-18595 LAD3453_P02_D06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 220	3508	TTCAACATCAAGGACTACTATATGCAC	ADI-18595 LAD3453_P02_D06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 220	3509	WIDPENGNTIYDPKFQG	ADI-18595 LAD3453_P02_D06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 220	3510	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-18595 LAD3453_P02_D06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 220	3511	ARDGYARYYFDY	ADI-18595 LAD3453_P02_D06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 220	3512	GCTAGAGACGGTTACGCCAGATATTACTTTGACTAC	ADI-18595 LAD3453_P02_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 220	3513	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18595 LAD3453_P02_D06	Light chain variable region("LC") nucleic acid sequence
Ab 220	3514	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18595 LAD3453_P02_D06	Light chain variable region ("LC") amino acid sequence
Ab 220	3515	KSSQSLLNSRTRKNYLA	ADI-18595 LAD3453_P02_D06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 220	3516	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18595 LAD3453_P02_D06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 220	3517	WASTRES	ADI-18595 LAD3453_P02_D06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 220	3518	TGGGCATCTACCCGGGAATCC	ADI-18595 LAD3453_P02_D06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 220	3519	KQSYNLRT	ADI-18595 LAD3453_P02_D06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 220	3520	AAGCAGAGTTACAATTTGAGAACT	ADI-18595 LAD3453_P02_D06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 221	3521	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGCCACCATAACCGCGGACACGTCCGCCAACACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGACGGATACGCGAGATACTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18596 LAD3453_P02_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 221	3522	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDPENGNTIYDPKFQGRATITADTSANTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18596 LAD3453_P02_F06	Heavy chain variable region ("HC") amino acid sequence
Ab 221	3523	FNIKDYYMH	ADI-18596 LAD3453_P02_F06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 221	3524	TTCAACATCAAGGACTACTATATGCAC	ADI-18596 LAD3453_P02_F06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 221	3525	WIDPENGNTIYDPKFQG	ADI-18596 LAD3453_P02_F06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 221	3526	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-18596 LAD3453_P02_F06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 221	3527	ARDGYARYYFDY	ADI-18596 LAD3453_P02_F06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 221	3528	GCGAGAGACGGATACGCGAGATACTACTTTGACTAC	ADI-18596 LAD3453_P02_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 221	3529	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18596 LAD3453_P02_F06	Light chain variable region("LC") nucleic acid sequence
Ab 221	3530	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18596 LAD3453_P02_F06	Light chain variable region ("LC") amino acid sequence
Ab 221	3531	KSSQSLLNSRTRKNYLA	ADI-18596 LAD3453_P02_F06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 221	3532	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18596 LAD3453_P02_F06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 221	3533	WASTRES	ADI-18596 LAD3453_P02_F06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 221	3534	TGGGCATCTACCCGGGAATCC	ADI-18596 LAD3453_P02_F06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 221	3535	KQSYNLRT	ADI-18596 LAD3453_P02_F06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 221	3536	AAGCAGAGTTACAATTTGAGAACT	ADI-18596 LAD3453_P02_F06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 222	3537	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGCAGAGTCACCATGACCGCGGACACGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGACGGTTATGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-18597 LAD3453_P03_B03	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 222	3538	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWIGWIDPENGNTIYDPKFQGRVTMTADTSTSTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-18597 LAD3453_P03_B03	Heavy chain variable region ("HC") amino acid sequence
Ab 222	3539	FNIKDYYMH	ADI-18597 LAD3453_P03_B03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 222	3540	TTCAACATCAAGGACTACTATATGCAC	ADI-18597 LAD3453_P03_B03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 222	3541	WIDPENGNTIYDPKFQG	ADI-18597 LAD3453_P03_B03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 222	3542	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCGAAGTTCCAGGGC	ADI-18597 LAD3453_P03_B03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 222	3543	ARDGYARYYFDY	ADI-18597 LAD3453_P03_B03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 222	3544	GCGAGGGACGGTTATGCTAGATATTACTTTGACTAC	ADI-18597 LAD3453_P03_B03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 222	3545	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18597 LAD3453_P03_B03	Light chain variable region("LC") nucleic acid sequence
Ab 222	3546	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	ADI-18597 LAD3453_P03_B03	Light chain variable region ("LC") amino acid sequence
Ab 222	3547	KSSQSLLNSRTRKNYLA	ADI-18597 LAD3453_P03_B03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 222	3548	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-18597 LAD3453_P03_B03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 222	3549	WASTRES	ADI-18597 LAD3453_P03_B03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 222	3550	TGGGCATCTACCCGGGAATCC	ADI-18597 LAD3453_P03_B03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 222	3551	KQSYNLRT	ADI-18597 LAD3453_P03_B03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 222	3552	AAGCAGAGTTACAATTTGAGAACT	ADI-18597 LAD3453_P03_B03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 223	3553	CAGGTCCAGCTTGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAAGGCTTCGGGATACCCCTTCAGTTCCTATCCTATGCATTGGGTGCGCCAGGCCCCCGGACAAAGGCTTGAGTGGATGGGATGGATCAACGTTGACAATGAGAACACAAAATATTCATGGAAGTTCCGGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAGTTTACATGGAGCTGAGCAGTCTGATATCTGAAGACACGGCTGTGTATTACTGTGGGAGAGACTGGGACGGGGCGATCCGTGTCTTGGACTACTGGGGCCAGGGAACCCT	ADI-18965 SAD4931_P05_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 223	3554	QVQLVQSGAEVKKPGASVKISCKASGYPFSSYPMHWVRQAPGQRLEWMGWINVDNENTKYSWKFRGRVTITRDTSASTVYMELSSLISEDTAVYYCGRDWDGAIRVLDYWGQGTLVTVSS	ADI-18965 SAD4931_P05_F07	Heavy chain variable region ("HC") amino acid sequence
Ab 223	3555	YPFSSYPMH	ADI-18965 SAD4931_P05_F07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 223	3556	TACCCCTTCAGTTCCTATCCTATGCAT	ADI-18965 SAD4931_P05_F07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 223	3557	WINVDNENTKYSWKFRG	ADI-18965 SAD4931_P05_F07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 223	3558	TGGATCAACGTTGACAATGAGAACACAAAATATTCATGGAAGTTCCGGGGC	ADI-18965 SAD4931_P05_F07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 223	3559	GRDWDGAIRVLDY	ADI-18965 SAD4931_P05_F07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 223	3560	GGGAGAGACTGGGACGGGGCGATCCGTGTCTTGGACTAC	ADI-18965 SAD4931_P05_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 223	3561	GATATTGTGATGACTCAGACTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCACCTGCAAGTCCAGCCAGAGTGTTTTATTCAGCTCCGACAATAAGAACTACTTAGCTTGGTACCAGCAGAAACCGGGACAGCCTCCTAAATTGCTCATTTACTGGGCATCTATCCGGGAATCCGGGGTCCCTGACCGATTCGGTGGCAGCGGGTCTGGGACACATTTCACTCTCACCATCACCAGCGTGCAGGCTGCAGATGTGGCAGTTTATTACTGTCAGCAATATTATGGTAATTTCCCCACCTTCGGCCAAGGGACACGACTGGAGATTAAA	ADI-18965 SAD4931_P05_F07	Light chain variable region("LC") nucleic acid sequence
Ab 223	3562	DIVMTQTPDSLAVSLGERATITCKSSQSVLFSSDNKNYLAWYQQKPGQPPKLLIYWASIRESGVPDRFGGSGSGTHFTLTITSVQAADVAVYYCQQYYGNFPTFGQGTRLEIK	ADI-18965 SAD4931_P05_F07	Light chain variable region ("LC") amino acid sequence
Ab 223	3563	KSSQSVLFSSDNKNYLA	ADI-18965 SAD4931_P05_F07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 223	3564	AAGTCCAGCCAGAGTGTTTTATTCAGCTCCGACAATAAGAACTACTTAGCT	ADI-18965 SAD4931_P05_F07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 223	3565	WASIRES	ADI-18965 SAD4931_P05_F07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 223	3566	TGGGCATCTATCCGGGAATCC	ADI-18965 SAD4931_P05_F07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 223	3567	QQYYGNFPT	ADI-18965 SAD4931_P05_F07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 223	3568	CAGCAATATTATGGTAATTTCCCCACC	ADI-18965 SAD4931_P05_F07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 224	3569	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20564 SAD5574_P03_C02	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 224	3570	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20564 SAD5574_P03_C02	Heavy chain variable region ("HC") amino acid sequence
Ab 224	3571	FNIKDYYMH	ADI-20564 SAD5574_P03_C02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 224	3572	TTCAACATCAAGGACTACTATATGCAC	ADI-20564 SAD5574_P03_C02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 224	3573	WIDLENGNTIYDPKFQG	ADI-20564 SAD5574_P03_C02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 224	3574	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20564 SAD5574_P03_C02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 224	3575	ARDGYARYYFDY	ADI-20564 SAD5574_P03_C02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 224	3576	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20564 SAD5574_P03_C02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 224	3577	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20564 SAD5574_P03_C02	Light chain variable region("LC") nucleic acid sequence
Ab 224	3578	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	ADI-20564 SAD5574_P03_C02	Light chain variable region ("LC") amino acid sequence
Ab 224	3579	KSSQSLLNSRTRKNYLA	ADI-20564 SAD5574_P03_C02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 224	3580	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20564 SAD5574_P03_C02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 224	3581	WASTRES	ADI-20564 SAD5574_P03_C02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 224	3582	TGGGCATCTACCCGGGAATCC	ADI-20564 SAD5574_P03_C02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 224	3583	KQSYFRRA	ADI-20564 SAD5574_P03_C02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 224	3584	AAGCAATCTTATTTTCGGAGAGCT	ADI-20564 SAD5574_P03_C02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 225	3585	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACACCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCCGGGCAAAGGCTTGAGTGGATGGGATGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGGTCTGAAGACACGGCGGTGTACTACTGCGCGAGGGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-20565 SAD5574_P03_C06	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 225	3586	QVQLVQSGAEVKKPGASVKVSCKASGFNTKDYYMHWVRQAPGQRLEWMGWIGPENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20565 SAD5574_P03_C06	Heavy chain variable region ("HC") amino acid sequence
Ab 225	3587	FNTKDYYMH	ADI-20565 SAD5574_P03_C06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 225	3588	TTCAACACCAAGGACTACTATATGCAC	ADI-20565 SAD5574_P03_C06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 225	3589	WIGPENGNTIYDPKFQG	ADI-20565 SAD5574_P03_C06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 225	3590	TGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20565 SAD5574_P03_C06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 225	3591	ARDGYARYYFDY	ADI-20565 SAD5574_P03_C06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 225	3592	GCGAGGGATGGATACGCTAGATATTACTTTGACTAC	ADI-20565 SAD5574_P03_C06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 225	3593	GACATCGTAATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20565 SAD5574_P03_C06	Light chain variable region("LC") nucleic acid sequence
Ab 225	3594	DIVMTQSPDSLAVSLGERATINCRSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20565 SAD5574_P03_C06	Light chain variable region ("LC") amino acid sequence
Ab 225	3595	RSSQSLLNSRTRKNYLA	ADI-20565 SAD5574_P03_C06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 225	3596	AGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20565 SAD5574_P03_C06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 225	3597	WASTRES	ADI-20565 SAD5574_P03_C06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 225	3598	TGGGCATCTACCCGGGAATCC	ADI-20565 SAD5574_P03_C06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 225	3599	KQSYSRRT	ADI-20565 SAD5574_P03_C06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 225	3600	AAGCAATCTTATTCTCGGAGAACT	ADI-20565 SAD5574_P03_C06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 226	3601	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCCGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20566 SAD5574_P03_G09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 226	3602	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20566 SAD5574_P03_G09	Heavy chain variable region ("HC") amino acid sequence
Ab 226	3603	FNIKDYYMH	ADI-20566 SAD5574_P03_G09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 226	3604	TTCAACATCAAGGACTACTATATGCAC	ADI-20566 SAD5574_P03_G09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 226	3605	WIDLENGNTIYDPKFQG	ADI-20566 SAD5574_P03_G09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 226	3606	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20566 SAD5574_P03_G09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 226	3607	ARDGYARYYFDY	ADI-20566 SAD5574_P03_G09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 226	3608	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20566 SAD5574_P03_G09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 226	3609	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGACTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20566 SAD5574_P03_G09	Light chain variable region("LC") nucleic acid sequence
Ab 226	3610	DIVMTQSPDSLAVSLGERATINCKSSQSLLNGRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGTGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20566 SAD5574_P03_G09	Light chain variable region ("LC") amino acid sequence
Ab 226	3611	KSSQSLLNGRTRKNYLA	ADI-20566 SAD5574_P03_G09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 226	3612	AAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTTAGCT	ADI-20566 SAD5574_P03_G09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 226	3613	WASTRES	ADI-20566 SAD5574_P03_G09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 226	3614	TGGGCATCTACCCGGGAATCC	ADI-20566 SAD5574_P03_G09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 226	3615	KQSYSRRT	ADI-20566 SAD5574_P03_G09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 226	3616	AAGCAATCTTATTCTCGGAGAACT	ADI-20566 SAD5574_P03_G09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 227	3617	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAGGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20567 SAD5574_P03_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 227	3618	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20567 SAD5574_P03_F09	Heavy chain variable region ("HC") amino acid sequence
Ab 227	3619	FNIKDYYMH	ADI-20567 SAD5574_P03_F09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 227	3620	TTCAACATCAAGGACTACTATATGCAC	ADI-20567 SAD5574_P03_F09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 227	3621	WIDLENGNTIYDPKFQG	ADI-20567 SAD5574_P03_F09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 227	3622	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20567 SAD5574_P03_F09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 227	3623	ARDGYARYYFDY	ADI-20567 SAD5574_P03_F09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 227	3624	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20567 SAD5574_P03_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 227	3625	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20567 SAD5574_P03_F09	Light chain variable region("LC") nucleic acid sequence
Ab 227	3626	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	ADI-20567 SAD5574_P03_F09	Light chain variable region ("LC") amino acid sequence
Ab 227	3627	KSSQSLLNSRTRKNYLA	ADI-20567 SAD5574_P03_F09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 227	3628	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20567 SAD5574_P03_F09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 227	3629	WASTRES	ADI-20567 SAD5574_P03_F09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 227	3630	TGGGCATCTACCCGGGAATCC	ADI-20567 SAD5574_P03_F09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 227	3631	KQSYFRRA	ADI-20567 SAD5574_P03_F09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 227	3632	AAGCAATCTTATTTTCGGAGAGCT	ADI-20567 SAD5574_P03_F09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 228	3633	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20568 SAD5574_P03_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 228	3634	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20568 SAD5574_P03_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 228	3635	FNIKDYYMH	ADI-20568 SAD5574_P03_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 228	3636	TTCAACATCAAGGACTACTATATGCAC	ADI-20568 SAD5574_P03_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 228	3637	WIDLENGNTIYDPKFQG	ADI-20568 SAD5574_P03_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 228	3638	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20568 SAD5574_P03_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 228	3639	ARDGYARYYFDY	ADI-20568 SAD5574_P03_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 228	3640	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20568 SAD5574_P03_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 228	3641	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20568 SAD5574_P03_A01	Light chain variable region("LC") nucleic acid sequence
Ab 228	3642	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20568 SAD5574_P03_A01	Light chain variable region ("LC") amino acid sequence
Ab 228	3643	KSSQSLLNSRTRKNYLA	ADI-20568 SAD5574_P03_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 228	3644	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20568 SAD5574_P03_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 228	3645	WASTRES	ADI-20568 SAD5574_P03_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 228	3646	TGGGCATCTACCCGGGAATCC	ADI-20568 SAD5574_P03_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 228	3647	KQSYSRRT	ADI-20568 SAD5574_P03_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 228	3648	AAGCAATCTTATTCTCGGAGAACT	ADI-20568 SAD5574_P03_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 229	3649	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20569 SAD5574_P03_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 229	3650	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20569 SAD5574_P03_A05	Heavy chain variable region ("HC") amino acid sequence
Ab 229	3651	FNIKDYYMH	ADI-20569 SAD5574_P03_A05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 229	3652	TTCAACATCAAGGACTACTATATGCAC	ADI-20569 SAD5574_P03_A05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 229	3653	WIDLENGNTIYDPKFQG	ADI-20569 SAD5574_P03_A05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 229	3654	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20569 SAD5574_P03_A05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 229	3655	ARDGYARYYFDY	ADI-20569 SAD5574_P03_A05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 229	3656	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20569 SAD5574_P03_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 229	3657	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGGGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-20569 SAD5574_P03_A05	Light chain variable region("LC") nucleic acid sequence
Ab 229	3658	DIVMTQSPDSLAVSLGGRATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20569 SAD5574_P03_A05	Light chain variable region ("LC") amino acid sequence
Ab 229	3659	KSSQSLLNSRTRKNYLA	ADI-20569 SAD5574_P03_A05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 229	3660	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20569 SAD5574_P03_A05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 229	3661	WASTRES	ADI-20569 SAD5574_P03_A05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 229	3662	TGGGCATCTACCCGGGAATCC	ADI-20569 SAD5574_P03_A05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 229	3663	KQSYSRRT	ADI-20569 SAD5574_P03_A05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 229	3664	AAGCAATCTTATTCTCGGAGAACT	ADI-20569 SAD5574_P03_A05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 230	3665	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACACCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCCGGGCAAAGGCTTGAGTGGATGGGATGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGGTCTGAAGACACGGCGGTGTACTACTGCGCGAGGGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-20570 SAD5574_P03_G06	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 230	3666	QVQLVQSGAEVKKPGASVKVSCKASGFNTKDYYMHWVRQAPGQRLEWMGWIGPENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20570 SAD5574_P03_G06	Heavy chain variable region ("HC") amino acid sequence
Ab 230	3667	FNTKDYYMH	ADI-20570 SAD5574_P03_G06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 230	3668	TTCAACACCAAGGACTACTATATGCAC	ADI-20570 SAD5574_P03_G06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 230	3669	WIGPENGNTIYDPKFQG	ADI-20570 SAD5574_P03_G06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 230	3670	TGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20570 SAD5574_P03_G06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 230	3671	ARDGYARYYFDY	ADI-20570 SAD5574_P03_G06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 230	3672	GCGAGGGATGGATACGCTAGATATTACTTTGACTAC	ADI-20570 SAD5574_P03_G06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 230	3673	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGCCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20570 SAD5574_P03_G06	Light chain variable region("LC") nucleic acid sequence
Ab 230	3674	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20570 SAD5574_P03_G06	Light chain variable region ("LC") amino acid sequence
Ab 230	3675	KSSQSLLNSRTRKNYLA	ADI-20570 SAD5574_P03_G06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 230	3676	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20570 SAD5574_P03_G06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 230	3677	WASTRES	ADI-20570 SAD5574_P03_G06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 230	3678	TGGGCATCTACCCGGGAATCC	ADI-20570 SAD5574_P03_G06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 230	3679	KQSYSRRT	ADI-20570 SAD5574_P03_G06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 230	3680	AAGCAATCTTATTCTCGGAGAACT	ADI-20570 SAD5574_P03_G06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 231	3681	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20571 SAD5574_P03_B03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 231	3682	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20571 SAD5574_P03_B03	Heavy chain variable region ("HC") amino acid sequence
Ab 231	3683	FNIKDYYMH	ADI-20571 SAD5574_P03_B03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 231	3684	TTCAACATCAAGGACTACTATATGCAC	ADI-20571 SAD5574_P03_B03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 231	3685	WIDLENGNTIYDPKFQG	ADI-20571 SAD5574_P03_B03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 231	3686	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20571 SAD5574_P03_B03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 231	3687	ARDGYARYYFDY	ADI-20571 SAD5574_P03_B03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 231	3688	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20571 SAD5574_P03_B03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 231	3689	GACATCGTAATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTATCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20571 SAD5574_P03_B03	Light chain variable region("LC") nucleic acid sequence
Ab 231	3690	DIVMTQSPDSLAVSLGERATINCRSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASIRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20571 SAD5574_P03_B03	Light chain variable region ("LC") amino acid sequence
Ab 231	3691	RSSQSLLNSRTRKNYLA	ADI-20571 SAD5574_P03_B03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 231	3692	AGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20571 SAD5574_P03_B03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 231	3693	WASIRES	ADI-20571 SAD5574_P03_B03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 231	3694	TGGGCATCTATCCGGGAATCC	ADI-20571 SAD5574_P03_B03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 231	3695	KQSYSRRT	ADI-20571 SAD5574_P03_B03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 231	3696	AAGCAATCTTATTCTCGGAGAACT	ADI-20571 SAD5574_P03_B03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 232	3697	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20572 SAD5574_P03_H06	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 232	3698	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20572 SAD5574_P03_H06	Heavy chain variable region ("HC") amino acid sequence
Ab 232	3699	FNIKDYYMH	ADI-20572 SAD5574_P03_H06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 232	3700	TTCAACATCAAGGACTACTATATGCAC	ADI-20572 SAD5574_P03_H06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 232	3701	WIDLENGNTIYDPKFQG	ADI-20572 SAD5574_P03_H06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 232	3702	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20572 SAD5574_P03_H06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 232	3703	ARDGYARYYFDY	ADI-20572 SAD5574_P03_H06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 232	3704	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20572 SAD5574_P03_H06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 232	3705	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20572 SAD5574_P03_H06	Light chain variable region("LC") nucleic acid sequence
Ab 232	3706	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	ADI-20572 SAD5574_P03_H06	Light chain variable region ("LC") amino acid sequence
Ab 232	3707	KSSQSLLNSRTRKNYLA	ADI-20572 SAD5574_P03_H06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 232	3708	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20572 SAD5574_P03_H06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 232	3709	WASTRES	ADI-20572 SAD5574_P03_H06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 232	3710	TGGGCATCTACCCGGGAATCC	ADI-20572 SAD5574_P03_H06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 232	3711	KQSYFRRA	ADI-20572 SAD5574_P03_H06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 232	3712	AAGCAATCTTATTTTCGGAGAGCT	ADI-20572 SAD5574_P03_H06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 233	3713	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20573 SAD5574_P03_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 233	3714	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20573 SAD5574_P03_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 233	3715	FNIKDYYMH	ADI-20573 SAD5574_P03_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 233	3716	TTCAACATCAAGGACTACTATATGCAC	ADI-20573 SAD5574_P03_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 233	3717	WIDLENGNTIYDPKFQG	ADI-20573 SAD5574_P03_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 233	3718	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20573 SAD5574_P03_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 233	3719	ARDGYARYYFDY	ADI-20573 SAD5574_P03_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 233	3720	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20573 SAD5574_P03_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 233	3721	GACATCGTAATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20573 SAD5574_P03_A02	Light chain variable region("LC") nucleic acid sequence
Ab 233	3722	DIVMTQSPDSLAVSLGERATINCRSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20573 SAD5574_P03_A02	Light chain variable region ("LC") amino acid sequence
Ab 233	3723	RSSQSLLNSRTRKNYLA	ADI-20573 SAD5574_P03_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 233	3724	AGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20573 SAD5574_P03_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 233	3725	WASTRES	ADI-20573 SAD5574_P03_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 233	3726	TGGGCATCTACCCGGGAATCC	ADI-20573 SAD5574_P03_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 233	3727	KQSYSRRT	ADI-20573 SAD5574_P03_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 233	3728	AAGCAATCTTATTCTCGGAGAACT	ADI-20573 SAD5574_P03_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 234	3729	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20574 SAD5574_P03_A08	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 234	3730	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20574 SAD5574_P03_A08	Heavy chain variable region ("HC") amino acid sequence
Ab 234	3731	FNIKDYYMH	ADI-20574 SAD5574_P03_A08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 234	3732	TTCAACATCAAGGACTACTATATGCAC	ADI-20574 SAD5574_P03_A08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 234	3733	WIDLENGNTIYDPKFQG	ADI-20574 SAD5574_P03_A08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 234	3734	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20574 SAD5574_P03_A08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 234	3735	ARDGYARYYFDY	ADI-20574 SAD5574_P03_A08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 234	3736	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20574 SAD5574_P03_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 234	3737	GGCATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-20574 SAD5574_P03_A08	Light chain variable region("LC") nucleic acid sequence
Ab 234	3738	GIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20574 SAD5574_P03_A08	Light chain variable region ("LC") amino acid sequence
Ab 234	3739	KSSQSLLNSRTRKNYLA	ADI-20574 SAD5574_P03_A08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 234	3740	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20574 SAD5574_P03_A08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 234	3741	WASTRES	ADI-20574 SAD5574_P03_A08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 234	3742	TGGGCATCTACCCGGGAATCC	ADI-20574 SAD5574_P03_A08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 234	3743	KQSYSRRT	ADI-20574 SAD5574_P03_A08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 234	3744	AAGCAATCTTATTCTCGGAGAACT	ADI-20574 SAD5574_P03_A08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 235	3745	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20575 SAD5574_P03_H05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 235	3746	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20575 SAD5574_P03_H05	Heavy chain variable region ("HC") amino acid sequence
Ab 235	3747	FNIKDYYMH	ADI-20575 SAD5574_P03_H05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 235	3748	TTCAACATCAAGGACTACTATATGCAC	ADI-20575 SAD5574_P03_H05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 235	3749	WIDLENGNTIYDPKFQG	ADI-20575 SAD5574_P03_H05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 235	3750	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20575 SAD5574_P03_H05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 235	3751	ARDGYARYYFDY	ADI-20575 SAD5574_P03_H05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 235	3752	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20575 SAD5574_P03_H05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 235	3753	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20575 SAD5574_P03_H05	Light chain variable region("LC") nucleic acid sequence
Ab 235	3754	DIVMTQSPDSLAVSLGERATINCKSSQSLLNGRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20575 SAD5574_P03_H05	Light chain variable region ("LC") amino acid sequence
Ab 235	3755	KSSQSLLNGRTRKNYLA	ADI-20575 SAD5574_P03_H05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 235	3756	AAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTTAGCT	ADI-20575 SAD5574_P03_H05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 235	3757	WASTRES	ADI-20575 SAD5574_P03_H05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 235	3758	TGGGCATCTACCCGGGAATCC	ADI-20575 SAD5574_P03_H05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 235	3759	KQSYSRRT	ADI-20575 SAD5574_P03_H05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 235	3760	AAGCAATCTTATTCTCGGAGAACT	ADI-20575 SAD5574_P03_H05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 236	3761	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGACAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20576 SAD5574_P03_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 236	3762	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLDNGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20576 SAD5574_P03_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 236	3763	FNIKDYYMH	ADI-20576 SAD5574_P03_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 236	3764	TTCAACATCAAGGACTACTATATGCAC	ADI-20576 SAD5574_P03_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 236	3765	WIDLDNGNTIYDPKFQG	ADI-20576 SAD5574_P03_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 236	3766	TGGATCGACCTTGACAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20576 SAD5574_P03_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 236	3767	ARDGYARYYFDY	ADI-20576 SAD5574_P03_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 236	3768	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20576 SAD5574_P03_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 236	3769	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGCCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20576 SAD5574_P03_A03	Light chain variable region("LC") nucleic acid sequence
Ab 236	3770	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20576 SAD5574_P03_A03	Light chain variable region ("LC") amino acid sequence
Ab 236	3771	KSSQSLLNSRTRKNYLA	ADI-20576 SAD5574_P03_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 236	3772	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20576 SAD5574_P03_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 236	3773	WASTRES	ADI-20576 SAD5574_P03_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 236	3774	TGGGCATCTACCCGGGAATCC	ADI-20576 SAD5574_P03_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 236	3775	KQSYSRRT	ADI-20576 SAD5574_P03_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 236	3776	AAGCAATCTTATTCTCGGAGAACT	ADI-20576 SAD5574_P03_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 237	3777	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCCGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20577 SAD5574_P03_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 237	3778	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20577 SAD5574_P03_F11	Heavy chain variable region ("HC") amino acid sequence
Ab 237	3779	FNIKDYYMH	ADI-20577 SAD5574_P03_F11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 237	3780	TTCAACATCAAGGACTACTATATGCAC	ADI-20577 SAD5574_P03_F11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 237	3781	WIDLENGNTIYDPKFQG	ADI-20577 SAD5574_P03_F11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 237	3782	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20577 SAD5574_P03_F11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 237	3783	ARDGYARYYFDY	ADI-20577 SAD5574_P03_F11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 237	3784	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20577 SAD5574_P03_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 237	3785	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGACTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20577 SAD5574_P03_F11	Light chain variable region("LC") nucleic acid sequence
Ab 237	3786	DIVMTQSPDSLAVSLGERATINCKSSQSLLNGRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGTGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20577 SAD5574_P03_F11	Light chain variable region ("LC") amino acid sequence
Ab 237	3787	KSSQSLLNGRTRKNYLA	ADI-20577 SAD5574_P03_F11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 237	3788	AAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTTAGCT	ADI-20577 SAD5574_P03_F11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 237	3789	WASTRES	ADI-20577 SAD5574_P03_F11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 237	3790	TGGGCATCTACCCGGGAATCC	ADI-20577 SAD5574_P03_F11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 237	3791	KQSYSRRT	ADI-20577 SAD5574_P03_F11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 237	3792	AAGCAATCTTATTCTCGGAGAACT	ADI-20577 SAD5574_P03_F11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 238	3793	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGAACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20578 SAD5574_P03_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTTTCCTCA		
Ab 238	3794	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRNTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20578 SAD5574_P03_B05	Heavy chain variable region ("HC") amino acid sequence
Ab 238	3795	FNIKDYYMH	ADI-20578 SAD5574_P03_B05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 238	3796	TTCAACATCAAGGACTACTATATGCAC	ADI-20578 SAD5574_P03_B05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 238	3797	WIDLENGNTIYDPKFQG	ADI-20578 SAD5574_P03_B05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 238	3798	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20578 SAD5574_P03_B05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 238	3799	ARDGYARYYFDY	ADI-20578 SAD5574_P03_B05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 238	3800	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20578 SAD5574_P03_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 238	3801	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20578 SAD5574_P03_B05	Light chain variable region("LC") nucleic acid sequence
Ab 238	3802	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20578 SAD5574_P03_B05	Light chain variable region ("LC") amino acid sequence
Ab 238	3803	KSSQSLLNSRTRKNYLA	ADI-20578 SAD5574_P03_B05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 238	3804	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20578 SAD5574_P03_B05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 238	3805	WASTRES	ADI-20578 SAD5574_P03_B05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 238	3806	TGGGCATCTACCCGGGAATCC	ADI-20578 SAD5574_P03_B05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 238	3807	KQSYSRRT	ADI-20578 SAD5574_P03_B05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 238	3808	AAGCAATCTTATTCTCGGAGAACT	ADI-20578 SAD5574_P03_B05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 239	3809	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20579 SAD5574_P03_D04	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 239	3810	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20579 SAD5574_P03_D04	Heavy chain variable region ("HC") amino acid sequence
Ab 239	3811	FNIKDYYMH	ADI-20579 SAD5574_P03_D04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 239	3812	TTCAACATCAAGGACTACTATATGCAC	ADI-20579 SAD5574_P03_D04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 239	3813	WIDLENGNTIYDPKFQG	ADI-20579 SAD5574_P03_D04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 239	3814	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20579 SAD5574_P03_D04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 239	3815	ARDGYARYYFDY	ADI-20579 SAD5574_P03_D04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 239	3816	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20579 SAD5574_P03_D04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 239	3817	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGCCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20579 SAD5574_P03_D04	Light chain variable region("LC") nucleic acid sequence
Ab 239	3818	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20579 SAD5574_P03_D04	Light chain variable region ("LC") amino acid sequence
Ab 239	3819	KSSQSLLNSRTRKNYLA	ADI-20579 SAD5574_P03_D04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 239	3820	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20579 SAD5574_P03_D04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 239	3821	WASTRES	ADI-20579 SAD5574_P03_D04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 239	3822	TGGGCATCTACCCGGGAATCC	ADI-20579 SAD5574_P03_D04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 239	3823	KQSYSRRT	ADI-20579 SAD5574_P03_D04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 239	3824	AAGCAATCTTATTCTCGGAGAACT	ADI-20579 SAD5574_P03_D04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 240	3825	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20580 SAD5574_P03_A04	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 240	3826	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20580 SAD5574_P03_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 240	3827	FNIKDYYMH	ADI-20580 SAD5574_P03_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 240	3828	TTCAACATCAAGGACTACTATATGCAC	ADI-20580 SAD5574_P03_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 240	3829	WIDLENGNTIYDPKFQG	ADI-20580 SAD5574_P03_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 240	3830	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20580 SAD5574_P03_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 240	3831	ARDGYARYYFDY	ADI-20580 SAD5574_P03_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 240	3832	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20580 SAD5574_P03_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 240	3833	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20580 SAD5574_P03_A04	Light chain variable region("LC") nucleic acid sequence
Ab 240	3834	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20580 SAD5574_P03_A04	Light chain variable region ("LC") amino acid sequence
Ab 240	3835	KSSQSLLNSRTRKNYLA	ADI-20580 SAD5574_P03_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 240	3836	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20580 SAD5574_P03_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 240	3837	WASTRES	ADI-20580 SAD5574_P03_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 240	3838	TGGGCATCTACCCGGGAATCC	ADI-20580 SAD5574_P03_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 240	3839	KQSYSRRT	ADI-20580 SAD5574_P03_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 240	3840	AAGCAATCTTATTCTCGGAGAACT	ADI-20580 SAD5574_P03_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 241	3841	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGACTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGGCTCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTCGACTACTGGGGCCAAGGAACCCTG	ADI-20581 SAD5574_P03_B06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 241	3842	QVQLVQSGAEVKKPGASVKVSCKASGLNIKDYYMHWVRQAPGQRLEWMGWIGSENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20581 SAD5574_P03_B06	Heavy chain variable region ("HC") amino acid sequence
Ab 241	3843	LNIKDYYMH	ADI-20581 SAD5574_P03_B06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 241	3844	CTCAACATCAAGGACTACTATATGCAC	ADI-20581 SAD5574_P03_B06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 241	3845	WIGSENGNTIYDPKFQG	ADI-20581 SAD5574_P03_B06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 241	3846	TGGATCGGCTCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20581 SAD5574_P03_B06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 241	3847	ARDGYARYYFDY	ADI-20581 SAD5574_P03_B06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 241	3848	GCGAGAGATGGATACGCTAGATATTACTTCGACTAC	ADI-20581 SAD5574_P03_B06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 241	3849	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGCCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20581 SAD5574_P03_B06	Light chain variable region("LC") nucleic acid sequence
Ab 241	3850	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20581 SAD5574_P03_B06	Light chain variable region ("LC") amino acid sequence
Ab 241	3851	KSSQSLLNSRTRKNYLA	ADI-20581 SAD5574_P03_B06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 241	3852	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20581 SAD5574_P03_B06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 241	3853	WASTRES	ADI-20581 SAD5574_P03_B06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 241	3854	TGGGCATCTACCCGGGAATCC	ADI-20581 SAD5574_P03_B06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 241	3855	KQSYSRRT	ADI-20581 SAD5574_P03_B06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 241	3856	AAGCAATCTTATTCTCGGAGAACT	ADI-20581 SAD5574_P03_B06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 242	3857	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGACTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20582 SAD5574_P03_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 242	3858	QVQLVQSGAEVKKPGASVKVSCKASGLNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20582 SAD5574_P03_C08	Heavy chain variable region ("HC") amino acid sequence
Ab 242	3859	LNIKDYYMH	ADI-20582 SAD5574_P03_C08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 242	3860	CTCAACATCAAGGACTACTATATGCAC	ADI-20582 SAD5574_P03_C08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 242	3861	WIDLENGNTIYDPKFQG	ADI-20582 SAD5574_P03_C08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 242	3862	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20582 SAD5574_P03_C08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 242	3863	ARDGYARYYFDY	ADI-20582 SAD5574_P03_C08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 242	3864	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20582 SAD5574_P03_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 242	3865	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-20582 SAD5574_P03_C08	Light chain variable region("LC") nucleic acid sequence
Ab 242	3866	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20582 SAD5574_P03_C08	Light chain variable region ("LC") amino acid sequence
Ab 242	3867	KSSQSLLNSRTGKNYLA	ADI-20582 SAD5574_P03_C08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 242	3868	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-20582 SAD5574_P03_C08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 242	3869	WASTRES	ADI-20582 SAD5574_P03_C08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 242	3870	TGGGCATCTACCCGGGAATCC	ADI-20582 SAD5574_P03_C08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 242	3871	KQSYSRRT	ADI-20582 SAD5574_P03_C08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 242	3872	AAGCAATCTTATTCTCGGAGAACT	ADI-20582 SAD5574_P03_C08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 243	3873	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACACCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCCGGGCAAAGGCTTGAGTGGATGGGATGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGGTCTGAAGACACGGCGGTGTACTACTGCGCGAGGGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-20583 SAD5574_P03_B11	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 243	3874	QVQLVQSGAEVKKPGASVKVSCKASGFNTKDYYMHWVRQAPGQRLEWMGWIGPENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20583 SAD5574_P03_B11	Heavy chain variable region ("HC") amino acid sequence
Ab 243	3875	FNTKDYYMH	ADI-20583 SAD5574_P03_B11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 243	3876	TTCAACACCAAGGACTACTATATGCAC	ADI-20583 SAD5574_P03_B11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 243	3877	WIGPENGNTIYDPKFQG	ADI-20583 SAD5574_P03_B11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 243	3878	TGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-20583 SAD5574_P03_B11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 243	3879	ARDGYARYYFDY	ADI-20583 SAD5574_P03_B11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 243	3880	GCGAGGGATGGATACGCTAGATATTACTTTGACTAC	ADI-20583 SAD5574_P03_B11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 243	3881	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAACAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20583 SAD5574_P03_B11	Light chain variable region("LC") nucleic acid sequence
Ab 243	3882	DIVMTQSPDSLAVSLGERATINCKSSQSLLNNRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-20583 SAD5574_P03_B11	Light chain variable region ("LC") amino acid sequence
Ab 243	3883	KSSQSLLNNRTRKNYLA	ADI-20583 SAD5574_P03_B11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 243	3884	AAGTCCAGCCAGAGTCTTTTAAACAACAGAACCAGAAAGAACTACTTAGCT	ADI-20583 SAD5574_P03_B11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 243	3885	WASTRES	ADI-20583 SAD5574_P03_B11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 243	3886	TGGGCATCTACCCGGGAATCC	ADI-20583 SAD5574_P03_B11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 243	3887	KQSYSRRT	ADI-20583 SAD5574_P03_B11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 243	3888	AAGCAATCTTATTCTCGGAGAACT	ADI-20583 SAD5574_P03_B11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 244	3889	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20584 SAD5574_P03_D10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 244	3890	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20584 SAD5574_P03_D10	Heavy chain variable region ("HC") amino acid sequence
Ab 244	3891	FNIKDYYMH	ADI-20584 SAD5574_P03_D10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 244	3892	TTCAACATCAAGGACTACTATATGCAC	ADI-20584 SAD5574_P03_D10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 244	3893	WIDLENGNTIYDPKFQG	ADI-20584 SAD5574_P03_D10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 244	3894	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAATTTCAGGGC	ADI-20584 SAD5574_P03_D10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 244	3895	ARDGYARYYFDY	ADI-20584 SAD5574_P03_D10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 244	3896	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20584 SAD5574_P03_D10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 244	3897	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTCGGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20584 SAD5574_P03_D10	Light chain variable region("LC") nucleic acid sequence
Ab 244	3898	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	ADI-20584 SAD5574_P03_D10	Light chain variable region ("LC") amino acid sequence
Ab 244	3899	KSSQSLLNSRTRKNYLA	ADI-20584 SAD5574_P03_D10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 244	3900	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20584 SAD5574_P03_D10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 244	3901	WASTRES	ADI-20584 SAD5574_P03_D10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 244	3902	TGGGCATCTACCCGGGAATCC	ADI-20584 SAD5574_P03_D10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 244	3903	KQSYFRRA	ADI-20584 SAD5574_P03_D10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 244	3904	AAGCAATCTTATTTTCGGAGAGCT	ADI-20584 SAD5574_P03_D10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 245	3905	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCGCCTGCAAGGCTTCTGGATCCAATATCAAGGACTACTATGTGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGGCCCTGAAAATGGTAACACAGTCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-20585 SAD5402_P01_G02	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 245	3906	QVQLVQSGAEVKKPGASVKVACKASGSNIKDYYVHWVRQAPGQRLEWMGWIGPENGNTVYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-20585 SAD5402_P01_G02	Heavy chain variable region ("HC") amino acid sequence
Ab 245	3907	SNIKDYYVH	ADI-20585 SAD5402_P01_G02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 245	3908	TCCAATATCAAGGACTACTATGTGCAC	ADI-20585 SAD5402_P01_G02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 245	3909	WIGPENGNTVYDPKFQG	ADI-20585 SAD5402_P01_G02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 245	3910	TGGATCGGCCCTGAAAATGGTAACACAGTCTATGACCCGAAGTTTCAGGGC	ADI-20585 SAD5402_P01_G02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 245	3911	ARDGYARYYFDY	ADI-20585 SAD5402_P01_G02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 245	3912	GCGAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-20585 SAD5402_P01_G02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 245	3913	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20585 SAD5402_P01_G02	Light chain variable region("LC") nucleic acid sequence
Ab 245	3914	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-20585 SAD5402_P01_G02	Light chain variable region ("LC") amino acid sequence
Ab 245	3915	KSSQSLLNSRTRKNYLA	ADI-20585 SAD5402_P01_G02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 245	3916	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20585 SAD5402_P01_G02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 245	3917	WASTRES	ADI-20585 SAD5402_P01_G02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 245	3918	TGGGCATCTACCCGGGAATCC	ADI-20585 SAD5402_P01_G02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 245	3919	KQSYSLRT	ADI-20585 SAD5402_P01_G02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 245	3920	AAGCAATCTTATTCTCTGAGAACT	ADI-20585 SAD5402_P01_G02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 246	3921	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCCACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCTAGAGATGGCTCATATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-20818 SAD5399_P01_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 246	3922	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSHYIHWVRQAPGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	ADI-20818 SAD5399_P01_C01	Heavy chain variable region ("HC") amino acid sequence
Ab 246	3923	YTFTSHYIH	ADI-20818 SAD5399_P01_C01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 246	3924	TACACCTTCACCAGCCACTATATACAC	ADI-20818 SAD5399_P01_C01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 246	3925	WIYPGDGSTKYNEKFKG	ADI-20818 SAD5399_P01_C01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 246	3926	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTTCAAGGGC	ADI-20818 SAD5399_P01_C01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 246	3927	ARDGSYYFDY	ADI-20818 SAD5399_P01_C01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 246	3928	GCTAGAGATGGCTCATATTACTTTGACTAC	ADI-20818 SAD5399_P01_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 246	3929	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20818 SAD5399_P01_C01	Light chain variable region("LC") nucleic acid sequence
Ab 246	3930	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-20818 SAD5399_P01_C01	Light chain variable region ("LC") amino acid sequence
Ab 246	3931	KSSQSLLNSRTRKNYLA	ADI-20818 SAD5399_P01_C01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 246	3932	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20818 SAD5399_P01_C01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 246	3933	WASTRES	ADI-20818 SAD5399_P01_C01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 246	3934	TGGGCATCTACCCGGGAATCC	ADI-20818 SAD5399_P01_C01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 246	3935	KQSYSLRT	ADI-20818 SAD5399_P01_C01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 246	3936	AAGCAATCTTATTCTCTGAGAACT	ADI-20818 SAD5399_P01_C01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 247	3937	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTCCTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGGTAATGTTGACACAAGGTACAACGAGAAGTTCAAGGGCAGAGTCACCATAACCGCGGACAAGTCCGCGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCGAGGGATTACGGATACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-20820 SAD5400_P01_F07	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 247	3938	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQAPGQGLEWIGWIYPGNVDTRYNEKFKGRVTITADKSASTAYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	ADI-20820 SAD5400_P01_F07	Heavy chain variable region ("HC") amino acid sequence
Ab 247	3939	YTFTSSYIH	ADI-20820 SAD5400_P01_F07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 247	3940	TACACCTTCACCAGCTCCTATATACAC	ADI-20820 SAD5400_P01_F07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 247	3941	WIYPGNVDTRYNEKFKG	ADI-20820 SAD5400_P01_F07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 247	3942	TGGATCTACCCTGGTAATGTTGACACAAGGTACAACGAGAAGTTCAAGGGC	ADI-20820 SAD5400_P01_F07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 247	3943	ARDYGYYFDY	ADI-20820 SAD5400_P01_F07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 247	3944	GCGAGGGATTACGGATACTACTTTGACTAC	ADI-20820 SAD5400_P01_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 247	3945	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20820 SAD5400_P01_F07	Light chain variable region("LC") nucleic acid sequence
Ab 247	3946	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-20820 SAD5400_P01_F07	Light chain variable region ("LC") amino acid sequence
Ab 247	3947	KSSQSLLNSRTRKNYLA	ADI-20820 SAD5400_P01_F07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 247	3948	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-20820 SAD5400_P01_F07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 247	3949	WASTRES	ADI-20820 SAD5400_P01_F07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 247	3950	TGGGCATCTACCCGGGAATCC	ADI-20820 SAD5400_P01_F07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 247	3951	KQSYSLRT	ADI-20820 SAD5400_P01_F07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 247	3952	AAGCAATCTTATTCTCTGAGAACT	ADI-20820 SAD5400_P01_F07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 248	3953	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCGCGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACGCCAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-21097 SAD5574_P03_D07	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 248	3954	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVSS	ADI-21097 SAD5574_P03_D07	Heavy chain variable region ("HC") amino acid sequence
Ab 248	3955	FNIKDYYMH	ADI-21097 SAD5574_P03_D07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 248	3956	TTCAACATCAAGGACTACTATATGCAC	ADI-21097 SAD5574_P03_D07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 248	3957	WIDPENGNTIYDPKFQG	ADI-21097 SAD5574_P03_D07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 248	3958	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21097 SAD5574_P03_D07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 248	3959	ARDGYARYYFDY	ADI-21097 SAD5574_P03_D07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 248	3960	GCTAGAGACGGTTACGCCAGATATTACTTTGACTAC	ADI-21097 SAD5574_P03_D07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 248	3961	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-21097 SAD5574_P03_D07	Light chain variable region("LC") nucleic acid sequence
Ab 248	3962	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-21097 SAD5574_P03_D07	Light chain variable region ("LC") amino acid sequence
Ab 248	3963	KSSQSLLNSRTRKNYLA	ADI-21097 SAD5574_P03_D07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 248	3964	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	ADI-21097 SAD5574_P03_D07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 248	3965	WASTRES	ADI-21097 SAD5574_P03_D07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 248	3966	TGGGCATCTACCCGGGAATCC	ADI-21097 SAD5574_P03_D07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 248	3967	KQSYSLRT	ADI-21097 SAD5574_P03_D07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 248	3968	AAGCAATCTTATTCTCTGAGAACT	ADI-21097 SAD5574_P03_D07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 249	3969	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-21959 SAD5837_P01_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 249	3970	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYYFDYWGQGTLVTVSS	ADI-21959 SAD5837_P01_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 249	3971	FNIKDYYMH	ADI-21959 SAD5837_P01_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 249	3972	TTCAACATCAAGGACTACTATATGCAC	ADI-21959 SAD5837_P01_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 249	3973	WIDLENGNTIYDPKFQG	ADI-21959 SAD5837_P01_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 249	3974	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21959 SAD5837_P01_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 249	3975	ARDGYGRYYFDY	ADI-21959 SAD5837_P01_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 249	3976	GCGAGAGATGGATACGGGAGATATTACTTTGACTAC	ADI-21959 SAD5837_P01_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 249	3977	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21959 SAD5837_P01_E02	Light chain variable region("LC") nucleic acid sequence
Ab 249	3978	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21959 SAD5837_P01_E02	Light chain variable region ("LC") amino acid sequence
Ab 249	3979	KSSQSLLNSRTGKNYLA	ADI-21959 SAD5837_P01_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 249	3980	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21959 SAD5837_P01_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 249	3981	WASTRES	ADI-21959 SAD5837_P01_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 249	3982	TGGGCATCTACCCGGGAATCC	ADI-21959 SAD5837_P01_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 249	3983	KQSYSRRT	ADI-21959 SAD5837_P01_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 249	3984	AAGCAATCTTATTCTCGGAGAACT	ADI-21959 SAD5837_P01_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 250	3985	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGACATTTGGGGCCAAGGAACCCTGG	ADI-21963 SAD5837_P01_F07	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 250	3986	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDIWGQGTLVTVSS	ADI-21963 SAD5837_P01_F07	Heavy chain variable region ("HC") amino acid sequence
Ab 250	3987	FNIKDYYMH	ADI-21963 SAD5837_P01_F07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 250	3988	TTCAACATCAAGGACTACTATATGCAC	ADI-21963 SAD5837_P01_F07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 250	3989	WIDLENGNTIYDPKFQG	ADI-21963 SAD5837_P01_F07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 250	3990	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21963 SAD5837_P01_F07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 250	3991	ARDGYARYYFDI	ADI-21963 SAD5837_P01_F07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 250	3992	GCGAGAGATGGATACGCTAGATATTACTTTGACATT	ADI-21963 SAD5837_P01_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 250	3993	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21963 SAD5837_P01_F07	Light chain variable region("LC") nucleic acid sequence
Ab 250	3994	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21963 SAD5837_P01_F07	Light chain variable region ("LC") amino acid sequence
Ab 250	3995	KSSQSLLNSRTGKNYLA	ADI-21963 SAD5837_P01_F07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 250	3996	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21963 SAD5837_P01_F07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 250	3997	WASTRES	ADI-21963 SAD5837_P01_F07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 250	3998	TGGGCATCTACCCGGGAATCC	ADI-21963 SAD5837_P01_F07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 250	3999	KQSYSRRT	ADI-21963 SAD5837_P01_F07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 250	4000	AAGCAATCTTATTCTCGGAGAACT	ADI-21963 SAD5837_P01_F07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 251	4001	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTACTTTGACGCTTGGGGCCAAGGAACCCTG	ADI-21965 SAD5837_P01_D09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 251	4002	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYYFDAWGQGTLVTVSS	ADI-21965 SAD5837_P01_D09	Heavy chain variable region ("HC") amino acid sequence
Ab 251	4003	FNIKDYYMH	ADI-21965 SAD5837_P01_D09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 251	4004	TTCAACATCAAGGACTACTATATGCAC	ADI-21965 SAD5837_P01_D09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 251	4005	WIDLENGNTIYDPKFQG	ADI-21965 SAD5837_P01_D09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 251	4006	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21965 SAD5837_P01_D09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 251	4007	ARDGYGRYYFDA	ADI-21965 SAD5837_P01_D09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 251	4008	GCGAGAGATGGATACGGGAGATATTACTTTGACGCT	ADI-21965 SAD5837_P01_D09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 251	4009	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21965 SAD5837_P01_D09	Light chain variable region("LC") nucleic acid sequence
Ab 251	4010	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21965 SAD5837_P01_D09	Light chain variable region ("LC") amino acid sequence
Ab 251	4011	KSSQSLLNSRTGKNYLA	ADI-21965 SAD5837_P01_D09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 251	4012	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21965 SAD5837_P01_D09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 251	4013	WASTRES	ADI-21965 SAD5837_P01_D09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 251	4014	TGGGCATCTACCCGGGAATCC	ADI-21965 SAD5837_P01_D09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 251	4015	KQSYSRRT	ADI-21965 SAD5837_P01_D09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 251	4016	AAGCAATCTTATTCTCGGAGAACT	ADI-21965 SAD5837_P01_D09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 252	4017	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTTTTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-21967 SAD5837_P01_C11	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 252	4018	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYFFDYWGQGTLVTVSS	ADI-21967 SAD5837_P01_C11	Heavy chain variable region ("HC") amino acid sequence
Ab 252	4019	FNIKDYYMH	ADI-21967 SAD5837_P01_C11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 252	4020	TTCAACATCAAGGACTACTATATGCAC	ADI-21967 SAD5837_P01_C11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 252	4021	WIDLENGNTIYDPKFQG	ADI-21967 SAD5837_P01_C11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 252	4022	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21967 SAD5837_P01_C11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 252	4023	ARDGYARYFFDY	ADI-21967 SAD5837_P01_C11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 252	4024	GCGAGAGATGGATACGCTAGATATTTTTTTGACTAC	ADI-21967 SAD5837_P01_C11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 252	4025	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21967 SAD5837_P01_C11	Light chain variable region("LC") nucleic acid sequence
Ab 252	4026	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21967 SAD5837_P01_C11	Light chain variable region ("LC") amino acid sequence
Ab 252	4027	KSSQSLLNSRTGKNYLA	ADI-21967 SAD5837_P01_C11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 252	4028	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21967 SAD5837_P01_C11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 252	4029	WASTRES	ADI-21967 SAD5837_P01_C11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 252	4030	TGGGCATCTACCCGGGAATCC	ADI-21967 SAD5837_P01_C11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 252	4031	KQSYSRRT	ADI-21967 SAD5837_P01_C11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 252	4032	AAGCAATCTTATTCTCGGAGAACT	ADI-21967 SAD5837_P01_C11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 253	4033	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTTTGACTACTGGGGCCAAGGAACCCTG	ADI-21970 SAD5837_P02_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 253	4034	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFFDYWGQGTLVTVSS	ADI-21970 SAD5837_P02_B02	Heavy chain variable region ("HC") amino acid sequence
Ab 253	4035	FNIKDYYMH	ADI-21970 SAD5837_P02_B02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 253	4036	TTCAACATCAAGGACTACTATATGCAC	ADI-21970 SAD5837_P02_B02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 253	4037	WIDLENGNTIYDPKFQG	ADI-21970 SAD5837_P02_B02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 253	4038	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21970 SAD5837_P02_B02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 253	4039	ARDGYGRYFFDY	ADI-21970 SAD5837_P02_B02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 253	4040	GCGAGAGATGGATACGGGAGATATTTTTTTGACTAC	ADI-21970 SAD5837_P02_B02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 253	4041	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21970 SAD5837_P02_B02	Light chain variable region("LC") nucleic acid sequence
Ab 253	4042	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21970 SAD5837_P02_B02	Light chain variable region ("LC") amino acid sequence
Ab 253	4043	KSSQSLLNSRTGKNYLA	ADI-21970 SAD5837_P02_B02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 253	4044	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTGGCT	ADI-21970 SAD5837_P02_B02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 253	4045	WASTRES	ADI-21970 SAD5837_P02_B02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 253	4046	TGGGCATCTACCCGGGAATCC	ADI-21970 SAD5837_P02_B02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 253	4047	KQSYSRRT	ADI-21970 SAD5837_P02_B02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 253	4048	AAGCAATCTTATTCTCGGAGAACT	ADI-21970 SAD5837_P02_B02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 254	4049	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTACTACGACTACTGGGGCCAAGGAACCCTG	ADI-21971 SAD5837_P02_C03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 254	4050	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYYYDYWGQGTLVTVSS	ADI-21971 SAD5837_P02_C03	Heavy chain variable region ("HC") amino acid sequence
Ab 254	4051	FNIKDYYMH	ADI-21971 SAD5837_P02_C03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 254	4052	TTCAACATCAAGGACTACTATATGCAC	ADI-21971 SAD5837_P02_C03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 254	4053	WIDLENGNTIYDPKFQG	ADI-21971 SAD5837_P02_C03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 254	4054	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21971 SAD5837_P02_C03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 254	4055	ARDGYGRYYYDY	ADI-21971 SAD5837_P02_C03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 254	4056	GCGAGAGATGGATACGGGAGATATTACTACGACTAC	ADI-21971 SAD5837_P02_C03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 254	4057	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21971 SAD5837_P02_C03	Light chain variable region("LC") nucleic acid sequence
Ab 254	4058	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21971 SAD5837_P02_C03	Light chain variable region ("LC") amino acid sequence
Ab 254	4059	KSSQSLLNSRTGKNYLA	ADI-21971 SAD5837_P02_C03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 254	4060	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21971 SAD5837_P02_C03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 254	4061	WASTRES	ADI-21971 SAD5837_P02_C03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 254	4062	TGGGCATCTACCCGGGAATCC	ADI-21971 SAD5837_P02_C03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 254	4063	KQSYSRRT	ADI-21971 SAD5837_P02_C03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 254	4064	AAGCAATCTTATTCTCGGAGAACT	ADI-21971 SAD5837_P02_C03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 255	4065	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTACTACGACGTGTGGGGCCAAGGAACCCTG	ADI-21972 SAD5837_P02_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 255	4066	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYYYDVWGQGTLVTVSS	ADI-21972 SAD5837_P02_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 255	4067	FNIKDYYMH	ADI-21972 SAD5837_P02_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 255	4068	TTCAACATCAAGGACTACTATATGCAC	ADI-21972 SAD5837_P02_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 255	4069	WIDLENGNTIYDPKFQG	ADI-21972 SAD5837_P02_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 255	4070	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21972 SAD5837_P02_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 255	4071	ARDGYGRYYYDV	ADI-21972 SAD5837_P02_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 255	4072	GCGAGAGATGGATACGGGAGATATTACTACGACGTG	ADI-21972 SAD5837_P02_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 255	4073	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21972 SAD5837_P02_A04	Light chain variable region("LC") nucleic acid sequence
Ab 255	4074	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21972 SAD5837_P02_A04	Light chain variable region ("LC") amino acid sequence
Ab 255	4075	KSSQSLLNSRTGKNYLA	ADI-21972 SAD5837_P02_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 255	4076	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21972 SAD5837_P02_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 255	4077	WASTRES	ADI-21972 SAD5837_P02_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 255	4078	TGGGCATCTACCCGGGAATCC	ADI-21972 SAD5837_P02_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 255	4079	KQSYSRRT	ADI-21972 SAD5837_P02_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 255	4080	AAGCAATCTTATTCTCGGAGAACT	ADI-21972 SAD5837_P02_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 256	4081	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACTACTGGGGCCAAGGAACCCTG	ADI-21973 SAD5837_P02_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 256	4082	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDYWGQGTLVTVSS	ADI-21973 SAD5837_P02_B05	Heavy chain variable region ("HC") amino acid sequence
Ab 256	4083	FNIKDYYMH	ADI-21973 SAD5837_P02_B05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 256	4084	TTCAACATCAAGGACTACTATATGCAC	ADI-21973 SAD5837_P02_B05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 256	4085	WIDLENGNTIYDPKFQG	ADI-21973 SAD5837_P02_B05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 256	4086	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21973 SAD5837_P02_B05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 256	4087	ARDGYGRYFYDY	ADI-21973 SAD5837_P02_B05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 256	4088	GCGAGAGATGGATACGGGAGATATTTTTACGACTAC	ADI-21973 SAD5837_P02_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 256	4089	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21973 SAD5837_P02_B05	Light chain variable region("LC") nucleic acid sequence
Ab 256	4090	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21973 SAD5837_P02_B05	Light chain variable region ("LC") amino acid sequence
Ab 256	4091	KSSQSLLNSRTGKNYLA	ADI-21973 SAD5837_P02_B05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 256	4092	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21973 SAD5837_P02_B05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 256	4093	WASTRES	ADI-21973 SAD5837_P02_B05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 256	4094	TGGGCATCTACCCGGGAATCC	ADI-21973 SAD5837_P02_B05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 256	4095	KQSYSRRT	ADI-21973 SAD5837_P02_B05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 256	4096	AAGCAATCTTATTCTCGGAGAACT	ADI-21973 SAD5837_P02_B05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 257	4097	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTTTGACGTGTGGGGCCAAGGAACCCTG	ADI-21974 SAD5837_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 257	4098	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFFDVWGQGTLVTVSS	ADI-21974 SAD5837_P02_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 257	4099	FNIKDYYMH	ADI-21974 SAD5837_P02_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 257	4100	TTCAACATCAAGGACTACTATATGCAC	ADI-21974 SAD5837_P02_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 257	4101	WIDLENGNTIYDPKFQG	ADI-21974 SAD5837_P02_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 257	4102	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21974 SAD5837_P02_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 257	4103	ARDGYGRYFFDV	ADI-21974 SAD5837_P02_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 257	4104	GCGAGAGATGGATACGGGAGATATTTTTTTGACGTG	ADI-21974 SAD5837_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 257	4105	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21974 SAD5837_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 257	4106	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21974 SAD5837_P02_A06	Light chain variable region ("LC") amino acid sequence
Ab 257	4107	KSSQSLLNSRTGKNYLA	ADI-21974 SAD5837_P02_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 257	4108	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	ADI-21974 SAD5837_P02_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 257	4109	WASTRES	ADI-21974 SAD5837_P02_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 257	4110	TGGGCATCTACCCGGGAATCC	ADI-21974 SAD5837_P02_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 257	4111	KQSYSRRT	ADI-21974 SAD5837_P02_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 257	4112	AAGCAATCTTATTCTCGGAGAACT	ADI-21974 SAD5837_P02_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 258	4113	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTTTTTTGACATATGGGGCCAAGGAACCCTGG	ADI-21975 SAD5837_P02_F08	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 258	4114	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYFFDIWGQGTLVTVSS	ADI-21975 SAD5837_P02_F08	Heavy chain variable region ("HC") amino acid sequence
Ab 258	4115	FNIKDYYMH	ADI-21975 SAD5837_P02_F08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 258	4116	TTCAACATCAAGGACTACTATATGCAC	ADI-21975 SAD5837_P02_F08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 258	4117	WIDLENGNTIYDPKFQG	ADI-21975 SAD5837_P02_F08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 258	4118	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21975 SAD5837_P02_F08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 258	4119	ARDGYARYFFDI	ADI-21975 SAD5837_P02_F08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 258	4120	GCGAGAGATGGATACGCTAGATATTTTTTTGACATA	ADI-21975 SAD5837_P02_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 258	4121	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21975 SAD5837_P02_F08	Light chain variable region("LC") nucleic acid sequence
Ab 258	4122	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21975 SAD5837_P02_F08	Light chain variable region ("LC") amino acid sequence
Ab 258	4123	KSSQSLLNSRTGKNYLA	ADI-21975 SAD5837_P02_F08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 258	4124	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	ADI-21975 SAD5837_P02_F08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 258	4125	WASTRES	ADI-21975 SAD5837_P02_F08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 258	4126	TGGGCATCTACCCGGGAATCC	ADI-21975 SAD5837_P02_F08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 258	4127	KQSYSRRT	ADI-21975 SAD5837_P02_F08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 258	4128	AAGCAATCTTATTCTCGGAGAACT	ADI-21975 SAD5837_P02_F08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 259	4129	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTTTTTTGACGTGTGGGGCCAAGGAACCCTGG	ADI-21976 SAD5837_P02_B09	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 259	4130	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYFFDVWGQGTLVTVSS	ADI-21976 SAD5837_P02_B09	Heavy chain variable region ("HC") amino acid sequence
Ab 259	4131	FNIKDYYMH	ADI-21976 SAD5837_P02_B09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 259	4132	TTCAACATCAAGGACTACTATATGCAC	ADI-21976 SAD5837_P02_B09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 259	4133	WIDLENGNTIYDPKFQG	ADI-21976 SAD5837_P02_B09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 259	4134	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21976 SAD5837_P02_B09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 259	4135	ARDGYARYFFDV	ADI-21976 SAD5837_P02_B09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 259	4136	GCGAGAGATGGATACGCTAGATATTTTTTTGACGTG	ADI-21976 SAD5837_P02_B09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 259	4137	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21976 SAD5837_P02_B09	Light chain variable region("LC") nucleic acid sequence
Ab 259	4138	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21976 SAD5837_P02_B09	Light chain variable region ("LC") amino acid sequence
Ab 259	4139	KSSQSLLNSRTGKNYLA	ADI-21976 SAD5837_P02_B09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 259	4140	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21976 SAD5837_P02_B09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 259	4141	WASTRES	ADI-21976 SAD5837_P02_B09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 259	4142	TGGGCATCTACCCGGGAATCC	ADI-21976 SAD5837_P02_B09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 259	4143	KQSYSRRT	ADI-21976 SAD5837_P02_B09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 259	4144	AAGCAATCTTATTCTCGGAGAACT	ADI-21976 SAD5837_P02_B09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 260	4145	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTTTTACGACGTCTGGGGCCAAGGAACCCTGG	ADI-21977 SAD5837_P02_B11	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 260	4146	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYFYDVWGQGTLVTVSS	ADI-21977 SAD5837_P02_B11	Heavy chain variable region ("HC") amino acid sequence
Ab 260	4147	FNIKDYYMH	ADI-21977 SAD5837_P02_B11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 260	4148	TTCAACATCAAGGACTACTATATGCAC	ADI-21977 SAD5837_P02_B11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 260	4149	WIDLENGNTIYDPKFQG	ADI-21977 SAD5837_P02_B11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 260	4150	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21977 SAD5837_P02_B11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 260	4151	ARDGYARYFYDV	ADI-21977 SAD5837_P02_B11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 260	4152	GCGAGAGATGGATACGCTAGATATTTTTACGACGTC	ADI-21977 SAD5837_P02_B11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 260	4153	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21977 SAD5837_P02_B11	Light chain variable region("LC") nucleic acid sequence
Ab 260	4154	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21977 SAD5837_P02_B11	Light chain variable region ("LC") amino acid sequence
Ab 260	4155	KSSQSLLNSRTGKNYLA	ADI-21977 SAD5837_P02_B11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 260	4156	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21977 SAD5837_P02_B11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 260	4157	WASTRES	ADI-21977 SAD5837_P02_B11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 260	4158	TGGGCATCTACCCGGGAATCC	ADI-21977 SAD5837_P02_B11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 260	4159	KQSYSRRT	ADI-21977 SAD5837_P02_B11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 260	4160	AAGCAATCTTATTCTCGGAGAACT	ADI-21977 SAD5837_P02_B11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 261	4161	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-21978 SAD5837_P04_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 261	4162	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-21978 SAD5837_P04_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 261	4163	FNIKDYYMH	ADI-21978 SAD5837_P04_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 261	4164	TTCAACATCAAGGACTACTATATGCAC	ADI-21978 SAD5837_P04_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 261	4165	WIDLENGNTIYDPKFQG	ADI-21978 SAD5837_P04_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 261	4166	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21978 SAD5837_P04_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 261	4167	ARDGYGRYFYDV	ADI-21978 SAD5837_P04_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 261	4168	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-21978 SAD5837_P04_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 261	4169	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21978 SAD5837_P04_A01	Light chain variable region("LC") nucleic acid sequence
Ab 261	4170	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21978 SAD5837_P04_A01	Light chain variable region ("LC") amino acid sequence
Ab 261	4171	KSSQSLLNSRTGKNYLA	ADI-21978 SAD5837_P04_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 261	4172	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21978 SAD5837_P04_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 261	4173	WASTRES	ADI-21978 SAD5837_P04_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 261	4174	TGGGCATCTACCCGGGAATCC	ADI-21978 SAD5837_P04_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 261	4175	KQSYSRRT	ADI-21978 SAD5837_P04_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 261	4176	AAGCAATCTTATTCTCGGAGAACT	ADI-21978 SAD5837_P04_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 262	4177	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTTTTACGACTACTGGGGCCAAGGAACCCTGG	ADI-21979 SAD5837_P04_A03	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 262	4178	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYFYDYWGQGTLVTVSS	ADI-21979 SAD5837_P04_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 262	4179	FNIKDYYMH	ADI-21979 SAD5837_P04_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 262	4180	TTCAACATCAAGGACTACTATATGCAC	ADI-21979 SAD5837_P04_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 262	4181	WIDLENGNTIYDPKFQG	ADI-21979 SAD5837_P04_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 262	4182	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21979 SAD5837_P04_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 262	4183	ARDGYARYFYDY	ADI-21979 SAD5837_P04_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 262	4184	GCGAGAGATGGATACGCTAGATATTTTTACGACTAC	ADI-21979 SAD5837_P04_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 262	4185	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21979 SAD5837_P04_A03	Light chain variable region("LC") nucleic acid sequence
Ab 262	4186	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21979 SAD5837_P04_A03	Light chain variable region ("LC") amino acid sequence
Ab 262	4187	KSSQSLLNSRTGKNYLA	ADI-21979 SAD5837_P04_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 262	4188	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21979 SAD5837_P04_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 262	4189	WASTRES	ADI-21979 SAD5837_P04_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 262	4190	TGGGCATCTACCCGGGAATCC	ADI-21979 SAD5837_P04_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 262	4191	KQSYSRRT	ADI-21979 SAD5837_P04_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 262	4192	AAGCAATCTTATTCTCGGAGAACT	ADI-21979 SAD5837_P04_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 263	4193	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-22523 LAD4606_P01_H12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 263	4194	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-22523 LAD4606_P01_H12	Heavy chain variable region ("HC") amino acid sequence
Ab 263	4195	FNIKDYYMH	ADI-22523 LAD4606_P01_H12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 263	4196	TTCAACATCAAGGACTACTATATGCAC	ADI-22523 LAD4606_P01_H12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 263	4197	WIDLENGNTIYDPKFQG	ADI-22523 LAD4606_P01_H12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 263	4198	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-22523 LAD4606_P01_H12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 263	4199	ARDGYGRYFYDV	ADI-22523 LAD4606_P01_H12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 263	4200	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-22523 LAD4606_P01_H12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 263	4201	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-22523 LAD4606_P01_H12	Light chain variable region("LC") nucleic acid sequence
Ab 263	4202	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-22523 LAD4606_P01_H12	Light chain variable region ("LC") amino acid sequence
Ab 263	4203	KSSQSLLNSRTGKNYLA	ADI-22523 LAD4606_P01_H12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 263	4204	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-22523 LAD4606_P01_H12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 263	4205	WASTRES	ADI-22523 LAD4606_P01_H12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 263	4206	TGGGCATCTACCCGGGAATCC	ADI-22523 LAD4606_P01_H12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 263	4207	KQSYSRRT	ADI-22523 LAD4606_P01_H12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 263	4208	AAGCAATCTTATTCTCGGAGAACT	ADI-22523 LAD4606_P01_H12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 264	4209	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23639 LAD4707_P01_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 264	4210	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23639 LAD4707_P01_D01	Heavy chain variable region ("HC") amino acid sequence
Ab 264	4211	FNIKDYYMH	ADI-23639 LAD4707_P01_D01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 264	4212	TTCAACATCAAGGACTACTATATGCAC	ADI-23639 LAD4707_P01_D01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 264	4213	WIDPENGNTIYDPKFQG	ADI-23639 LAD4707_P01_D01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 264	4214	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23639 LAD4707_P01_D01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 264	4215	ARDGYGRYFYDV	ADI-23639 LAD4707_P01_D01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 264	4216	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23639 LAD4707_P01_D01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 264	4217	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23639 LAD4707_P01_D01	Light chain variable region("LC") nucleic acid sequence
Ab 264	4218	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23639 LAD4707_P01_D01	Light chain variable region ("LC") amino acid sequence
Ab 264	4219	KSSQSLLNSRTGKNYLA	ADI-23639 LAD4707_P01_D01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 264	4220	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23639 LAD4707_P01_D01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 264	4221	WASTRES	ADI-23639 LAD4707_P01_D01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 264	4222	TGGGCATCTACCCGGGAATCC	ADI-23639 LAD4707_P01_D01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 264	4223	KQSYSRRT	ADI-23639 LAD4707_P01_D01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 264	4224	AAGCAATCTTATTCTCGGAGAACT	ADI-23639 LAD4707_P01_D01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 265	4225	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCGCGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23640 LAD4708_P01_H02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 265	4226	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23640 LAD4708_P01_H02	Heavy chain variable region ("HC") amino acid sequence
Ab 265	4227	FNIKDYYMH	ADI-23640 LAD4708_P01_H02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 265	4228	TTCAACATCAAGGACTACTATATGCAC	ADI-23640 LAD4708_P01_H02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 265	4229	WIDPENGNTIYDPKFQG	ADI-23640 LAD4708_P01_H02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 265	4230	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23640 LAD4708_P01_H02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 265	4231	ARDGYGRYFYDV	ADI-23640 LAD4708_P01_H02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 265	4232	GCTAGAGACGGTTACGGGAGATATTTTTACGACGTG	ADI-23640 LAD4708_P01_H02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 265	4233	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23640 LAD4708_P01_H02	Light chain variable region("LC") nucleic acid sequence
Ab 265	4234	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23640 LAD4708_P01_H02	Light chain variable region ("LC") amino acid sequence
Ab 265	4235	KSSQSLLNSRTGKNYLA	ADI-23640 LAD4708_P01_H02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 265	4236	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23640 LAD4708_P01_H02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 265	4237	WASTRES	ADI-23640 LAD4708_P01_H02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 265	4238	TGGGCATCTACCCGGGAATCC	ADI-23640 LAD4708_P01_H02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 265	4239	KQSYSRRT	ADI-23640 LAD4708_P01_H02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 265	4240	AAGCAATCTTATTCTCGGAGAACT	ADI-23640 LAD4708_P01_H02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 266	4241	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23641 LAD4709_P01_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 266	4242	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23641 LAD4709_P01_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 266	4243	FNIKDYYMH	ADI-23641 LAD4709_P01_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 266	4244	TTCAACATCAAGGACTACTATATGCAC	ADI-23641 LAD4709_P01_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 266	4245	WIDLENGNTIYDPKFQG	ADI-23641 LAD4709_P01_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 266	4246	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23641 LAD4709_P01_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 266	4247	ARDGYGRYFYDV	ADI-23641 LAD4709_P01_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 266	4248	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23641 LAD4709_P01_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 266	4249	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23641 LAD4709_P01_E03	Light chain variable region("LC") nucleic acid sequence
Ab 266	4250	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-23641 LAD4709_P01_E03	Light chain variable region ("LC") amino acid sequence
Ab 266	4251	KSSQSLLNSRTGKNYLA	ADI-23641 LAD4709_P01_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 266	4252	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23641 LAD4709_P01_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 266	4253	WASTRES	ADI-23641 LAD4709_P01_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 266	4254	TGGGCATCTACCCGGGAATCC	ADI-23641 LAD4709_P01_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 266	4255	KQSYSLRT	ADI-23641 LAD4709_P01_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 266	4256	AAGCAATCTTATTCTCTGAGAACT	ADI-23641 LAD4709_P01_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 267	4257	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23642 LAD4710_P01_C04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 267	4258	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23642 LAD4710_P01_C04	Heavy chain variable region ("HC") amino acid sequence
Ab 267	4259	FNIKDYYMH	ADI-23642 LAD4710_P01_C04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 267	4260	TTCAACATCAAGGACTACTATATGCAC	ADI-23642 LAD4710_P01_C04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 267	4261	WIDPENGNTIYDPKFQG	ADI-23642 LAD4710_P01_C04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 267	4262	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23642 LAD4710_P01_C04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 267	4263	ARDGYGRYFYDV	ADI-23642 LAD4710_P01_C04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 267	4264	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23642 LAD4710_P01_C04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 267	4265	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23642 LAD4710_P01_C04	Light chain variable region("LC") nucleic acid sequence
Ab 267	4266	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-23642 LAD4710_P01_C04	Light chain variable region ("LC") amino acid sequence
Ab 267	4267	KSSQSLLNSRTGKNYLA	ADI-23642 LAD4710_P01_C04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 267	4268	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23642 LAD4710_P01_C04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 267	4269	WASTRES	ADI-23642 LAD4710_P01_C04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 267	4270	TGGGCATCTACCCGGGAATCC	ADI-23642 LAD4710_P01_C04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 267	4271	KQSYSLRT	ADI-23642 LAD4710_P01_C04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 267	4272	AAGCAATCTTATTCTCTGAGAACT	ADI-23642 LAD4710_P01_C04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 268	4273	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCGCGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23643 LAD4711_P01_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 268	4274	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23643 LAD4711_P01_C05	Heavy chain variable region ("HC") amino acid sequence
Ab 268	4275	FNIKDYYMH	ADI-23643 LAD4711_P01_C05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 268	4276	TTCAACATCAAGGACTACTATATGCAC	ADI-23643 LAD4711_P01_C05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 268	4277	WIDPENGNTIYDPKFQG	ADI-23643 LAD4711_P01_C05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 268	4278	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23643 LAD4711_P01_C05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 268	4279	ARDGYGRYFYDV	ADI-23643 LAD4711_P01_C05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 268	4280	GCTAGAGACGGTTACGGGAGATATTTTTACGACGTG	ADI-23643 LAD4711_P01_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 268	4281	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23643 LAD4711_P01_C05	Light chain variable region("LC") nucleic acid sequence
Ab 268	4282	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-23643 LAD4711_P01_C05	Light chain variable region ("LC") amino acid sequence
Ab 268	4283	KSSQSLLNSRTGKNYLA	ADI-23643 LAD4711_P01_C05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 268	4284	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23643 LAD4711_P01_C05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 268	4285	WASTRES	ADI-23643 LAD4711_P01_C05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 268	4286	TGGGCATCTACCCGGGAATCC	ADI-23643 LAD4711_P01_C05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 268	4287	KQSYSLRT	ADI-23643 LAD4711_P01_C05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 268	4288	AAGCAATCTTATTCTCTGAGAACT	ADI-23643 LAD4711_P01_C05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 269	4289	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23644 LAD4758_P02_H01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 269	4290	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23644 LAD4758_P02_H01	Heavy chain variable region ("HC") amino acid sequence
Ab 269	4291	FNIKDYYMH	ADI-23644 LAD4758_P02_H01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 269	4292	TTCAACATCAAGGACTACTATATGCAC	ADI-23644 LAD4758_P02_H01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 269	4293	WIDLEEGNTIYDPKFQG	ADI-23644 LAD4758_P02_H01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 269	4294	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23644 LAD4758_P02_H01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 269	4295	ARDGYGRYFYDV	ADI-23644 LAD4758_P02_H01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 269	4296	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23644 LAD4758_P02_H01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 269	4297	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23644 LAD4758_P02_H01	Light chain variable region("LC") nucleic acid sequence
Ab 269	4298	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23644 LAD4758_P02_H01	Light chain variable region ("LC") amino acid sequence
Ab 269	4299	KSSQSLLESRTGKNYLA	ADI-23644 LAD4758_P02_H01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 269	4300	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23644 LAD4758_P02_H01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 269	4301	WASTRES	ADI-23644 LAD4758_P02_H01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 269	4302	TGGGCATCTACCCGGGAATCC	ADI-23644 LAD4758_P02_H01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 269	4303	KQSYSRRT	ADI-23644 LAD4758_P02_H01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 269	4304	AAGCAATCTTATTCTCGGAGAACT	ADI-23644 LAD4758_P02_H01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 270	4305	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23645 LAD4759_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 270	4306	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23645 LAD4759_P02_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 270	4307	FNIKDYYMH	ADI-23645 LAD4759_P02_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 270	4308	TTCAACATCAAGGACTACTATATGCAC	ADI-23645 LAD4759_P02_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 270	4309	WIDLENGNTIYQPKFQG	ADI-23645 LAD4759_P02_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 270	4310	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23645 LAD4759_P02_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 270	4311	ARDGYGRYFYDV	ADI-23645 LAD4759_P02_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 270	4312	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23645 LAD4759_P02_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 270	4313	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23645 LAD4759_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 270	4314	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23645 LAD4759_P02_A02	Light chain variable region ("LC") amino acid sequence
Ab 270	4315	KSSQSLLESRTGKNYLA	ADI-23645 LAD4759_P02_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 270	4316	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23645 LAD4759_P02_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 270	4317	WASTRES	ADI-23645 LAD4759_P02_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 270	4318	TGGGCATCTACCCGGGAATCC	ADI-23645 LAD4759_P02_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 270	4319	KQSYSRRT	ADI-23645 LAD4759_P02_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 270	4320	AAGCAATCTTATTCTCGGAGAACT	ADI-23645 LAD4759_P02_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 271	4321	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23646 LAD4760_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 271	4322	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23646 LAD4760_P02_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 271	4323	FNIKDYYMH	ADI-23646 LAD4760_P02_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 271	4324	TTCAACATCAAGGACTACTATATGCAC	ADI-23646 LAD4760_P02_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 271	4325	WIDLENGNTIYDPKFQG	ADI-23646 LAD4760_P02_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 271	4326	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23646 LAD4760_P02_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 271	4327	AREGYGRYFYDV	ADI-23646 LAD4760_P02_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 271	4328	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23646 LAD4760_P02_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 271	4329	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23646 LAD4760_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 271	4330	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23646 LAD4760_P02_A03	Light chain variable region ("LC") amino acid sequence
Ab 271	4331	KSSQSLLESRTGKNYLA	ADI-23646 LAD4760_P02_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 271	4332	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23646 LAD4760_P02_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 271	4333	WASTRES	ADI-23646 LAD4760_P02_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 271	4334	TGGGCATCTACCCGGGAATCC	ADI-23646 LAD4760_P02_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 271	4335	KQSYSRRT	ADI-23646 LAD4760_P02_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 271	4336	AAGCAATCTTATTCTCGGAGAACT	ADI-23646 LAD4760_P02_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 272	4337	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23647 LAD4761_P02_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 272	4338	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23647 LAD4761_P02_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 272	4339	FNIKDYYMH	ADI-23647 LAD4761_P02_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 272	4340	TTCAACATCAAGGACTACTATATGCAC	ADI-23647 LAD4761_P02_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 272	4341	WIDLEEGNTIYQPKFQG	ADI-23647 LAD4761_P02_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 272	4342	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23647 LAD4761_P02_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 272	4343	ARDGYGRYFYDV	ADI-23647 LAD4761_P02_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 272	4344	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23647 LAD4761_P02_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 272	4345	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23647 LAD4761_P02_A04	Light chain variable region("LC") nucleic acid sequence
Ab 272	4346	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23647 LAD4761_P02_A04	Light chain variable region ("LC") amino acid sequence
Ab 272	4347	KSSQSLLESRTGKNYLA	ADI-23647 LAD4761_P02_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 272	4348	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23647 LAD4761_P02_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 272	4349	WASTRES	ADI-23647 LAD4761_P02_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 272	4350	TGGGCATCTACCCGGGAATCC	ADI-23647 LAD4761_P02_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 272	4351	KQSYSRRT	ADI-23647 LAD4761_P02_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 272	4352	AAGCAATCTTATTCTCGGAGAACT	ADI-23647 LAD4761_P02_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 273	4353	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23648 LAD4762_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 273	4354	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23648 LAD4762_P02_A05	Heavy chain variable region ("HC") amino acid sequence
Ab 273	4355	FNIKDYYMH	ADI-23648 LAD4762_P02_A05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 273	4356	TTCAACATCAAGGACTACTATATGCAC	ADI-23648 LAD4762_P02_A05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 273	4357	WIDLENGNTIYQPKFQG	ADI-23648 LAD4762_P02_A05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 273	4358	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23648 LAD4762_P02_A05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 273	4359	AREGYGRYFYDV	ADI-23648 LAD4762_P02_A05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 273	4360	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23648 LAD4762_P02_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 273	4361	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23648 LAD4762_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 273	4362	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23648 LAD4762_P02_A05	Light chain variable region ("LC") amino acid sequence
Ab 273	4363	KSSQSLLESRTGKNYLA	ADI-23648 LAD4762_P02_A05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 273	4364	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23648 LAD4762_P02_A05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 273	4365	WASTRES	ADI-23648 LAD4762_P02_A05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 273	4366	TGGGCATCTACCCGGGAATCC	ADI-23648 LAD4762_P02_A05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 273	4367	KQSYSRRT	ADI-23648 LAD4762_P02_A05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 273	4368	AAGCAATCTTATTCTCGGAGAACT	ADI-23648 LAD4762_P02_A05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 274	4369	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23649 LAD4763_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 274	4370	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23649 LAD4763_P02_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 274	4371	FNIKDYYMH	ADI-23649 LAD4763_P02_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 274	4372	TTCAACATCAAGGACTACTATATGCAC	ADI-23649 LAD4763_P02_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 274	4373	WIDLEEGNTIYDPKFQG	ADI-23649 LAD4763_P02_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 274	4374	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23649 LAD4763_P02_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 274	4375	AREGYGRYFYDV	ADI-23649 LAD4763_P02_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 274	4376	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23649 LAD4763_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 274	4377	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23649 LAD4763_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 274	4378	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23649 LAD4763_P02_A06	Light chain variable region ("LC") amino acid sequence
Ab 274	4379	KSSQSLLESRTGKNYLA	ADI-23649 LAD4763_P02_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 274	4380	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23649 LAD4763_P02_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 274	4381	WASTRES	ADI-23649 LAD4763_P02_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 274	4382	TGGGCATCTACCCGGGAATCC	ADI-23649 LAD4763_P02_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 274	4383	KQSYSRRT	ADI-23649 LAD4763_P02_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 274	4384	AAGCAATCTTATTCTCGGAGAACT	ADI-23649 LAD4763_P02_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 275	4385	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23650 LAD4764_P02_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 275	4386	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23650 LAD4764_P02_A07	Heavy chain variable region ("HC") amino acid sequence
Ab 275	4387	FNIKDYYMH	ADI-23650 LAD4764_P02_A07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 275	4388	TTCAACATCAAGGACTACTATATGCAC	ADI-23650 LAD4764_P02_A07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 275	4389	WIDLEEGNTIYQPKFQG	ADI-23650 LAD4764_P02_A07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 275	4390	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23650 LAD4764_P02_A07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 275	4391	AREGYGRYFYDV	ADI-23650 LAD4764_P02_A07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 275	4392	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23650 LAD4764_P02_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 275	4393	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23650 LAD4764_P02_A07	Light chain variable region("LC") nucleic acid sequence
Ab 275	4394	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23650 LAD4764_P02_A07	Light chain variable region ("LC") amino acid sequence
Ab 275	4395	KSSQSLLESRTGKNYLA	ADI-23650 LAD4764_P02_A07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 275	4396	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23650 LAD4764_P02_A07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 275	4397	WASTRES	ADI-23650 LAD4764_P02_A07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 275	4398	TGGGCATCTACCCGGGAATCC	ADI-23650 LAD4764_P02_A07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 275	4399	KQSYSRRT	ADI-23650 LAD4764_P02_A07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 275	4400	AAGCAATCTTATTCTCGGAGAACT	ADI-23650 LAD4764_P02_A07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 276	4401	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23651 LAD4765_P02_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 276	4402	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23651 LAD4765_P02_A08	Heavy chain variable region ("HC") amino acid sequence
Ab 276	4403	FNIKDYYMH	ADI-23651 LAD4765_P02_A08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 276	4404	TTCAACATCAAGGACTACTATATGCAC	ADI-23651 LAD4765_P02_A08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 276	4405	WIDLENGNTIYDPKFQG	ADI-23651 LAD4765_P02_A08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 276	4406	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23651 LAD4765_P02_A08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 276	4407	ARDGYGRYFYDV	ADI-23651 LAD4765_P02_A08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 276	4408	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23651 LAD4765_P02_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 276	4409	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23651 LAD4765_P02_A08	Light chain variable region("LC") nucleic acid sequence
Ab 276	4410	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23651 LAD4765_P02_A08	Light chain variable region ("LC") amino acid sequence
Ab 276	4411	KSSQSLLESRTGKNYLA	ADI-23651 LAD4765_P02_A08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 276	4412	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23651 LAD4765_P02_A08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 276	4413	WASTRES	ADI-23651 LAD4765_P02_A08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 276	4414	TGGGCATCTACCCGGGAATCC	ADI-23651 LAD4765_P02_A08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 276	4415	KQSYSRRT	ADI-23651 LAD4765_P02_A08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 276	4416	AAGCAATCTTATTCTCGGAGAACT	ADI-23651 LAD4765_P02_A08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 277	4417	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23652 LAD4766_P02_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 277	4418	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23652 LAD4766_P02_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 277	4419	FNIKDYYMH	ADI-23652 LAD4766_P02_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 277	4420	TTCAACATCAAGGACTACTATATGCAC	ADI-23652 LAD4766_P02_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 277	4421	WIDLEEGNTIYDPKFQG	ADI-23652 LAD4766_P02_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 277	4422	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23652 LAD4766_P02_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 277	4423	ARDGYGRYFYDV	ADI-23652 LAD4766_P02_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 277	4424	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23652 LAD4766_P02_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 277	4425	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23652 LAD4766_P02_A09	Light chain variable region("LC") nucleic acid sequence
Ab 277	4426	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23652 LAD4766_P02_A09	Light chain variable region ("LC") amino acid sequence
Ab 277	4427	KSSQSLLNSRTGKNYLA	ADI-23652 LAD4766_P02_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 277	4428	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23652 LAD4766_P02_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 277	4429	WASTRES	ADI-23652 LAD4766_P02_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 277	4430	TGGGCATCTACCCGGGAATCC	ADI-23652 LAD4766_P02_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 277	4431	KQSYSRRT	ADI-23652 LAD4766_P02_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 277	4432	AAGCAATCTTATTCTCGGAGAACT	ADI-23652 LAD4766_P02_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 278	4433	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23653 LAD4767_P02_A10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 278	4434	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23653 LAD4767_P02_A10	Heavy chain variable region ("HC") amino acid sequence
Ab 278	4435	FNIKDYYMH	ADI-23653 LAD4767_P02_A10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 278	4436	TTCAACATCAAGGACTACTATATGCAC	ADI-23653 LAD4767_P02_A10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 278	4437	WIDLENGNTIYQPKFQG	ADI-23653 LAD4767_P02_A10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 278	4438	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23653 LAD4767_P02_A10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 278	4439	ARDGYGRYFYDV	ADI-23653 LAD4767_P02_A10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 278	4440	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23653 LAD4767_P02_A10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 278	4441	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23653 LAD4767_P02_A10	Light chain variable region("LC") nucleic acid sequence
Ab 278	4442	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23653 LAD4767_P02_A10	Light chain variable region ("LC") amino acid sequence
Ab 278	4443	KSSQSLLNSRTGKNYLA	ADI-23653 LAD4767_P02_A10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 278	4444	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23653 LAD4767_P02_A10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 278	4445	WASTRES	ADI-23653 LAD4767_P02_A10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 278	4446	TGGGCATCTACCCGGGAATCC	ADI-23653 LAD4767_P02_A10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 278	4447	KQSYSRRT	ADI-23653 LAD4767_P02_A10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 278	4448	AAGCAATCTTATTCTCGGAGAACT	ADI-23653 LAD4767_P02_A10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 279	4449	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23654 LAD4768_P02_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 279	4450	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23654 LAD4768_P02_F11	Heavy chain variable region ("HC") amino acid sequence
Ab 279	4451	FNIKDYYMH	ADI-23654 LAD4768_P02_F11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 279	4452	TTCAACATCAAGGACTACTATATGCAC	ADI-23654 LAD4768_P02_F11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 279	4453	WIDLENGNTIYDPKFQG	ADI-23654 LAD4768_P02_F11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 279	4454	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23654 LAD4768_P02_F11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 279	4455	AREGYGRYFYDV	ADI-23654 LAD4768_P02_F11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 279	4456	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23654 LAD4768_P02_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 279	4457	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23654 LAD4768_P02_F11	Light chain variable region("LC") nucleic acid sequence
Ab 279	4458	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23654 LAD4768_P02_F11	Light chain variable region ("LC") amino acid sequence
Ab 279	4459	KSSQSLLNSRTGKNYLA	ADI-23654 LAD4768_P02_F11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 279	4460	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23654 LAD4768_P02_F11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 279	4461	WASTRES	ADI-23654 LAD4768_P02_F11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 279	4462	TGGGCATCTACCCGGGAATCC	ADI-23654 LAD4768_P02_F11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 279	4463	KQSYSRRT	ADI-23654 LAD4768_P02_F11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 279	4464	AAGCAATCTTATTCTCGGAGAACT	ADI-23654 LAD4768_P02_F11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 280	4465	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23655 LAD4769_P02_H01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 280	4466	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23655 LAD4769_P02_H01	Heavy chain variable region ("HC") amino acid sequence
Ab 280	4467	FNIKDYYMH	ADI-23655 LAD4769_P02_H01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 280	4468	TTCAACATCAAGGACTACTATATGCAC	ADI-23655 LAD4769_P02_H01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 280	4469	WIDLEEGNTIYQPKFQG	ADI-23655 LAD4769_P02_H01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 280	4470	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23655 LAD4769_P02_H01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 280	4471	ARDGYGRYFYDV	ADI-23655 LAD4769_P02_H01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 280	4472	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23655 LAD4769_P02_H01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 280	4473	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23655 LAD4769_P02_H01	Light chain variable region("LC") nucleic acid sequence
Ab 280	4474	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23655 LAD4769_P02_H01	Light chain variable region ("LC") amino acid sequence
Ab 280	4475	KSSQSLLNSRTGKNYLA	ADI-23655 LAD4769_P02_H01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 280	4476	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23655 LAD4769_P02_H01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 280	4477	WASTRES	ADI-23655 LAD4769_P02_H01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 280	4478	TGGGCATCTACCCGGGAATCC	ADI-23655 LAD4769_P02_H01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 280	4479	KQSYSRRT	ADI-23655 LAD4769_P02_H01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 280	4480	AAGCAATCTTATTCTCGGAGAACT	ADI-23655 LAD4769_P02_H01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 281	4481	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23656 LAD4770_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 281	4482	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23656 LAD4770_P02_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 281	4483	FNIKDYYMH	ADI-23656 LAD4770_P02_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 281	4484	TTCAACATCAAGGACTACTATATGCAC	ADI-23656 LAD4770_P02_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 281	4485	WIDLENGNTIYQPKFQG	ADI-23656 LAD4770_P02_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 281	4486	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23656 LAD4770_P02_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 281	4487	AREGYGRYFYDV	ADI-23656 LAD4770_P02_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 281	4488	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23656 LAD4770_P02_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 281	4489	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23656 LAD4770_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 281	4490	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23656 LAD4770_P02_A02	Light chain variable region ("LC") amino acid sequence
Ab 281	4491	KSSQSLLNSRTGKNYLA	ADI-23656 LAD4770_P02_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 281	4492	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23656 LAD4770_P02_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 281	4493	WASTRES	ADI-23656 LAD4770_P02_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 281	4494	TGGGCATCTACCCGGGAATCC	ADI-23656 LAD4770_P02_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 281	4495	KQSYSRRT	ADI-23656 LAD4770_P02_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 281	4496	AAGCAATCTTATTCTCGGAGAACT	ADI-23656 LAD4770_P02_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 282	4497	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23657 LAD4771_P02_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 282	4498	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23657 LAD4771_P02_H03	Heavy chain variable region ("HC") amino acid sequence
Ab 282	4499	FNIKDYYMH	ADI-23657 LAD4771_P02_H03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 282	4500	TTCAACATCAAGGACTACTATATGCAC	ADI-23657 LAD4771_P02_H03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 282	4501	WIDLEEGNTIYDPKFQG	ADI-23657 LAD4771_P02_H03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 282	4502	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23657 LAD4771_P02_H03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 282	4503	AREGYGRYFYDV	ADI-23657 LAD4771_P02_H03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 282	4504	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23657 LAD4771_P02_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 282	4505	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23657 LAD4771_P02_H03	Light chain variable region("LC") nucleic acid sequence
Ab 282	4506	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23657 LAD4771_P02_H03	Light chain variable region ("LC") amino acid sequence
Ab 282	4507	KSSQSLLNSRTGKNYLA	ADI-23657 LAD4771_P02_H03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 282	4508	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23657 LAD4771_P02_H03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 282	4509	WASTRES	ADI-23657 LAD4771_P02_H03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 282	4510	TGGGCATCTACCCGGGAATCC	ADI-23657 LAD4771_P02_H03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 282	4511	KQSYSRRT	ADI-23657 LAD4771_P02_H03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 282	4512	AAGCAATCTTATTCTCGGAGAACT	ADI-23657 LAD4771_P02_H03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 283	4513	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGAAGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23658 LAD4772_P02_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 283	4514	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTVSS	ADI-23658 LAD4772_P02_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 283	4515	FNIKDYYMH	ADI-23658 LAD4772_P02_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 283	4516	TTCAACATCAAGGACTACTATATGCAC	ADI-23658 LAD4772_P02_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 283	4517	WIDLEEGNTIYQPKFQG	ADI-23658 LAD4772_P02_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 283	4518	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGTTTCAGGGC	ADI-23658 LAD4772_P02_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 283	4519	AREGYGRYFYDV	ADI-23658 LAD4772_P02_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 283	4520	GCGAGAGAAGGATACGGGAGATATTTTTACGACGTG	ADI-23658 LAD4772_P02_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 283	4521	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23658 LAD4772_P02_A04	Light chain variable region("LC") nucleic acid sequence
Ab 283	4522	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23658 LAD4772_P02_A04	Light chain variable region ("LC") amino acid sequence
Ab 283	4523	KSSQSLLNSRTGKNYLA	ADI-23658 LAD4772_P02_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 283	4524	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23658 LAD4772_P02_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 283	4525	WASTRES	ADI-23658 LAD4772_P02_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 283	4526	TGGGCATCTACCCGGGAATCC	ADI-23658 LAD4772_P02_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 283	4527	KQSYSRRT	ADI-23658 LAD4772_P02_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 283	4528	AAGCAATCTTATTCTCGGAGAACT	ADI-23658 LAD4772_P02_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 284	4529	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23659 LAD4779_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 284	4530	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23659 LAD4779_P01_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 284	4531	FNIKDYYMH	ADI-23659 LAD4779_P01_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 284	4532	TTCAACATCAAGGACTACTATATGCAC	ADI-23659 LAD4779_P01_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 284	4533	WIDLENANTIYDPKFQG	ADI-23659 LAD4779_P01_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 284	4534	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23659 LAD4779_P01_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 284	4535	ARDGYGRYFYDV	ADI-23659 LAD4779_P01_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 284	4536	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23659 LAD4779_P01_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 284	4537	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23659 LAD4779_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 284	4538	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23659 LAD4779_P01_A04	Light chain variable region ("LC") amino acid sequence
Ab 284	4539	KSSQSLLNARTGKNYLA	ADI-23659 LAD4779_P01_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 284	4540	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-23659 LAD4779_P01_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 284	4541	WASTRES	ADI-23659 LAD4779_P01_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 284	4542	TGGGCATCTACCCGGGAATCC	ADI-23659 LAD4779_P01_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 284	4543	KQSYSRRT	ADI-23659 LAD4779_P01_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 284	4544	AAGCAATCTTATTCTCGGAGAACT	ADI-23659 LAD4779_P01_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 285	4545	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23660 LAD4780_P01_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 285	4546	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23660 LAD4780_P01_B05	Heavy chain variable region ("HC") amino acid sequence
Ab 285	4547	FNIKDYYMH	ADI-23660 LAD4780_P01_B05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 285	4548	TTCAACATCAAGGACTACTATATGCAC	ADI-23660 LAD4780_P01_B05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 285	4549	WIDLENGNTIYDAKFQG	ADI-23660 LAD4780_P01_B05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 285	4550	TGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-23660 LAD4780_P01_B05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 285	4551	ARDGYGRYFYDV	ADI-23660 LAD4780_P01_B05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 285	4552	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23660 LAD4780_P01_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 285	4553	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23660 LAD4780_P01_B05	Light chain variable region("LC") nucleic acid sequence
Ab 285	4554	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23660 LAD4780_P01_B05	Light chain variable region ("LC") amino acid sequence
Ab 285	4555	KSSQSLLNARTGKNYLA	ADI-23660 LAD4780_P01_B05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 285	4556	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-23660 LAD4780_P01_B05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 285	4557	WASTRES	ADI-23660 LAD4780_P01_B05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 285	4558	TGGGCATCTACCCGGGAATCC	ADI-23660 LAD4780_P01_B05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 285	4559	KQSYSRRT	ADI-23660 LAD4780_P01_B05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 285	4560	AAGCAATCTTATTCTCGGAGAACT	ADI-23660 LAD4780_P01_B05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 286	4561	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23661 LAD4781_P01_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 286	4562	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-23661 LAD4781_P01_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 286	4563	FNIKDYYMH	ADI-23661 LAD4781_P01_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 286	4564	TTCAACATCAAGGACTACTATATGCAC	ADI-23661 LAD4781_P01_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 286	4565	WIDLENGNTIYDPKFQG	ADI-23661 LAD4781_P01_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 286	4566	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23661 LAD4781_P01_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 286	4567	ARDAYGRYFYDV	ADI-23661 LAD4781_P01_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 286	4568	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-23661 LAD4781_P01_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 286	4569	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23661 LAD4781_P01_A06	Light chain variable region("LC") nucleic acid sequence
Ab 286	4570	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23661 LAD4781_P01_A06	Light chain variable region ("LC") amino acid sequence
Ab 286	4571	KSSQSLLNARTGKNYLA	ADI-23661 LAD4781_P01_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 286	4572	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-23661 LAD4781_P01_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 286	4573	WASTRES	ADI-23661 LAD4781_P01_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 286	4574	TGGGCATCTACCCGGGAATCC	ADI-23661 LAD4781_P01_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 286	4575	KQSYSRRT	ADI-23661 LAD4781_P01_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 286	4576	AAGCAATCTTATTCTCGGAGAACT	ADI-23661 LAD4781_P01_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 287	4577	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23663 LAD4783_P01_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 287	4578	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-23663 LAD4783_P01_C08	Heavy chain variable region ("HC") amino acid sequence
Ab 287	4579	FNIKDYYMH	ADI-23663 LAD4783_P01_C08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 287	4580	TTCAACATCAAGGACTACTATATGCAC	ADI-23663 LAD4783_P01_C08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 287	4581	WIDLENGNTIYDAKFQG	ADI-23663 LAD4783_P01_C08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 287	4582	TGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-23663 LAD4783_P01_C08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 287	4583	ARDAYGRYFYDV	ADI-23663 LAD4783_P01_C08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 287	4584	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-23663 LAD4783_P01_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 287	4585	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23663 LAD4783_P01_C08	Light chain variable region("LC") nucleic acid sequence
Ab 287	4586	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23663 LAD4783_P01_C08	Light chain variable region ("LC") amino acid sequence
Ab 287	4587	KSSQSLLNARTGKNYLA	ADI-23663 LAD4783_P01_C08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 287	4588	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-23663 LAD4783_P01_C08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 287	4589	WASTRES	ADI-23663 LAD4783_P01_C08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 287	4590	TGGGCATCTACCCGGGAATCC	ADI-23663 LAD4783_P01_C08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 287	4591	KQSYSRRT	ADI-23663 LAD4783_P01_C08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 287	4592	AAGCAATCTTATTCTCGGAGAACT	ADI-23663 LAD4783_P01_C08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 288	4593	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23664 LAD4784_P01_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 288	4594	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-23664 LAD4784_P01_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 288	4595	FNIKDYYMH	ADI-23664 LAD4784_P01_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 288	4596	TTCAACATCAAGGACTACTATATGCAC	ADI-23664 LAD4784_P01_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 288	4597	WIDLENANTIYDPKFQG	ADI-23664 LAD4784_P01_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 288	4598	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23664 LAD4784_P01_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 288	4599	ARDAYGRYFYDV	ADI-23664 LAD4784_P01_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 288	4600	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-23664 LAD4784_P01_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 288	4601	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23664 LAD4784_P01_A09	Light chain variable region("LC") nucleic acid sequence
Ab 288	4602	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23664 LAD4784_P01_A09	Light chain variable region ("LC") amino acid sequence
Ab 288	4603	KSSQSLLNARTGKNYLA	ADI-23664 LAD4784_P01_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 288	4604	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-23664 LAD4784_P01_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 288	4605	WASTRES	ADI-23664 LAD4784_P01_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 288	4606	TGGGCATCTACCCGGGAATCC	ADI-23664 LAD4784_P01_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 288	4607	KQSYSRRT	ADI-23664 LAD4784_P01_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 288	4608	AAGCAATCTTATTCTCGGAGAACT	ADI-23664 LAD4784_P01_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 289	4609	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCCTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23667 LAD4787_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 289	4610	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23667 LAD4787_P01_A12	Heavy chain variable region ("HC") amino acid sequence
Ab 289	4611	FNIKDYYMH	ADI-23667 LAD4787_P01_A12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 289	4612	TTCAACATCAAGGACTACTATATGCAC	ADI-23667 LAD4787_P01_A12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 289	4613	WIDLENANTIYDPKFQG	ADI-23667 LAD4787_P01_A12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 289	4614	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23667 LAD4787_P01_A12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 289	4615	ARDGYGRYFYDV	ADI-23667 LAD4787_P01_A12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 289	4616	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23667 LAD4787_P01_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 289	4617	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23667 LAD4787_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 289	4618	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23667 LAD4787_P01_A12	Light chain variable region ("LC") amino acid sequence
Ab 289	4619	KSSQSLLNSRTGKNYLA	ADI-23667 LAD4787_P01_A12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 289	4620	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23667 LAD4787_P01_A12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 289	4621	WASTRES	ADI-23667 LAD4787_P01_A12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 289	4622	TGGGCATCTACCCGGGAATCC	ADI-23667 LAD4787_P01_A12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 289	4623	KQSYSRRT	ADI-23667 LAD4787_P01_A12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 289	4624	AAGCAATCTTATTCTCGGAGAACT	ADI-23667 LAD4787_P01_A12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 290	4625	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23668 LAD4788_P01_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 290	4626	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23668 LAD4788_P01_C01	Heavy chain variable region ("HC") amino acid sequence
Ab 290	4627	FNIKDYYMH	ADI-23668 LAD4788_P01_C01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 290	4628	TTCAACATCAAGGACTACTATATGCAC	ADI-23668 LAD4788_P01_C01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 290	4629	WIDLENGNTIYDAKFQG	ADI-23668 LAD4788_P01_C01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 290	4630	TGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-23668 LAD4788_P01_C01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 290	4631	ARDGYGRYFYDV	ADI-23668 LAD4788_P01_C01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 290	4632	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23668 LAD4788_P01_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 290	4633	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23668 LAD4788_P01_C01	Light chain variable region("LC") nucleic acid sequence
Ab 290	4634	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23668 LAD4788_P01_C01	Light chain variable region ("LC") amino acid sequence
Ab 290	4635	KSSQSLLNSRTGKNYLA	ADI-23668 LAD4788_P01_C01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 290	4636	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23668 LAD4788_P01_C01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 290	4637	WASTRES	ADI-23668 LAD4788_P01_C01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 290	4638	TGGGCATCTACCCGGGAATCC	ADI-23668 LAD4788_P01_C01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 290	4639	KQSYSRRT	ADI-23668 LAD4788_P01_C01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 290	4640	AAGCAATCTTATTCTCGGAGAACT	ADI-23668 LAD4788_P01_C01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 291	4641	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23669 LAD4789_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 291	4642	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-23669 LAD4789_P01_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 291	4643	FNIKDYYMH	ADI-23669 LAD4789_P01_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 291	4644	TTCAACATCAAGGACTACTATATGCAC	ADI-23669 LAD4789_P01_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 291	4645	WIDLENGNTIYDPKFQG	ADI-23669 LAD4789_P01_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 291	4646	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23669 LAD4789_P01_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 291	4647	ARDAYGRYFYDV	ADI-23669 LAD4789_P01_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 291	4648	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-23669 LAD4789_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 291	4649	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23669 LAD4789_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 291	4650	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23669 LAD4789_P01_A02	Light chain variable region ("LC") amino acid sequence
Ab 291	4651	KSSQSLLNSRTGKNYLA	ADI-23669 LAD4789_P01_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 291	4652	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23669 LAD4789_P01_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 291	4653	WASTRES	ADI-23669 LAD4789_P01_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 291	4654	TGGGCATCTACCCGGGAATCC	ADI-23669 LAD4789_P01_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 291	4655	KQSYSRRT	ADI-23669 LAD4789_P01_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 291	4656	AAGCAATCTTATTCTCGGAGAACT	ADI-23669 LAD4789_P01_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 292	4657	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23670 LAD4790_P01_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 292	4658	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-23670 LAD4790_P01_H03	Heavy chain variable region ("HC") amino acid sequence
Ab 292	4659	FNIKDYYMH	ADI-23670 LAD4790_P01_H03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 292	4660	TTCAACATCAAGGACTACTATATGCAC	ADI-23670 LAD4790_P01_H03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 292	4661	WIDLENANTIYDAKFQG	ADI-23670 LAD4790_P01_H03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 292	4662	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-23670 LAD4790_P01_H03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 292	4663	ARDGYGRYFYDV	ADI-23670 LAD4790_P01_H03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 292	4664	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-23670 LAD4790_P01_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 292	4665	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23670 LAD4790_P01_H03	Light chain variable region("LC") nucleic acid sequence
Ab 292	4666	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23670 LAD4790_P01_H03	Light chain variable region ("LC") amino acid sequence
Ab 292	4667	KSSQSLLNSRTGKNYLA	ADI-23670 LAD4790_P01_H03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 292	4668	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23670 LAD4790_P01_H03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 292	4669	WASTRES	ADI-23670 LAD4790_P01_H03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 292	4670	TGGGCATCTACCCGGGAATCC	ADI-23670 LAD4790_P01_H03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 292	4671	KQSYSRRT	ADI-23670 LAD4790_P01_H03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 292	4672	AAGCAATCTTATTCTCGGAGAACT	ADI-23670 LAD4790_P01_H03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 293	4673	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23671 LAD4791_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 293	4674	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-23671 LAD4791_P01_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 293	4675	FNIKDYYMH	ADI-23671 LAD4791_P01_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 293	4676	TTCAACATCAAGGACTACTATATGCAC	ADI-23671 LAD4791_P01_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 293	4677	WIDLENGNTIYDAKFQG	ADI-23671 LAD4791_P01_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 293	4678	TGGATCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-23671 LAD4791_P01_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 293	4679	ARDAYGRYFYDV	ADI-23671 LAD4791_P01_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 293	4680	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-23671 LAD4791_P01_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 293	4681	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23671 LAD4791_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 293	4682	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23671 LAD4791_P01_A04	Light chain variable region ("LC") amino acid sequence
Ab 293	4683	KSSQSLLNSRTGKNYLA	ADI-23671 LAD4791_P01_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 293	4684	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23671 LAD4791_P01_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 293	4685	WASTRES	ADI-23671 LAD4791_P01_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 293	4686	TGGGCATCTACCCGGGAATCC	ADI-23671 LAD4791_P01_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 293	4687	KQSYSRRT	ADI-23671 LAD4791_P01_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 293	4688	AAGCAATCTTATTCTCGGAGAACT	ADI-23671 LAD4791_P01_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 294	4689	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23672 LAD4792_P01_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 294	4690	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-23672 LAD4792_P01_A05	Heavy chain variable region ("HC") amino acid sequence
Ab 294	4691	FNIKDYYMH	ADI-23672 LAD4792_P01_A05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 294	4692	TTCAACATCAAGGACTACTATATGCAC	ADI-23672 LAD4792_P01_A05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 294	4693	WIDLENANTIYDPKFQG	ADI-23672 LAD4792_P01_A05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 294	4694	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-23672 LAD4792_P01_A05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 294	4695	ARDAYGRYFYDV	ADI-23672 LAD4792_P01_A05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 294	4696	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-23672 LAD4792_P01_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 294	4697	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23672 LAD4792_P01_A05	Light chain variable region("LC") nucleic acid sequence
Ab 294	4698	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23672 LAD4792_P01_A05	Light chain variable region ("LC") amino acid sequence
Ab 294	4699	KSSQSLLNSRTGKNYLA	ADI-23672 LAD4792_P01_A05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 294	4700	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23672 LAD4792_P01_A05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 294	4701	WASTRES	ADI-23672 LAD4792_P01_A05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 294	4702	TGGGCATCTACCCGGGAATCC	ADI-23672 LAD4792_P01_A05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 294	4703	KQSYSRRT	ADI-23672 LAD4792_P01_A05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 294	4704	AAGCAATCTTATTCTCGGAGAACT	ADI-23672 LAD4792_P01_A05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 295	4705	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23673 LAD4793_P01_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 295	4706	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-23673 LAD4793_P01_D06	Heavy chain variable region ("HC") amino acid sequence
Ab 295	4707	FNIKDYYMH	ADI-23673 LAD4793_P01_D06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 295	4708	TTCAACATCAAGGACTACTATATGCAC	ADI-23673 LAD4793_P01_D06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 295	4709	WIDLENANTIYDAKFQG	ADI-23673 LAD4793_P01_D06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 295	4710	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-23673 LAD4793_P01_D06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 295	4711	ARDAYGRYFYDV	ADI-23673 LAD4793_P01_D06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 295	4712	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-23673 LAD4793_P01_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 295	4713	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23673 LAD4793_P01_D06	Light chain variable region("LC") nucleic acid sequence
Ab 295	4714	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-23673 LAD4793_P01_D06	Light chain variable region ("LC") amino acid sequence
Ab 295	4715	KSSQSLLNSRTGKNYLA	ADI-23673 LAD4793_P01_D06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 295	4716	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-23673 LAD4793_P01_D06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 295	4717	WASTRES	ADI-23673 LAD4793_P01_D06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 295	4718	TGGGCATCTACCCGGGAATCC	ADI-23673 LAD4793_P01_D06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 295	4719	KQSYSRRT	ADI-23673 LAD4793_P01_D06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 295	4720	AAGCAATCTTATTCTCGGAGAACT	ADI-23673 LAD4793_P01_D06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 296	4721	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24403 BAD24629_D09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 296	4722	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24403 BAD24629_D09	Heavy chain variable region ("HC") amino acid sequence
Ab 296	4723	FNIKDYYMH	ADI-24403 BAD24629_D09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 296	4724	TTCAACATCAAGGACTACTATATGCAC	ADI-24403 BAD24629_D09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 296	4725	WIDLENGNTIYDPKFQG	ADI-24403 BAD24629_D09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 296	4726	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24403 BAD24629_D09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 296	4727	ARDGYGRYFYDV	ADI-24403 BAD24629_D09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 296	4728	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24403 BAD24629_D09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 296	4729	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24403 BAD24629_D09	Light chain variable region("LC") nucleic acid sequence
Ab 296	4730	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24403 BAD24629_D09	Light chain variable region ("LC") amino acid sequence
Ab 296	4731	KSSQSLLNSRTGKNYLA	ADI-24403 BAD24629_D09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 296	4732	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24403 BAD24629_D09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 296	4733	WASTRES	ADI-24403 BAD24629_D09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 296	4734	TGGGCATCTACCCGGGAATCC	ADI-24403 BAD24629_D09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 296	4735	KQSYSRRT	ADI-24403 BAD24629_D09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 296	4736	AAGCAATCTTATTCTCGGAGAACT	ADI-24403 BAD24629_D09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 297	4737	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24404 BAD24629_H09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 297	4738	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24404 BAD24629_H09	Heavy chain variable region ("HC") amino acid sequence
Ab 297	4739	FNIKDYYMH	ADI-24404 BAD24629_H09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 297	4740	TTCAACATCAAGGACTACTATATGCAC	ADI-24404 BAD24629_H09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 297	4741	WIDLENGNTIYDPKFQG	ADI-24404 BAD24629_H09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 297	4742	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24404 BAD24629_H09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 297	4743	ARDGYGRYFYDV	ADI-24404 BAD24629_H09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 297	4744	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24404 BAD24629_H09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 297	4745	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24404 BAD24629_H09	Light chain variable region("LC") nucleic acid sequence
Ab 297	4746	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24404 BAD24629_H09	Light chain variable region ("LC") amino acid sequence
Ab 297	4747	KSSQSLLNSRTGKNYLA	ADI-24404 BAD24629_H09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 297	4748	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24404 BAD24629_H09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 297	4749	WASTRES	ADI-24404 BAD24629_H09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 297	4750	TGGGCATCTACCCGGGAATCC	ADI-24404 BAD24629_H09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 297	4751	KQSYSRRT	ADI-24404 BAD24629_H09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 297	4752	AAGCAATCTTATTCTCGGAGAACT	ADI-24404 BAD24629_H09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 298	4753	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24405 BAD24629_C10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 298	4754	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24405 BAD24629_C10	Heavy chain variable region ("HC") amino acid sequence
Ab 298	4755	FNIKDYYMH	ADI-24405 BAD24629_C10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 298	4756	TTCAACATCAAGGACTACTATATGCAC	ADI-24405 BAD24629_C10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 298	4757	WIDLENGNTIYDPKFQG	ADI-24405 BAD24629_C10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 298	4758	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24405 BAD24629_C10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 298	4759	ARDGYGRYFYDV	ADI-24405 BAD24629_C10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 298	4760	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24405 BAD24629_C10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 298	4761	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24405 BAD24629_C10	Light chain variable region("LC") nucleic acid sequence
Ab 298	4762	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24405 BAD24629_C10	Light chain variable region ("LC") amino acid sequence
Ab 298	4763	KSSQSLLNSRTGKNYLA	ADI-24405 BAD24629_C10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 298	4764	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24405 BAD24629_C10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 298	4765	WASTRES	ADI-24405 BAD24629_C10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 298	4766	TGGGCATCTACCCGGGAATCC	ADI-24405 BAD24629_C10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 298	4767	KQSYSRRT	ADI-24405 BAD24629_C10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 298	4768	AAGCAATCTTATTCTCGGAGAACT	ADI-24405 BAD24629_C10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 299	4769	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24407 BAD24629_C11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 299	4770	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24407 BAD24629_C11	Heavy chain variable region ("HC") amino acid sequence
Ab 299	4771	FNIKDYYMH	ADI-24407 BAD24629_C11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 299	4772	TTCAACATCAAGGACTACTATATGCAC	ADI-24407 BAD24629_C11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 299	4773	WIDLENGNTIYDPKFQG	ADI-24407 BAD24629_C11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 299	4774	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24407 BAD24629_C11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 299	4775	ARDGYGRYFYDV	ADI-24407 BAD24629_C11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 299	4776	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24407 BAD24629_C11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 299	4777	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24407 BAD24629_C11	Light chain variable region("LC") nucleic acid sequence
Ab 299	4778	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24407 BAD24629_C11	Light chain variable region ("LC") amino acid sequence
Ab 299	4779	KSSQSLLNSRTGKNYLA	ADI-24407 BAD24629_C11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 299	4780	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24407 BAD24629_C11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 299	4781	WASTRES	ADI-24407 BAD24629_C11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 299	4782	TGGGCATCTACCCGGGAATCC	ADI-24407 BAD24629_C11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 299	4783	KQSYSRRT	ADI-24407 BAD24629_C11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 299	4784	AAGCAATCTTATTCTCGGAGAACT	ADI-24407 BAD24629_C11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 300	4785	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24408 BAD24629_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 300	4786	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24408 BAD24629_F11	Heavy chain variable region ("HC") amino acid sequence
Ab 300	4787	FNIKDYYMH	ADI-24408 BAD24629_F11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 300	4788	TTCAACATCAAGGACTACTATATGCAC	ADI-24408 BAD24629_F11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 300	4789	WIDLENGNTIYDPKFQG	ADI-24408 BAD24629_F11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 300	4790	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24408 BAD24629_F11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 300	4791	ARDGYGRYFYDV	ADI-24408 BAD24629_F11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 300	4792	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24408 BAD24629_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 300	4793	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24408 BAD24629_F11	Light chain variable region("LC") nucleic acid sequence
Ab 300	4794	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24408 BAD24629_F11	Light chain variable region ("LC") amino acid sequence
Ab 300	4795	KSSQSLLNSRTGKNYLA	ADI-24408 BAD24629_F11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 300	4796	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24408 BAD24629_F11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 300	4797	WASTRES	ADI-24408 BAD24629_F11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 300	4798	TGGGCATCTACCCGGGAATCC	ADI-24408 BAD24629_F11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 300	4799	KQSYSRRT	ADI-24408 BAD24629_F11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 300	4800	AAGCAATCTTATTCTCGGAGAACT	ADI-24408 BAD24629_F11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 301	4801	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24409 BAD24629_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 301	4802	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24409 BAD24629_A12	Heavy chain variable region ("HC") amino acid sequence
Ab 301	4803	FNIKDYYMH	ADI-24409 BAD24629_A12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 301	4804	TTCAACATCAAGGACTACTATATGCAC	ADI-24409 BAD24629_A12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 301	4805	WIDLENGNTIYDPKFQG	ADI-24409 BAD24629_A12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 301	4806	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24409 BAD24629_A12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 301	4807	ARDGYGRYFYDV	ADI-24409 BAD24629_A12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 301	4808	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24409 BAD24629_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 301	4809	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24409 BAD24629_A12	Light chain variable region("LC") nucleic acid sequence
Ab 301	4810	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24409 BAD24629_A12	Light chain variable region ("LC") amino acid sequence
Ab 301	4811	KSSQSLLNSRTGKNYLA	ADI-24409 BAD24629_A12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 301	4812	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24409 BAD24629_A12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 301	4813	WASTRES	ADI-24409 BAD24629_A12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 301	4814	TGGGCATCTACCCGGGAATCC	ADI-24409 BAD24629_A12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 301	4815	KQSYSRRT	ADI-24409 BAD24629_A12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 301	4816	AAGCAATCTTATTCTCGGAGAACT	ADI-24409 BAD24629_A12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 302	4817	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24410 BAD24629_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 302	4818	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24410 BAD24629_F12	Heavy chain variable region ("HC") amino acid sequence
Ab 302	4819	FNIKDYYMH	ADI-24410 BAD24629_F12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 302	4820	TTCAACATCAAGGACTACTATATGCAC	ADI-24410 BAD24629_F12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 302	4821	WIDLENGNTIYDPKFQG	ADI-24410 BAD24629_F12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 302	4822	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24410 BAD24629_F12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 302	4823	ARDGYGRYFYDV	ADI-24410 BAD24629_F12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 302	4824	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24410 BAD24629_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 302	4825	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24410 BAD24629_F12	Light chain variable region("LC") nucleic acid sequence
Ab 302	4826	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24410 BAD24629_F12	Light chain variable region ("LC") amino acid sequence
Ab 302	4827	KSSQSLLNSRTGKNYLA	ADI-24410 BAD24629_F12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 302	4828	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24410 BAD24629_F12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 302	4829	WASTRES	ADI-24410 BAD24629_F12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 302	4830	TGGGCATCTACCCGGGAATCC	ADI-24410 BAD24629_F12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 302	4831	KQSYSRRT	ADI-24410 BAD24629_F12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 302	4832	AAGCAATCTTATTCTCGGAGAACT	ADI-24410 BAD24629_F12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 303	4833	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24411 BAD24630_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 303	4834	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24411 BAD24630_C01	Heavy chain variable region ("HC") amino acid sequence
Ab 303	4835	FNIKDYYMH	ADI-24411 BAD24630_C01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 303	4836	TTCAACATCAAGGACTACTATATGCAC	ADI-24411 BAD24630_C01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 303	4837	WIDLENGNTIYDPKFQG	ADI-24411 BAD24630_C01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 303	4838	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24411 BAD24630_C01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 303	4839	ARDGYGRYFYDV	ADI-24411 BAD24630_C01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 303	4840	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24411 BAD24630_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 303	4841	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24411 BAD24630_C01	Light chain variable region("LC") nucleic acid sequence
Ab 303	4842	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24411 BAD24630_C01	Light chain variable region ("LC") amino acid sequence
Ab 303	4843	KSSQSLLNSRTGKNYLA	ADI-24411 BAD24630_C01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 303	4844	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24411 BAD24630_C01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 303	4845	WASTRES	ADI-24411 BAD24630_C01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 303	4846	TGGGCATCTACCCGGGAATCC	ADI-24411 BAD24630_C01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 303	4847	KQSYSRRT	ADI-24411 BAD24630_C01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 303	4848	AAGCAATCTTATTCTCGGAGAACT	ADI-24411 BAD24630_C01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 304	4849	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24412 BAD24630_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 304	4850	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24412 BAD24630_G01	Heavy chain variable region ("HC") amino acid sequence
Ab 304	4851	FNIKDYYMH	ADI-24412 BAD24630_G01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 304	4852	TTCAACATCAAGGACTACTATATGCAC	ADI-24412 BAD24630_G01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 304	4853	WIDLENGNTIYDPKFQG	ADI-24412 BAD24630_G01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 304	4854	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24412 BAD24630_G01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 304	4855	ARDGYGRYFYDV	ADI-24412 BAD24630_G01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 304	4856	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24412 BAD24630_G01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 304	4857	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24412 BAD24630_G01	Light chain variable region("LC") nucleic acid sequence
Ab 304	4858	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24412 BAD24630_G01	Light chain variable region ("LC") amino acid sequence
Ab 304	4859	KSSQSLLNSRTGKNYLA	ADI-24412 BAD24630_G01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 304	4860	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24412 BAD24630_G01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 304	4861	WASTRES	ADI-24412 BAD24630_G01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 304	4862	TGGGCATCTACCCGGGAATCC	ADI-24412 BAD24630_G01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 304	4863	KQSYSRRT	ADI-24412 BAD24630_G01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 304	4864	AAGCAATCTTATTCTCGGAGAACT	ADI-24412 BAD24630_G01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 305	4865	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24413 BAD24630_D02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 305	4866	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24413 BAD24630_D02	Heavy chain variable region ("HC") amino acid sequence
Ab 305	4867	FNIKDYYMH	ADI-24413 BAD24630_D02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 305	4868	TTCAACATCAAGGACTACTATATGCAC	ADI-24413 BAD24630_D02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 305	4869	WIDLENGNTIYDPKFQG	ADI-24413 BAD24630_D02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 305	4870	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24413 BAD24630_D02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 305	4871	ARDGYGRYFYDV	ADI-24413 BAD24630_D02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 305	4872	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24413 BAD24630_D02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 305	4873	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24413 BAD24630_D02	Light chain variable region("LC") nucleic acid sequence
Ab 305	4874	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24413 BAD24630_D02	Light chain variable region ("LC") amino acid sequence
Ab 305	4875	KSSQSLLNSRTGKNYLA	ADI-24413 BAD24630_D02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 305	4876	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24413 BAD24630_D02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 305	4877	WASTRES	ADI-24413 BAD24630_D02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 305	4878	TGGGCATCTACCCGGGAATCC	ADI-24413 BAD24630_D02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 305	4879	KQSYSRRT	ADI-24413 BAD24630_D02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 305	4880	AAGCAATCTTATTCTCGGAGAACT	ADI-24413 BAD24630_D02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 306	4881	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24414 BAD24734_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 306	4882	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24414 BAD24734_G01	Heavy chain variable region ("HC") amino acid sequence
Ab 306	4883	FNIKDYYMH	ADI-24414 BAD24734_G01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 306	4884	TTCAACATCAAGGACTACTATATGCAC	ADI-24414 BAD24734_G01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 306	4885	WIDLENGNTIYDPKFQG	ADI-24414 BAD24734_G01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 306	4886	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24414 BAD24734_G01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 306	4887	ARDGYGRYFYDV	ADI-24414 BAD24734_G01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 306	4888	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24414 BAD24734_G01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 306	4889	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24414 BAD24734_G01	Light chain variable region("LC") nucleic acid sequence
Ab 306	4890	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24414 BAD24734_G01	Light chain variable region ("LC") amino acid sequence
Ab 306	4891	KSSQSLLNSRTGKNYLA	ADI-24414 BAD24734_G01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 306	4892	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24414 BAD24734_G01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 306	4893	WASTRES	ADI-24414 BAD24734_G01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 306	4894	TGGGCATCTACCCGGGAATCC	ADI-24414 BAD24734_G01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 306	4895	KQSYSRRT	ADI-24414 BAD24734_G01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 306	4896	AAGCAATCTTATTCTCGGAGAACT	ADI-24414 BAD24734_G01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 307	4897	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24415 BAD24702_D04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 307	4898	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24415 BAD24702_D04	Heavy chain variable region ("HC") amino acid sequence
Ab 307	4899	FNIKDYYMH	ADI-24415 BAD24702_D04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 307	4900	TTCAACATCAAGGACTACTATATGCAC	ADI-24415 BAD24702_D04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 307	4901	WIDLENGNTIYDPKFQG	ADI-24415 BAD24702_D04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 307	4902	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24415 BAD24702_D04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 307	4903	ARDGYGRYFYDV	ADI-24415 BAD24702_D04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 307	4904	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24415 BAD24702_D04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 307	4905	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24415 BAD24702_D04	Light chain variable region("LC") nucleic acid sequence
Ab 307	4906	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24415 BAD24702_D04	Light chain variable region ("LC") amino acid sequence
Ab 307	4907	KSSQSLLNSRTGKNYLA	ADI-24415 BAD24702_D04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 307	4908	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24415 BAD24702_D04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 307	4909	WASTRES	ADI-24415 BAD24702_D04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 307	4910	TGGGCATCTACCCGGGAATCC	ADI-24415 BAD24702_D04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 307	4911	KQSYSRRT	ADI-24415 BAD24702_D04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 307	4912	AAGCAATCTTATTCTCGGAGAACT	ADI-24415 BAD24702_D04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 308	4913	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24416 BAD24702_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 308	4914	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24416 BAD24702_C05	Heavy chain variable region ("HC") amino acid sequence
Ab 308	4915	FNIKDYYMH	ADI-24416 BAD24702_C05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 308	4916	TTCAACATCAAGGACTACTATATGCAC	ADI-24416 BAD24702_C05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 308	4917	WIDLENGNTIYDPKFQG	ADI-24416 BAD24702_C05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 308	4918	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24416 BAD24702_C05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 308	4919	ARDGYGRYFYDV	ADI-24416 BAD24702_C05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 308	4920	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24416 BAD24702_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 308	4921	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24416 BAD24702_C05	Light chain variable region("LC") nucleic acid sequence
Ab 308	4922	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24416 BAD24702_C05	Light chain variable region ("LC") amino acid sequence
Ab 308	4923	KSSQSLLNSRTGKNYLA	ADI-24416 BAD24702_C05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 308	4924	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24416 BAD24702_C05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 308	4925	WASTRES	ADI-24416 BAD24702_C05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 308	4926	TGGGCATCTACCCGGGAATCC	ADI-24416 BAD24702_C05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 308	4927	KQSYSRRT	ADI-24416 BAD24702_C05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 308	4928	AAGCAATCTTATTCTCGGAGAACT	ADI-24416 BAD24702_C05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 309	4929	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24417 BAD24702_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 309	4930	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24417 BAD24702_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 309	4931	FNIKDYYMH	ADI-24417 BAD24702_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 309	4932	TTCAACATCAAGGACTACTATATGCAC	ADI-24417 BAD24702_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 309	4933	WIDLENGNTIYDPKFQG	ADI-24417 BAD24702_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 309	4934	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24417 BAD24702_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 309	4935	ARDGYGRYFYDV	ADI-24417 BAD24702_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 309	4936	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24417 BAD24702_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 309	4937	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24417 BAD24702_E05	Light chain variable region("LC") nucleic acid sequence
Ab 309	4938	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24417 BAD24702_E05	Light chain variable region ("LC") amino acid sequence
Ab 309	4939	KSSQSLLNSRTGKNYLA	ADI-24417 BAD24702_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 309	4940	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24417 BAD24702_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 309	4941	WASTRES	ADI-24417 BAD24702_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 309	4942	TGGGCATCTACCCGGGAATCC	ADI-24417 BAD24702_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 309	4943	KQSYSRRT	ADI-24417 BAD24702_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 309	4944	AAGCAATCTTATTCTCGGAGAACT	ADI-24417 BAD24702_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 310	4945	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCAGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24418 BAD24734_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 310	4946	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24418 BAD24734_B02	Heavy chain variable region ("HC") amino acid sequence
Ab 310	4947	FNIKDYYMH	ADI-24418 BAD24734_B02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 310	4948	TTCAACATCAAGGACTACTATATGCAC	ADI-24418 BAD24734_B02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 310	4949	WIDLENGNTIYDPKFQG	ADI-24418 BAD24734_B02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 310	4950	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24418 BAD24734_B02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 310	4951	ARDGYGRYFYDV	ADI-24418 BAD24734_B02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 310	4952	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24418 BAD24734_B02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 310	4953	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-24418 BAD24734_B02	Light chain variable region("LC") nucleic acid sequence
Ab 310	4954	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-24418 BAD24734_B02	Light chain variable region ("LC") amino acid sequence
Ab 310	4955	KSSQSLLNSRTGKNYLA	ADI-24418 BAD24734_B02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 310	4956	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24418 BAD24734_B02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 310	4957	WASTRES	ADI-24418 BAD24734_B02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 310	4958	TGGGCATCTACCCGGGAATCC	ADI-24418 BAD24734_B02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 310	4959	KQSYSRRT	ADI-24418 BAD24734_B02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 310	4960	AAGCAATCTTATTCTCGGAGAACT	ADI-24418 BAD24734_B02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 311	4961	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24434 BAD24631_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 311	4962	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24434 BAD24631_D01	Heavy chain variable region ("HC") amino acid sequence
Ab 311	4963	FNIKDYYMH	ADI-24434 BAD24631_D01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 311	4964	TTCAACATCAAGGACTACTATATGCAC	ADI-24434 BAD24631_D01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 311	4965	WIDLENGNTIYDPKFQG	ADI-24434 BAD24631_D01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 311	4966	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24434 BAD24631_D01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 311	4967	ARDGYGRYFYDV	ADI-24434 BAD24631_D01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 311	4968	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24434 BAD24631_D01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 311	4969	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24434 BAD24631_D01	Light chain variable region("LC") nucleic acid sequence
Ab 311	4970	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24434 BAD24631_D01	Light chain variable region ("LC") amino acid sequence
Ab 311	4971	KSSQSLLNSRTGKNYLA	ADI-24434 BAD24631_D01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 311	4972	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24434 BAD24631_D01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 311	4973	WASTRES	ADI-24434 BAD24631_D01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 311	4974	TGGGCATCTACCCGGGAATCC	ADI-24434 BAD24631_D01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 311	4975	KQSYSRRT	ADI-24434 BAD24631_D01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 311	4976	AAGCAATCTTATTCTCGGAGAACT	ADI-24434 BAD24631_D01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 312	4977	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24435 BAD24631_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 312	4978	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24435 BAD24631_G01	Heavy chain variable region ("HC") amino acid sequence
Ab 312	4979	FNIKDYYMH	ADI-24435 BAD24631_G01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 312	4980	TTCAACATCAAGGACTACTATATGCAC	ADI-24435 BAD24631_G01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 312	4981	WIDLENGNTIYDPKFQG	ADI-24435 BAD24631_G01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 312	4982	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24435 BAD24631_G01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 312	4983	ARDGYGRYFYDV	ADI-24435 BAD24631_G01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 312	4984	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24435 BAD24631_G01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 312	4985	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24435 BAD24631_G01	Light chain variable region("LC") nucleic acid sequence
Ab 312	4986	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24435 BAD24631_G01	Light chain variable region ("LC") amino acid sequence
Ab 312	4987	KSSQSLLNSRTGKNYLA	ADI-24435 BAD24631_G01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 312	4988	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24435 BAD24631_G01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 312	4989	WASTRES	ADI-24435 BAD24631_G01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 312	4990	TGGGCATCTACCCGGGAATCC	ADI-24435 BAD24631_G01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 312	4991	KQSYSRRT	ADI-24435 BAD24631_G01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 312	4992	AAGCAATCTTATTCTCGGAGAACT	ADI-24435 BAD24631_G01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 313	4993	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24436 BAD24631_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 313	4994	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24436 BAD24631_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 313	4995	FNIKDYYMH	ADI-24436 BAD24631_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 313	4996	TTCAACATCAAGGACTACTATATGCAC	ADI-24436 BAD24631_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 313	4997	WIDLENGNTIYDPKFQG	ADI-24436 BAD24631_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 313	4998	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24436 BAD24631_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 313	4999	ARDGYGRYFYDV	ADI-24436 BAD24631_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 313	5000	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24436 BAD24631_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 313	5001	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24436 BAD24631_A02	Light chain variable region("LC") nucleic acid sequence
Ab 313	5002	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24436 BAD24631_A02	Light chain variable region ("LC") amino acid sequence
Ab 313	5003	KSSQSLLNSRTGKNYLA	ADI-24436 BAD24631_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 313	5004	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24436 BAD24631_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 313	5005	WASTRES	ADI-24436 BAD24631_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 313	5006	TGGGCATCTACCCGGGAATCC	ADI-24436 BAD24631_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 313	5007	KQSYSRRT	ADI-24436 BAD24631_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 313	5008	AAGCAATCTTATTCTCGGAGAACT	ADI-24436 BAD24631_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 314	5009	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24437 BAD24631_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 314	5010	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24437 BAD24631_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 314	5011	FNIKDYYMH	ADI-24437 BAD24631_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 314	5012	TTCAACATCAAGGACTACTATATGCAC	ADI-24437 BAD24631_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 314	5013	WIDLENGNTIYDPKFQG	ADI-24437 BAD24631_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 314	5014	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24437 BAD24631_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 314	5015	ARDGYGRYFYDV	ADI-24437 BAD24631_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 314	5016	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24437 BAD24631_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 314	5017	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24437 BAD24631_E02	Light chain variable region("LC") nucleic acid sequence
Ab 314	5018	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24437 BAD24631_E02	Light chain variable region ("LC") amino acid sequence
Ab 314	5019	KSSQSLLNSRTGKNYLA	ADI-24437 BAD24631_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 314	5020	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24437 BAD24631_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 314	5021	WASTRES	ADI-24437 BAD24631_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 314	5022	TGGGCATCTACCCGGGAATCC	ADI-24437 BAD24631_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 314	5023	KQSYSRRT	ADI-24437 BAD24631_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 314	5024	AAGCAATCTTATTCTCGGAGAACT	ADI-24437 BAD24631_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 315	5025	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24438 BAD24734_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 315	5026	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24438 BAD24734_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 315	5027	FNIKDYYMH	ADI-24438 BAD24734_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 315	5028	TTCAACATCAAGGACTACTATATGCAC	ADI-24438 BAD24734_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 315	5029	WIDLENGNTIYDPKFQG	ADI-24438 BAD24734_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 315	5030	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24438 BAD24734_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 315	5031	ARDGYGRYFYDV	ADI-24438 BAD24734_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 315	5032	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24438 BAD24734_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 315	5033	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24438 BAD24734_A06	Light chain variable region("LC") nucleic acid sequence
Ab 315	5034	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24438 BAD24734_A06	Light chain variable region ("LC") amino acid sequence
Ab 315	5035	KSSQSLLNSRTGKNYLA	ADI-24438 BAD24734_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 315	5036	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24438 BAD24734_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 315	5037	WASTRES	ADI-24438 BAD24734_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 315	5038	TGGGCATCTACCCGGGAATCC	ADI-24438 BAD24734_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 315	5039	KQSYSRRT	ADI-24438 BAD24734_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 315	5040	AAGCAATCTTATTCTCGGAGAACT	ADI-24438 BAD24734_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 316	5041	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGATGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24439 BAD24631_G04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 316	5042	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPMFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24439 BAD24631_G04	Heavy chain variable region ("HC") amino acid sequence
Ab 316	5043	FNIKDYYMH	ADI-24439 BAD24631_G04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 316	5044	TTCAACATCAAGGACTACTATATGCAC	ADI-24439 BAD24631_G04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 316	5045	WIDLENGNTIYDPMFQG	ADI-24439 BAD24631_G04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 316	5046	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGATGTTTCAGGGC	ADI-24439 BAD24631_G04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 316	5047	ARDGYGRYFYDV	ADI-24439 BAD24631_G04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 316	5048	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24439 BAD24631_G04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 316	5049	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24439 BAD24631_G04	Light chain variable region("LC") nucleic acid sequence
Ab 316	5050	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24439 BAD24631_G04	Light chain variable region ("LC") amino acid sequence
Ab 316	5051	KSSQSLLNSRTGKNYLA	ADI-24439 BAD24631_G04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 316	5052	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24439 BAD24631_G04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 316	5053	WASTRES	ADI-24439 BAD24631_G04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 316	5054	TGGGCATCTACCCGGGAATCC	ADI-24439 BAD24631_G04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 316	5055	KQSYSRRT	ADI-24439 BAD24631_G04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 316	5056	AAGCAATCTTATTCTCGGAGAACT	ADI-24439 BAD24631_G04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 317	5057	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24440 BAD24631_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 317	5058	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24440 BAD24631_D05	Heavy chain variable region ("HC") amino acid sequence
Ab 317	5059	FNIKDYYMH	ADI-24440 BAD24631_D05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 317	5060	TTCAACATCAAGGACTACTATATGCAC	ADI-24440 BAD24631_D05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 317	5061	WIDLENGNTIYDPKFQG	ADI-24440 BAD24631_D05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 317	5062	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24440 BAD24631_D05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 317	5063	ARDGYGRYFYDV	ADI-24440 BAD24631_D05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 317	5064	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24440 BAD24631_D05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 317	5065	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24440 BAD24631_D05	Light chain variable region("LC") nucleic acid sequence
Ab 317	5066	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24440 BAD24631_D05	Light chain variable region ("LC") amino acid sequence
Ab 317	5067	KSSQSLLNSRTGKNYLA	ADI-24440 BAD24631_D05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 317	5068	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24440 BAD24631_D05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 317	5069	WASTRES	ADI-24440 BAD24631_D05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 317	5070	TGGGCATCTACCCGGGAATCC	ADI-24440 BAD24631_D05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 317	5071	KQSYSRRT	ADI-24440 BAD24631_D05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 317	5072	AAGCAATCTTATTCTCGGAGAACT	ADI-24440 BAD24631_D05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 318	5073	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24441 BAD24631_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 318	5074	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24441 BAD24631_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 318	5075	FNIKDYYMH	ADI-24441 BAD24631_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 318	5076	TTCAACATCAAGGACTACTATATGCAC	ADI-24441 BAD24631_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 318	5077	WIDLENGNTIYDPKFQG	ADI-24441 BAD24631_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 318	5078	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24441 BAD24631_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 318	5079	ARDGYGRYFYDV	ADI-24441 BAD24631_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 318	5080	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24441 BAD24631_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 318	5081	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24441 BAD24631_E05	Light chain variable region("LC") nucleic acid sequence
Ab 318	5082	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24441 BAD24631_E05	Light chain variable region ("LC") amino acid sequence
Ab 318	5083	KSSQSLLNSRTGKNYLA	ADI-24441 BAD24631_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 318	5084	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24441 BAD24631_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 318	5085	WASTRES	ADI-24441 BAD24631_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 318	5086	TGGGCATCTACCCGGGAATCC	ADI-24441 BAD24631_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 318	5087	KQSYSRRT	ADI-24441 BAD24631_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 318	5088	AAGCAATCTTATTCTCGGAGAACT	ADI-24441 BAD24631_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 319	5089	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24442 BAD24734_C07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 319	5090	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24442 BAD24734_C07	Heavy chain variable region ("HC") amino acid sequence
Ab 319	5091	FNIKDYYMH	ADI-24442 BAD24734_C07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 319	5092	TTCAACATCAAGGACTACTATATGCAC	ADI-24442 BAD24734_C07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 319	5093	WIDLENGNTIYDPKFQG	ADI-24442 BAD24734_C07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 319	5094	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24442 BAD24734_C07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 319	5095	ARDGYGRYFYDV	ADI-24442 BAD24734_C07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 319	5096	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24442 BAD24734_C07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 319	5097	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24442 BAD24734_C07	Light chain variable region("LC") nucleic acid sequence
Ab 319	5098	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24442 BAD24734_C07	Light chain variable region ("LC") amino acid sequence
Ab 319	5099	KSSQSLLNSRTGKNYLA	ADI-24442 BAD24734_C07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 319	5100	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24442 BAD24734_C07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 319	5101	WASTRES	ADI-24442 BAD24734_C07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 319	5102	TGGGCATCTACCCGGGAATCC	ADI-24442 BAD24734_C07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 319	5103	KQSYSRRT	ADI-24442 BAD24734_C07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 319	5104	AAGCAATCTTATTCTCGGAGAACT	ADI-24442 BAD24734_C07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 320	5105	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24443 BAD24631_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 320	5106	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24443 BAD24631_F06	Heavy chain variable region ("HC") amino acid sequence
Ab 320	5107	FNIKDYYMH	ADI-24443 BAD24631_F06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 320	5108	TTCAACATCAAGGACTACTATATGCAC	ADI-24443 BAD24631_F06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 320	5109	WIDLENGNTIYDPKFQG	ADI-24443 BAD24631_F06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 320	5110	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24443 BAD24631_F06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 320	5111	ARDGYGRYFYDV	ADI-24443 BAD24631_F06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 320	5112	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24443 BAD24631_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 320	5113	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24443 BAD24631_F06	Light chain variable region("LC") nucleic acid sequence
Ab 320	5114	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24443 BAD24631_F06	Light chain variable region ("LC") amino acid sequence
Ab 320	5115	KSSQSLLNSRTGKNYLA	ADI-24443 BAD24631_F06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 320	5116	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24443 BAD24631_F06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 320	5117	WASTRES	ADI-24443 BAD24631_F06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 320	5118	TGGGCATCTACCCGGGAATCC	ADI-24443 BAD24631_F06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 320	5119	KQSYSRRT	ADI-24443 BAD24631_F06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 320	5120	AAGCAATCTTATTCTCGGAGAACT	ADI-24443 BAD24631_F06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 321	5121	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24444 BAD24631_B07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 321	5122	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24444 BAD24631_B07	Heavy chain variable region ("HC") amino acid sequence
Ab 321	5123	FNIKDYYMH	ADI-24444 BAD24631_B07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 321	5124	TTCAACATCAAGGACTACTATATGCAC	ADI-24444 BAD24631_B07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 321	5125	WIDLENGNTIYDPKFQG	ADI-24444 BAD24631_B07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 321	5126	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24444 BAD24631_B07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 321	5127	ARDGYGRYFYDV	ADI-24444 BAD24631_B07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 321	5128	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24444 BAD24631_B07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 321	5129	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24444 BAD24631_B07	Light chain variable region("LC") nucleic acid sequence
Ab 321	5130	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24444 BAD24631_B07	Light chain variable region ("LC") amino acid sequence
Ab 321	5131	KSSQSLLNSRTGKNYLA	ADI-24444 BAD24631_B07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 321	5132	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24444 BAD24631_B07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 321	5133	WASTRES	ADI-24444 BAD24631_B07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 321	5134	TGGGCATCTACCCGGGAATCC	ADI-24444 BAD24631_B07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 321	5135	KQSYSRRT	ADI-24444 BAD24631_B07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 321	5136	AAGCAATCTTATTCTCGGAGAACT	ADI-24444 BAD24631_B07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 322	5137	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24445 BAD24631_H07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 322	5138	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24445 BAD24631_H07	Heavy chain variable region ("HC") amino acid sequence
Ab 322	5139	FNIKDYYMH	ADI-24445 BAD24631_H07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 322	5140	TTCAACATCAAGGACTACTATATGCAC	ADI-24445 BAD24631_H07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 322	5141	WIDLENGNTIYDPKFQG	ADI-24445 BAD24631_H07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 322	5142	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24445 BAD24631_H07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 322	5143	ARDGYGRYFYDV	ADI-24445 BAD24631_H07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 322	5144	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24445 BAD24631_H07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 322	5145	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24445 BAD24631_H07	Light chain variable region("LC") nucleic acid sequence
Ab 322	5146	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24445 BAD24631_H07	Light chain variable region ("LC") amino acid sequence
Ab 322	5147	KSSQSLLNSRTGKNYLA	ADI-24445 BAD24631_H07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 322	5148	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24445 BAD24631_H07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 322	5149	WASTRES	ADI-24445 BAD24631_H07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 322	5150	TGGGCATCTACCCGGGAATCC	ADI-24445 BAD24631_H07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 322	5151	KQSYSRRT	ADI-24445 BAD24631_H07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 322	5152	AAGCAATCTTATTCTCGGAGAACT	ADI-24445 BAD24631_H07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 323	5153	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24446 BAD24631_H08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 323	5154	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24446 BAD24631_H08	Heavy chain variable region ("HC") amino acid sequence
Ab 323	5155	FNIKDYYMH	ADI-24446 BAD24631_H08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 323	5156	TTCAACATCAAGGACTACTATATGCAC	ADI-24446 BAD24631_H08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 323	5157	WIDLENGNTIYDPKFQG	ADI-24446 BAD24631_H08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 323	5158	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24446 BAD24631_H08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 323	5159	ARDGYGRYFYDV	ADI-24446 BAD24631_H08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 323	5160	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24446 BAD24631_H08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 323	5161	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24446 BAD24631_H08	Light chain variable region("LC") nucleic acid sequence
Ab 323	5162	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24446 BAD24631_H08	Light chain variable region ("LC") amino acid sequence
Ab 323	5163	KSSQSLLNSRTGKNYLA	ADI-24446 BAD24631_H08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 323	5164	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24446 BAD24631_H08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 323	5165	WASTRES	ADI-24446 BAD24631_H08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 323	5166	TGGGCATCTACCCGGGAATCC	ADI-24446 BAD24631_H08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 323	5167	KQSYSRRT	ADI-24446 BAD24631_H08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 323	5168	AAGCAATCTTATTCTCGGAGAACT	ADI-24446 BAD24631_H08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 324	5169	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGAGGATGTCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24449 BAD24631_H12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 324	5170	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGGCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSS	ADI-24449 BAD24631_H12	Heavy chain variable region ("HC") amino acid sequence
Ab 324	5171	FNIKDYYMH	ADI-24449 BAD24631_H12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 324	5172	TTCAACATCAAGGACTACTATATGCAC	ADI-24449 BAD24631_H12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 324	5173	WIDLENGNTIYDPKFQG	ADI-24449 BAD24631_H12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 324	5174	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-24449 BAD24631_H12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 324	5175	ARDGYGRYFYDV	ADI-24449 BAD24631_H12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 324	5176	GCGAGAGATGGATACGGGAGATATTTTTACGACGTG	ADI-24449 BAD24631_H12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 324	5177	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCTGTGGGACCAAGGTCGAGATCAAA	ADI-24449 BAD24631_H12	Light chain variable region("LC") nucleic acid sequence
Ab 324	5178	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-24449 BAD24631_H12	Light chain variable region ("LC") amino acid sequence
Ab 324	5179	KSSQSLLNSRTGKNYLA	ADI-24449 BAD24631_H12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 324	5180	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-24449 BAD24631_H12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 324	5181	WASTRES	ADI-24449 BAD24631_H12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 324	5182	TGGGCATCTACCCGGGAATCC	ADI-24449 BAD24631_H12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 324	5183	KQSYSRRT	ADI-24449 BAD24631_H12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 324	5184	AAGCAATCTTATTCTCGGAGAACT	ADI-24449 BAD24631_H12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 325	5185	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26906 LAD5224_P03_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 325	5186	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-26906 LAD5224_P03_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 325	5187	FNIKDYYMH	ADI-26906 LAD5224_P03_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 325	5188	TTCAACATCAAGGACTACTATATGCAC	ADI-26906 LAD5224_P03_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 325	5189	WIDLENANTIYDAKFQG	ADI-26906 LAD5224_P03_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 325	5190	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26906 LAD5224_P03_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 325	5191	ARDAYGRYFYDV	ADI-26906 LAD5224_P03_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 325	5192	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-26906 LAD5224_P03_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 325	5193	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26906 LAD5224_P03_A01	Light chain variable region("LC") nucleic acid sequence
Ab 325	5194	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26906 LAD5224_P03_A01	Light chain variable region ("LC") amino acid sequence
Ab 325	5195	KSSQSLLNARTGKNYLA	ADI-26906 LAD5224_P03_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 325	5196	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26906 LAD5224_P03_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 325	5197	WASTRES	ADI-26906 LAD5224_P03_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 325	5198	TGGGCATCTACCCGGGAATCC	ADI-26906 LAD5224_P03_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 325	5199	KQSYSRRT	ADI-26906 LAD5224_P03_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 325	5200	AAGCAATCTTATTCTCGGAGAACT	ADI-26906 LAD5224_P03_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 326	5201	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26907 LAD5224_P03_D02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 326	5202	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVTVSS	ADI-26907 LAD5224_P03_D02	Heavy chain variable region ("HC") amino acid sequence
Ab 326	5203	FNIKDYYMH	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 326	5204	TTCAACATCAAGGACTACTATATGCAC	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 326	5205	WIDLENANTIYDAKFQG	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 326	5206	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 326	5207	GRDAYGRYFYDV	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 326	5208	GGTAGAGATGCGTACGGGAGATATTTTTACGACGTG	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 326	5209	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26907 LAD5224_P03_D02	Light chain variable region("LC") nucleic acid sequence
Ab 326	5210	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26907 LAD5224_P03_D02	Light chain variable region ("LC") amino acid sequence
Ab 326	5211	KSSQSLLNARTGKNYLA	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 326	5212	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 326	5213	WASTRES	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 326	5214	TGGGCATCTACCCGGGAATCC	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 326	5215	KQSYSRRT	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 326	5216	AAGCAATCTTATTCTCGGAGAACT	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 327	5217	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26908 LAD5224_P03_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 327	5218	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-26908 LAD5224_P03_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 327	5219	FNIKDYYMH	ADI-26908 LAD5224_P03_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 327	5220	TTCAACATCAAGGACTACTATATGCAC	ADI-26908 LAD5224_P03_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 327	5221	WIDLEEGNTIYDAKFQG	ADI-26908 LAD5224_P03_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 327	5222	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26908 LAD5224_P03_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 327	5223	ARDAYGRYFYDV	ADI-26908 LAD5224_P03_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 327	5224	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-26908 LAD5224_P03_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 327	5225	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26908 LAD5224_P03_A03	Light chain variable region("LC") nucleic acid sequence
Ab 327	5226	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26908 LAD5224_P03_A03	Light chain variable region ("LC") amino acid sequence
Ab 327	5227	KSSQSLLNARTGKNYLA	ADI-26908 LAD5224_P03_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 327	5228	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26908 LAD5224_P03_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 327	5229	WASTRES	ADI-26908 LAD5224_P03_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 327	5230	TGGGCATCTACCCGGGAATCC	ADI-26908 LAD5224_P03_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 327	5231	KQSYSRRT	ADI-26908 LAD5224_P03_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 327	5232	AAGCAATCTTATTCTCGGAGAACT	ADI-26908 LAD5224_P03_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 328	5233	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26909 LAD5224_P03_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 328	5234	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVTVSS	ADI-26909 LAD5224_P03_E03	Heavy chain variable region ("HC") amino acid sequence
Ab 328	5235	FNIKDYYMH	ADI-26909 LAD5224_P03_E03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 328	5236	TTCAACATCAAGGACTACTATATGCAC	ADI-26909 LAD5224_P03_E03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 328	5237	WIDLEEGNTIYDAKFQG	ADI-26909 LAD5224_P03_E03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 328	5238	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26909 LAD5224_P03_E03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 328	5239	GRDAYGRYFYDV	ADI-26909 LAD5224_P03_E03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 328	5240	GGTAGAGATGCGTACGGGAGATATTTTTACGACGTG	ADI-26909 LAD5224_P03_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 328	5241	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26909 LAD5224_P03_E03	Light chain variable region("LC") nucleic acid sequence
Ab 328	5242	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26909 LAD5224_P03_E03	Light chain variable region ("LC") amino acid sequence
Ab 328	5243	KSSQSLLNARTGKNYLA	ADI-26909 LAD5224_P03_E03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 328	5244	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26909 LAD5224_P03_E03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 328	5245	WASTRES	ADI-26909 LAD5224_P03_E03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 328	5246	TGGGCATCTACCCGGGAATCC	ADI-26909 LAD5224_P03_E03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 328	5247	KQSYSRRT	ADI-26909 LAD5224_P03_E03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 328	5248	AAGCAATCTTATTCTCGGAGAACT	ADI-26909 LAD5224_P03_E03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 329	5249	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCGTTACGGGGCTTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26910 LAD5224_P03_G04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 329	5250	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTVSS	ADI-26910 LAD5224_P03_G04	Heavy chain variable region ("HC") amino acid sequence
Ab 329	5251	FNIKDYYMH	ADI-26910 LAD5224_P03_G04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 329	5252	TTCAACATCAAGGACTACTATATGCAC	ADI-26910 LAD5224_P03_G04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 329	5253	WIDLENANTIYDAKFQG	ADI-26910 LAD5224_P03_G04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 329	5254	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26910 LAD5224_P03_G04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 329	5255	ARDRYGAYFYDV	ADI-26910 LAD5224_P03_G04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 329	5256	GCGAGAGATCGTTACGGGGCTTATTTTTACGACGTG	ADI-26910 LAD5224_P03_G04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 329	5257	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26910 LAD5224_P03_G04	Light chain variable region("LC") nucleic acid sequence
Ab 329	5258	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26910 LAD5224_P03_G04	Light chain variable region ("LC") amino acid sequence
Ab 329	5259	KSSQSLLNARTGKNYLA	ADI-26910 LAD5224_P03_G04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 329	5260	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26910 LAD5224_P03_G04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 329	5261	WASTRES	ADI-26910 LAD5224_P03_G04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 329	5262	TGGGCATCTACCCGGGAATCC	ADI-26910 LAD5224_P03_G04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 329	5263	KQSYSRRT	ADI-26910 LAD5224_P03_G04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 329	5264	AAGCAATCTTATTCTCGGAGAACT	ADI-26910 LAD5224_P03_G04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 330	5265	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26912 LAD5224_P03_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 330	5266	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTVSS	ADI-26912 LAD5224_P03_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 330	5267	FNIKDYYMH	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 330	5268	TTCAACATCAAGGACTACTATATGCAC	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 330	5269	WIDLENANTIYDAKFQG	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 330	5270	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 330	5271	ARDVLGRYFYDV	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 330	5272	GCGAGAGATGTGTTGGGGAGATATTTTTACGACGTG	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 330	5273	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26912 LAD5224_P03_E05	Light chain variable region("LC") nucleic acid sequence
Ab 330	5274	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26912 LAD5224_P03_E05	Light chain variable region ("LC") amino acid sequence
Ab 330	5275	KSSQSLLNARTGKNYLA	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 330	5276	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 330	5277	WASTRES	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 330	5278	TGGGCATCTACCCGGGAATCC	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 330	5279	KQSYSRRT	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 330	5280	AAGCAATCTTATTCTCGGAGAACT	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 331	5281	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCAGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26913 LAD5224_P03_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 331	5282	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVTVSS	ADI-26913 LAD5224_P03_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 331	5283	FNIKDYYMH	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 331	5284	TTCAACATCAAGGACTACTATATGCAC	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 331	5285	WIDLENANTIYDAKFQG	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 331	5286	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 331	5287	ARDQYGRYFYDV	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 331	5288	GCGAGAGATCAGTACGGGAGATATTTTTACGACGTG	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 331	5289	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26913 LAD5224_P03_A06	Light chain variable region("LC") nucleic acid sequence
Ab 331	5290	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26913 LAD5224_P03_A06	Light chain variable region ("LC") amino acid sequence
Ab 331	5291	KSSQSLLNARTGKNYLA	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 331	5292	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 331	5293	WASTRES	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 331	5294	TGGGCATCTACCCGGGAATCC	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 331	5295	KQSYSRRT	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 331	5296	AAGCAATCTTATTCTCGGAGAACT	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 332	5297	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26915 LAD5224_P03_G07	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 332	5298	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTVSS	ADI-26915 LAD5224_P03_G07	Heavy chain variable region ("HC") amino acid sequence
Ab 332	5299	FNIKDYYMH	ADI-26915 LAD5224_P03_G07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 332	5300	TTCAACATCAAGGACTACTATATGCAC	ADI-26915 LAD5224_P03_G07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 332	5301	WIDLEEGNTIYDAKFQG	ADI-26915 LAD5224_P03_G07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 332	5302	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26915 LAD5224_P03_G07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 332	5303	ARDVLGRYFYDV	ADI-26915 LAD5224_P03_G07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 332	5304	GCGAGAGATGTGTTGGGGAGATATTTTTACGACGTG	ADI-26915 LAD5224_P03_G07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 332	5305	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26915 LAD5224_P03_G07	Light chain variable region("LC") nucleic acid sequence
Ab 332	5306	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26915 LAD5224_P03_G07	Light chain variable region ("LC") amino acid sequence
Ab 332	5307	KSSQSLLNARTGKNYLA	ADI-26915 LAD5224_P03_G07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 332	5308	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26915 LAD5224_P03_G07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 332	5309	WASTRES	ADI-26915 LAD5224_P03_G07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 332	5310	TGGGCATCTACCCGGGAATCC	ADI-26915 LAD5224_P03_G07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 332	5311	KQSYSRRT	ADI-26915 LAD5224_P03_G07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 332	5312	AAGCAATCTTATTCTCGGAGAACT	ADI-26915 LAD5224_P03_G07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 333	5313	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACGGGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTG	ADI-26916 LAD5224_P03_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 333	5314	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTVSS	ADI-26916 LAD5224_P03_F08	Heavy chain variable region ("HC") amino acid sequence
Ab 333	5315	FNIKDYYMH	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 333	5316	TTCAACATCAAGGACTACTATATGCAC	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 333	5317	WIDLENANTIYDAKFQG	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 333	5318	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 333	5319	ARDVYGRYFYDL	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 333	5320	GCGAGAGATGTGTACGGGAGATATTTTTACGACCTT	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 333	5321	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26916 LAD5224_P03_F08	Light chain variable region("LC") nucleic acid sequence
Ab 333	5322	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26916 LAD5224_P03_F08	Light chain variable region ("LC") amino acid sequence
Ab 333	5323	KSSQSLLNARTGKNYLA	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 333	5324	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 333	5325	WASTRES	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 333	5326	TGGGCATCTACCCGGGAATCC	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 333	5327	KQSYSRRT	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 333	5328	AAGCAATCTTATTCTCGGAGAACT	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 334	5329	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26917 LAD5224_P03_B09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 334	5330	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGGYFYDVWGQGTLVTVSS	ADI-26917 LAD5224_P03_B09	Heavy chain variable region ("HC") amino acid sequence
Ab 334	5331	FNIKDYYMH	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 334	5332	TTCAACATCAAGGACTACTATATGCAC	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 334	5333	WIDLENANTIYDAKFQG	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 334	5334	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 334	5335	ARDAYGGYFYDV	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 334	5336	GCGAGAGATGCGTACGGGGGGTATTTTTACGACGTG	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 334	5337	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26917 LAD5224_P03_B09	Light chain variable region("LC") nucleic acid sequence
Ab 334	5338	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26917 LAD5224_P03_B09	Light chain variable region ("LC") amino acid sequence
Ab 334	5339	KSSQSLLNARTGKNYLA	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 334	5340	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 334	5341	WASTRES	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 334	5342	TGGGCATCTACCCGGGAATCC	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 334	5343	KQSYSRRT	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 334	5344	AAGCAATCTTATTCTCGGAGAACT	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 335	5345	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATAATTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26918 LAD5224_P03_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 335	5346	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVTVSS	ADI-26918 LAD5224_P03_E09	Heavy chain variable region ("HC") amino acid sequence
Ab 335	5347	FNIKDYYMH	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 335	5348	TTCAACATCAAGGACTACTATATGCAC	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 335	5349	WIDLENANTIYDAKFQG	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 335	5350	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 335	5351	ARDNYGGYFYDV	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 335	5352	GCGAGAGATAATTACGGGGGGTATTTTTACGACGTG	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 335	5353	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26918 LAD5224_P03_E09	Light chain variable region("LC") nucleic acid sequence
Ab 335	5354	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26918 LAD5224_P03_E09	Light chain variable region ("LC") amino acid sequence
Ab 335	5355	KSSQSLLNARTGKNYLA	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 335	5356	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 335	5357	WASTRES	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 335	5358	TGGGCATCTACCCGGGAATCC	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 335	5359	KQSYSRRT	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 335	5360	AAGCAATCTTATTCTCGGAGAACT	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 336	5361	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26919 LAD5225_P03_D10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 336	5362	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-26919 LAD5225_P03_D10	Heavy chain variable region ("HC") amino acid sequence
Ab 336	5363	FNIKDYYMH	ADI-26919 LAD5225_P03_D10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 336	5364	TTCAACATCAAGGACTACTATATGCAC	ADI-26919 LAD5225_P03_D10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 336	5365	WIDLENANTIYDAKFQG	ADI-26919 LAD5225_P03_D10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 336	5366	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26919 LAD5225_P03_D10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 336	5367	ARDAYGRYFYDV	ADI-26919 LAD5225_P03_D10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 336	5368	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-26919 LAD5225_P03_D10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 336	5369	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26919 LAD5225_P03_D10	Light chain variable region("LC") nucleic acid sequence
Ab 336	5370	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26919 LAD5225_P03_D10	Light chain variable region ("LC") amino acid sequence
Ab 336	5371	KSSQSLLNARTGKNYLA	ADI-26919 LAD5225_P03_D10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 336	5372	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26919 LAD5225_P03_D10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 336	5373	WASTRES	ADI-26919 LAD5225_P03_D10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 336	5374	TGGGCATCTACCCGGGAATCC	ADI-26919 LAD5225_P03_D10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 336	5375	KQSYSLRT	ADI-26919 LAD5225_P03_D10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 336	5376	AAGCAATCTTATTCTCTGAGAACT	ADI-26919 LAD5225_P03_D10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 337	5377	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26920 LAD5225_P03_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 337	5378	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVTVSS	ADI-26920 LAD5225_P03_A11	Heavy chain variable region ("HC") amino acid sequence
Ab 337	5379	FNIKDYYMH	ADI-26920 LAD5225_P03_A11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 337	5380	TTCAACATCAAGGACTACTATATGCAC	ADI-26920 LAD5225_P03_A11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 337	5381	WIDLENANTIYDAKFQG	ADI-26920 LAD5225_P03_A11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 337	5382	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26920 LAD5225_P03_A11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 337	5383	GRDAYGRYFYDV	ADI-26920 LAD5225_P03_A11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 337	5384	GGTAGAGATGCGTACGGGAGATATTTTTACGACGTG	ADI-26920 LAD5225_P03_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 337	5385	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26920 LAD5225_P03_A11	Light chain variable region("LC") nucleic acid sequence
Ab 337	5386	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26920 LAD5225_P03_A11	Light chain variable region ("LC") amino acid sequence
Ab 337	5387	KSSQSLLNARTGKNYLA	ADI-26920 LAD5225_P03_A11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 337	5388	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26920 LAD5225_P03_A11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 337	5389	WASTRES	ADI-26920 LAD5225_P03_A11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 337	5390	TGGGCATCTACCCGGGAATCC	ADI-26920 LAD5225_P03_A11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 337	5391	KQSYSLRT	ADI-26920 LAD5225_P03_A11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 337	5392	AAGCAATCTTATTCTCTGAGAACT	ADI-26920 LAD5225_P03_A11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 338	5393	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26921 LAD5225_P03_B12	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 338	5394	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-26921 LAD5225_P03_B12	Heavy chain variable region ("HC") amino acid sequence
Ab 338	5395	FNIKDYYMH	ADI-26921 LAD5225_P03_B12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 338	5396	TTCAACATCAAGGACTACTATATGCAC	ADI-26921 LAD5225_P03_B12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 338	5397	WIDLEEGNTIYDAKFQG	ADI-26921 LAD5225_P03_B12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 338	5398	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26921 LAD5225_P03_B12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 338	5399	ARDAYGRYFYDV	ADI-26921 LAD5225_P03_B12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 338	5400	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-26921 LAD5225_P03_B12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 338	5401	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26921 LAD5225_P03_B12	Light chain variable region("LC") nucleic acid sequence
Ab 338	5402	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26921 LAD5225_P03_B12	Light chain variable region ("LC") amino acid sequence
Ab 338	5403	KSSQSLLNARTGKNYLA	ADI-26921 LAD5225_P03_B12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 338	5404	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26921 LAD5225_P03_B12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 338	5405	WASTRES	ADI-26921 LAD5225_P03_B12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 338	5406	TGGGCATCTACCCGGGAATCC	ADI-26921 LAD5225_P03_B12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 338	5407	KQSYSLRT	ADI-26921 LAD5225_P03_B12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 338	5408	AAGCAATCTTATTCTCTGAGAACT	ADI-26921 LAD5225_P03_B12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 339	5409	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACGGGCTGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26924 LAD5225_P04_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 339	5410	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGRDAYGLYFYDVWGQGTLVTVSS	ADI-26924 LAD5225_P04_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 339	5411	FNIKDYYMH	ADI-26924 LAD5225_P04_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 339	5412	TTCAACATCAAGGACTACTATATGCAC	ADI-26924 LAD5225_P04_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 339	5413	WIDLENANTIYDAKFQG	ADI-26924 LAD5225_P04_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 339	5414	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26924 LAD5225_P04_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 339	5415	GRDAYGLYFYDV	ADI-26924 LAD5225_P04_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 339	5416	GGTAGAGATGCGTACGGGCTGTATTTTTACGACGTG	ADI-26924 LAD5225_P04_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 339	5417	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26924 LAD5225_P04_A02	Light chain variable region("LC") nucleic acid sequence
Ab 339	5418	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26924 LAD5225_P04_A02	Light chain variable region ("LC") amino acid sequence
Ab 339	5419	KSSQSLLNARTGKNYLA	ADI-26924 LAD5225_P04_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 339	5420	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26924 LAD5225_P04_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 339	5421	WASTRES	ADI-26924 LAD5225_P04_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 339	5422	TGGGCATCTACCCGGGAATCC	ADI-26924 LAD5225_P04_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 339	5423	KQSYSLRT	ADI-26924 LAD5225_P04_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 339	5424	AAGCAATCTTATTCTCTGAGAACT	ADI-26924 LAD5225_P04_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 340	5425	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26925 LAD5225_P04_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 340	5426	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTVSS	ADI-26925 LAD5225_P04_E02	Heavy chain variable region ("HC") amino acid sequence
Ab 340	5427	FNIKDYYMH	ADI-26925 LAD5225_P04_E02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 340	5428	TTCAACATCAAGGACTACTATATGCAC	ADI-26925 LAD5225_P04_E02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 340	5429	WIDLENANTIYDAKFQG	ADI-26925 LAD5225_P04_E02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 340	5430	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26925 LAD5225_P04_E02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 340	5431	ARDVLGRYFYDV	ADI-26925 LAD5225_P04_E02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 340	5432	GCGAGAGATGTGTTGGGGAGATATTTTTACGACGTG	ADI-26925 LAD5225_P04_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 340	5433	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26925 LAD5225_P04_E02	Light chain variable region("LC") nucleic acid sequence
Ab 340	5434	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26925 LAD5225_P04_E02	Light chain variable region ("LC") amino acid sequence
Ab 340	5435	KSSQSLLNARTGKNYLA	ADI-26925 LAD5225_P04_E02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 340	5436	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26925 LAD5225_P04_E02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 340	5437	WASTRES	ADI-26925 LAD5225_P04_E02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 340	5438	TGGGCATCTACCCGGGAATCC	ADI-26925 LAD5225_P04_E02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 340	5439	KQSYSLRT	ADI-26925 LAD5225_P04_E02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 340	5440	AAGCAATCTTATTCTCTGAGAACT	ADI-26925 LAD5225_P04_E02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 341	5441	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCGTTACGGGGCTTATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26927 LAD5225_P04_G03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 341	5442	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTVSS	ADI-26927 LAD5225_P04_G03	Heavy chain variable region ("HC") amino acid sequence
Ab 341	5443	FNIKDYYMH	ADI-26927 LAD5225_P04_G03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 341	5444	TTCAACATCAAGGACTACTATATGCAC	ADI-26927 LAD5225_P04_G03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 341	5445	WIDLEEGNTIYDAKFQG	ADI-26927 LAD5225_P04_G03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 341	5446	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26927 LAD5225_P04_G03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 341	5447	ARDRYGAYFYDV	ADI-26927 LAD5225_P04_G03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 341	5448	GCGAGAGATCGTTACGGGGCTTATTTTTACGACGTG	ADI-26927 LAD5225_P04_G03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 341	5449	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26927 LAD5225_P04_G03	Light chain variable region("LC") nucleic acid sequence
Ab 341	5450	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26927 LAD5225_P04_G03	Light chain variable region ("LC") amino acid sequence
Ab 341	5451	KSSQSLLNARTGKNYLA	ADI-26927 LAD5225_P04_G03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 341	5452	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26927 LAD5225_P04_G03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 341	5453	WASTRES	ADI-26927 LAD5225_P04_G03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 341	5454	TGGGCATCTACCCGGGAATCC	ADI-26927 LAD5225_P04_G03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 341	5455	KQSYSLRT	ADI-26927 LAD5225_P04_G03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 341	5456	AAGCAATCTTATTCTCTGAGAACT	ADI-26927 LAD5225_P04_G03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 342	5457	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACGGGCTGTATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26928 LAD5225_P04_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 342	5458	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGRDAYGLYFYDVWGQGTLVTVSS	ADI-26928 LAD5225_P04_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 342	5459	FNIKDYYMH	ADI-26928 LAD5225_P04_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 342	5460	TTCAACATCAAGGACTACTATATGCAC	ADI-26928 LAD5225_P04_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 342	5461	WIDLEEGNTIYDAKFQG	ADI-26928 LAD5225_P04_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 342	5462	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26928 LAD5225_P04_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 342	5463	GRDAYGLYFYDV	ADI-26928 LAD5225_P04_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 342	5464	GGTAGAGATGCGTACGGGCTGTATTTTTACGACGTG	ADI-26928 LAD5225_P04_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 342	5465	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26928 LAD5225_P04_A04	Light chain variable region("LC") nucleic acid sequence
Ab 342	5466	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26928 LAD5225_P04_A04	Light chain variable region ("LC") amino acid sequence
Ab 342	5467	KSSQSLLNARTGKNYLA	ADI-26928 LAD5225_P04_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 342	5468	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26928 LAD5225_P04_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 342	5469	WASTRES	ADI-26928 LAD5225_P04_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 342	5470	TGGGCATCTACCCGGGAATCC	ADI-26928 LAD5225_P04_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 342	5471	KQSYSLRT	ADI-26928 LAD5225_P04_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 342	5472	AAGCAATCTTATTCTCTGAGAACT	ADI-26928 LAD5225_P04_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 343	5473	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26929 LAD5225_P04_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 343	5474	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTVSS	ADI-26929 LAD5225_P04_E04	Heavy chain variable region ("HC") amino acid sequence
Ab 343	5475	FNIKDYYMH	ADI-26929 LAD5225_P04_E04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 343	5476	TTCAACATCAAGGACTACTATATGCAC	ADI-26929 LAD5225_P04_E04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 343	5477	WIDLEEGNTIYDAKFQG	ADI-26929 LAD5225_P04_E04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 343	5478	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26929 LAD5225_P04_E04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 343	5479	ARDVLGRYFYDV	ADI-26929 LAD5225_P04_E04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 343	5480	GCGAGAGATGTGTTGGGGAGATATTTTTACGACGTG	ADI-26929 LAD5225_P04_E04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 343	5481	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26929 LAD5225_P04_E04	Light chain variable region("LC") nucleic acid sequence
Ab 343	5482	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26929 LAD5225_P04_E04	Light chain variable region ("LC") amino acid sequence
Ab 343	5483	KSSQSLLNARTGKNYLA	ADI-26929 LAD5225_P04_E04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 343	5484	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26929 LAD5225_P04_E04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 343	5485	WASTRES	ADI-26929 LAD5225_P04_E04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 343	5486	TGGGCATCTACCCGGGAATCC	ADI-26929 LAD5225_P04_E04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 343	5487	KQSYSLRT	ADI-26929 LAD5225_P04_E04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 343	5488	AAGCAATCTTATTCTCTGAGAACT	ADI-26929 LAD5225_P04_E04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 344	5489	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACGGGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTG	ADI-26930 LAD5225_P04_F05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 344	5490	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTVSS	ADI-26930 LAD5225_P04_F05	Heavy chain variable region ("HC") amino acid sequence
Ab 344	5491	FNIKDYYMH	ADI-26930 LAD5225_P04_F05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 344	5492	TTCAACATCAAGGACTACTATATGCAC	ADI-26930 LAD5225_P04_F05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 344	5493	WIDLENANTIYDAKFQG	ADI-26930 LAD5225_P04_F05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 344	5494	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26930 LAD5225_P04_F05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 344	5495	ARDVYGRYFYDL	ADI-26930 LAD5225_P04_F05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 344	5496	GCGAGAGATGTGTACGGGAGATATTTTTACGACCTT	ADI-26930 LAD5225_P04_F05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 344	5497	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26930 LAD5225_P04_F05	Light chain variable region("LC") nucleic acid sequence
Ab 344	5498	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26930 LAD5225_P04_F05	Light chain variable region ("LC") amino acid sequence
Ab 344	5499	KSSQSLLNARTGKNYLA	ADI-26930 LAD5225_P04_F05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 344	5500	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26930 LAD5225_P04_F05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 344	5501	WASTRES	ADI-26930 LAD5225_P04_F05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 344	5502	TGGGCATCTACCCGGGAATCC	ADI-26930 LAD5225_P04_F05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 344	5503	KQSYSLRT	ADI-26930 LAD5225_P04_F05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 344	5504	AAGCAATCTTATTCTCTGAGAACT	ADI-26930 LAD5225_P04_F05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 345	5505	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATAATTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26932 LAD5225_P04_E06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 345	5506	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVTVSS	ADI-26932 LAD5225_P04_E06	Heavy chain variable region ("HC") amino acid sequence
Ab 345	5507	FNIKDYYMH	ADI-26932 LAD5225_P04_E06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 345	5508	TTCAACATCAAGGACTACTATATGCAC	ADI-26932 LAD5225_P04_E06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 345	5509	WIDLENANTIYDAKFQG	ADI-26932 LAD5225_P04_E06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 345	5510	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26932 LAD5225_P04_E06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 345	5511	ARDNYGGYFYDV	ADI-26932 LAD5225_P04_E06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 345	5512	GCGAGAGATAATTACGGGGGGTATTTTTACGACGTG	ADI-26932 LAD5225_P04_E06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 345	5513	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26932 LAD5225_P04_E06	Light chain variable region("LC") nucleic acid sequence
Ab 345	5514	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26932 LAD5225_P04_E06	Light chain variable region ("LC") amino acid sequence
Ab 345	5515	KSSQSLLNARTGKNYLA	ADI-26932 LAD5225_P04_E06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 345	5516	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26932 LAD5225_P04_E06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 345	5517	WASTRES	ADI-26932 LAD5225_P04_E06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 345	5518	TGGGCATCTACCCGGGAATCC	ADI-26932 LAD5225_P04_E06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 345	5519	KQSYSLRT	ADI-26932 LAD5225_P04_E06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 345	5520	AAGCAATCTTATTCTCTGAGAACT	ADI-26932 LAD5225_P04_E06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 346	5521	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26933 LAD5226_P04_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 346	5522	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-26933 LAD5226_P04_A07	Heavy chain variable region ("HC") amino acid sequence
Ab 346	5523	FNIKDYYMH	ADI-26933 LAD5226_P04_A07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 346	5524	TTCAACATCAAGGACTACTATATGCAC	ADI-26933 LAD5226_P04_A07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 346	5525	WIDLENANTIYDAKFQG	ADI-26933 LAD5226_P04_A07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 346	5526	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26933 LAD5226_P04_A07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 346	5527	ARDAYGRYFYDV	ADI-26933 LAD5226_P04_A07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 346	5528	GCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-26933 LAD5226_P04_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 346	5529	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26933 LAD5226_P04_A07	Light chain variable region("LC") nucleic acid sequence
Ab 346	5530	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26933 LAD5226_P04_A07	Light chain variable region ("LC") amino acid sequence
Ab 346	5531	KSSQSLLNARTGKNYLA	ADI-26933 LAD5226_P04_A07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 346	5532	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26933 LAD5226_P04_A07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 346	5533	WASTRES	ADI-26933 LAD5226_P04_A07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 346	5534	TGGGCATCTACCCGGGAATCC	ADI-26933 LAD5226_P04_A07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 346	5535	KQSYSIRT	ADI-26933 LAD5226_P04_A07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 346	5536	AAGCAATCTTATTCTATCAGAACT	ADI-26933 LAD5226_P04_A07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 347	5537	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26938 LAD5226_P04_E11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 347	5538	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTVSS	ADI-26938 LAD5226_P04_E11	Heavy chain variable region ("HC") amino acid sequence
Ab 347	5539	FNIKDYYMH	ADI-26938 LAD5226_P04_E11	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 347	5540	TTCAACATCAAGGACTACTATATGCAC	ADI-26938 LAD5226_P04_E11	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 347	5541	WIDLENANTIYDAKFQG	ADI-26938 LAD5226_P04_E11	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 347	5542	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26938 LAD5226_P04_E11	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 347	5543	ARDVLGRYFYDV	ADI-26938 LAD5226_P04_E11	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 347	5544	GCGAGAGATGTGTTGGGGAGATATTTTTACGACGTG	ADI-26938 LAD5226_P04_E11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 347	5545	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26938 LAD5226_P04_E11	Light chain variable region("LC") nucleic acid sequence
Ab 347	5546	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26938 LAD5226_P04_E11	Light chain variable region ("LC") amino acid sequence
Ab 347	5547	KSSQSLLNARTGKNYLA	ADI-26938 LAD5226_P04_E11	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 347	5548	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26938 LAD5226_P04_E11	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 347	5549	WASTRES	ADI-26938 LAD5226_P04_E11	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 347	5550	TGGGCATCTACCCGGGAATCC	ADI-26938 LAD5226_P04_E11	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 347	5551	KQSYSIRT	ADI-26938 LAD5226_P04_E11	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 347	5552	AAGCAATCTTATTCTATCAGAACT	ADI-26938 LAD5226_P04_E11	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 348	5553	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCAGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26939 LAD5226_P04_B12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 348	5554	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVTVSS	ADI-26939 LAD5226_P04_B12	Heavy chain variable region ("HC") amino acid sequence
Ab 348	5555	FNIKDYYMH	ADI-26939 LAD5226_P04_B12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 348	5556	TTCAACATCAAGGACTACTATATGCAC	ADI-26939 LAD5226_P04_B12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 348	5557	WIDLENANTIYDAKFQG	ADI-26939 LAD5226_P04_B12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 348	5558	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26939 LAD5226_P04_B12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 348	5559	ARDQYGRYFYDV	ADI-26939 LAD5226_P04_B12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 348	5560	GCGAGAGATCAGTACGGGAGATATTTTTACGACGTG	ADI-26939 LAD5226_P04_B12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 348	5561	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26939 LAD5226_P04_B12	Light chain variable region("LC") nucleic acid sequence
Ab 348	5562	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26939 LAD5226_P04_B12	Light chain variable region ("LC") amino acid sequence
Ab 348	5563	KSSQSLLNARTGKNYLA	ADI-26939 LAD5226_P04_B12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 348	5564	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26939 LAD5226_P04_B12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 348	5565	WASTRES	ADI-26939 LAD5226_P04_B12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 348	5566	TGGGCATCTACCCGGGAATCC	ADI-26939 LAD5226_P04_B12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 348	5567	KQSYSIRT	ADI-26939 LAD5226_P04_B12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 348	5568	AAGCAATCTTATTCTATCAGAACT	ADI-26939 LAD5226_P04_B12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 349	5569	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCGTTACGGGGCTTATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26940 LAD5226_P04_E12	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 349	5570	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTVSS	ADI-26940 LAD5226_P04_E12	Heavy chain variable region ("HC") amino acid sequence
Ab 349	5571	FNIKDYYMH	ADI-26940 LAD5226_P04_E12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 349	5572	TTCAACATCAAGGACTACTATATGCAC	ADI-26940 LAD5226_P04_E12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 349	5573	WIDLEEGNTIYDAKFQG	ADI-26940 LAD5226_P04_E12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 349	5574	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26940 LAD5226_P04_E12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 349	5575	ARDRYGAYFYDV	ADI-26940 LAD5226_P04_E12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 349	5576	GCGAGAGATCGTTACGGGGCTTATTTTTACGACGTG	ADI-26940 LAD5226_P04_E12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 349	5577	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26940 LAD5226_P04_E12	Light chain variable region("LC") nucleic acid sequence
Ab 349	5578	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26940 LAD5226_P04_E12	Light chain variable region ("LC") amino acid sequence
Ab 349	5579	KSSQSLLNARTGKNYLA	ADI-26940 LAD5226_P04_E12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 349	5580	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26940 LAD5226_P04_E12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 349	5581	WASTRES	ADI-26940 LAD5226_P04_E12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 349	5582	TGGGCATCTACCCGGGAATCC	ADI-26940 LAD5226_P04_E12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 349	5583	KQSYSIRT	ADI-26940 LAD5226_P04_E12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 349	5584	AAGCAATCTTATTCTATCAGAACT	ADI-26940 LAD5226_P04_E12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 350	5585	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCAGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26941 LAD5226_P05_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 350	5586	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVTVSS	ADI-26941 LAD5226_P05_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 350	5587	FNIKDYYMH	ADI-26941 LAD5226_P05_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 350	5588	TTCAACATCAAGGACTACTATATGCAC	ADI-26941 LAD5226_P05_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 350	5589	WIDLEEGNTIYDAKFQG	ADI-26941 LAD5226_P05_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 350	5590	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26941 LAD5226_P05_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 350	5591	ARDQYGRYFYDV	ADI-26941 LAD5226_P05_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 350	5592	GCGAGAGATCAGTACGGGAGATATTTTTACGACGTG	ADI-26941 LAD5226_P05_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 350	5593	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26941 LAD5226_P05_A02	Light chain variable region("LC") nucleic acid sequence
Ab 350	5594	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26941 LAD5226_P05_A02	Light chain variable region ("LC") amino acid sequence
Ab 350	5595	KSSQSLLNARTGKNYLA	ADI-26941 LAD5226_P05_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 350	5596	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26941 LAD5226_P05_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 350	5597	WASTRES	ADI-26941 LAD5226_P05_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 350	5598	TGGGCATCTACCCGGGAATCC	ADI-26941 LAD5226_P05_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 350	5599	KQSYSIRT	ADI-26941 LAD5226_P05_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 350	5600	AAGCAATCTTATTCTATCAGAACT	ADI-26941 LAD5226_P05_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 351	5601	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACGGGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTG	ADI-26942 LAD5226_P05_F02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 351	5602	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTVSS	ADI-26942 LAD5226_P05_F02	Heavy chain variable region ("HC") amino acid sequence
Ab 351	5603	FNIKDYYMH	ADI-26942 LAD5226_P05_F02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 351	5604	TTCAACATCAAGGACTACTATATGCAC	ADI-26942 LAD5226_P05_F02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 351	5605	WIDLENANTIYDAKFQG	ADI-26942 LAD5226_P05_F02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 351	5606	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26942 LAD5226_P05_F02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 351	5607	ARDVYGRYFYDL	ADI-26942 LAD5226_P05_F02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 351	5608	GCGAGAGATGTGTACGGGAGATATTTTTACGACCTT	ADI-26942 LAD5226_P05_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 351	5609	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26942 LAD5226_P05_F02	Light chain variable region("LC") nucleic acid sequence
Ab 351	5610	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26942 LAD5226_P05_F02	Light chain variable region ("LC") amino acid sequence
Ab 351	5611	KSSQSLLNARTGKNYLA	ADI-26942 LAD5226_P05_F02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 351	5612	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26942 LAD5226_P05_F02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 351	5613	WASTRES	ADI-26942 LAD5226_P05_F02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 351	5614	TGGGCATCTACCCGGGAATCC	ADI-26942 LAD5226_P05_F02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 351	5615	KQSYSIRT	ADI-26942 LAD5226_P05_F02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 351	5616	AAGCAATCTTATTCTATCAGAACT	ADI-26942 LAD5226_P05_F02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 352	5617	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26943 LAD5226_P05_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 352	5618	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGGYFYDVWGQGTLVTVSS	ADI-26943 LAD5226_P05_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 352	5619	FNIKDYYMH	ADI-26943 LAD5226_P05_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 352	5620	TTCAACATCAAGGACTACTATATGCAC	ADI-26943 LAD5226_P05_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 352	5621	WIDLENANTIYDAKFQG	ADI-26943 LAD5226_P05_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 352	5622	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26943 LAD5226_P05_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 352	5623	ARDAYGGYFYDV	ADI-26943 LAD5226_P05_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 352	5624	GCGAGAGATGCGTACGGGGGGTATTTTTACGACGTG	ADI-26943 LAD5226_P05_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 352	5625	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26943 LAD5226_P05_A03	Light chain variable region("LC") nucleic acid sequence
Ab 352	5626	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26943 LAD5226_P05_A03	Light chain variable region ("LC") amino acid sequence
Ab 352	5627	KSSQSLLNARTGKNYLA	ADI-26943 LAD5226_P05_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 352	5628	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26943 LAD5226_P05_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 352	5629	WASTRES	ADI-26943 LAD5226_P05_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 352	5630	TGGGCATCTACCCGGGAATCC	ADI-26943 LAD5226_P05_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 352	5631	KQSYSIRT	ADI-26943 LAD5226_P05_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 352	5632	AAGCAATCTTATTCTATCAGAACT	ADI-26943 LAD5226_P05_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 353	5633	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATAATTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26944 LAD5226_P05_G03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 353	5634	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVTVSS	ADI-26944 LAD5226_P05_G03	Heavy chain variable region ("HC") amino acid sequence
Ab 353	5635	FNIKDYYMH	ADI-26944 LAD5226_P05_G03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 353	5636	TTCAACATCAAGGACTACTATATGCAC	ADI-26944 LAD5226_P05_G03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 353	5637	WIDLENANTIYDAKFQG	ADI-26944 LAD5226_P05_G03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 353	5638	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26944 LAD5226_P05_G03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 353	5639	ARDNYGGYFYDV	ADI-26944 LAD5226_P05_G03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 353	5640	GCGAGAGATAATTACGGGGGGTATTTTTACGACGTG	ADI-26944 LAD5226_P05_G03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 353	5641	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26944 LAD5226_P05_G03	Light chain variable region("LC") nucleic acid sequence
Ab 353	5642	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	ADI-26944 LAD5226_P05_G03	Light chain variable region ("LC") amino acid sequence
Ab 353	5643	KSSQSLLNARTGKNYLA	ADI-26944 LAD5226_P05_G03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 353	5644	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26944 LAD5226_P05_G03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 353	5645	WASTRES	ADI-26944 LAD5226_P05_G03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 353	5646	TGGGCATCTACCCGGGAATCC	ADI-26944 LAD5226_P05_G03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 353	5647	KQSYSIRT	ADI-26944 LAD5226_P05_G03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 353	5648	AAGCAATCTTATTCTATCAGAACT	ADI-26944 LAD5226_P05_G03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 354	5649	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26945 LAD5227_P03_E06	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 354	5650	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVTVSS	ADI-26945 LAD5227_P03_E06	Heavy chain variable region ("HC") amino acid sequence
Ab 354	5651	FNIKDYYMH	ADI-26945 LAD5227_P03_E06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 354	5652	TTCAACATCAAGGACTACTATATGCAC	ADI-26945 LAD5227_P03_E06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 354	5653	WIDLEEGNTIYDAKFQG	ADI-26945 LAD5227_P03_E06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 354	5654	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26945 LAD5227_P03_E06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 354	5655	GRDAYGRYFYDV	ADI-26945 LAD5227_P03_E06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 354	5656	GGTAGAGATGCGTACGGGAGATATTTTTACGACGTG	ADI-26945 LAD5227_P03_E06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 354	5657	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26945 LAD5227_P03_E06	Light chain variable region("LC") nucleic acid sequence
Ab 354	5658	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26945 LAD5227_P03_E06	Light chain variable region ("LC") amino acid sequence
Ab 354	5659	KSSQSLLESRTGKNYLA	ADI-26945 LAD5227_P03_E06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 354	5660	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-26945 LAD5227_P03_E06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 354	5661	WASTRES	ADI-26945 LAD5227_P03_E06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 354	5662	TGGGCATCTACCCGGGAATCC	ADI-26945 LAD5227_P03_E06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 354	5663	KQSYSLRT	ADI-26945 LAD5227_P03_E06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 354	5664	AAGCAATCTTATTCTCTGAGAACT	ADI-26945 LAD5227_P03_E06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 355	5665	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26950 LAD5227_P03_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 355	5666	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTVSS	ADI-26950 LAD5227_P03_E10	Heavy chain variable region ("HC") amino acid sequence
Ab 355	5667	FNIKDYYMH	ADI-26950 LAD5227_P03_E10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 355	5668	TTCAACATCAAGGACTACTATATGCAC	ADI-26950 LAD5227_P03_E10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 355	5669	WIDLEEGNTIYDAKFQG	ADI-26950 LAD5227_P03_E10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 355	5670	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26950 LAD5227_P03_E10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 355	5671	ARDVLGRYFYDV	ADI-26950 LAD5227_P03_E10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 355	5672	GCGAGAGATGTGTTGGGGAGATATTTTTACGACGTG	ADI-26950 LAD5227_P03_E10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 355	5673	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26950 LAD5227_P03_E10	Light chain variable region("LC") nucleic acid sequence
Ab 355	5674	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26950 LAD5227_P03_E10	Light chain variable region ("LC") amino acid sequence
Ab 355	5675	KSSQSLLESRTGKNYLA	ADI-26950 LAD5227_P03_E10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 355	5676	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-26950 LAD5227_P03_E10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 355	5677	WASTRES	ADI-26950 LAD5227_P03_E10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 355	5678	TGGGCATCTACCCGGGAATCC	ADI-26950 LAD5227_P03_E10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 355	5679	KQSYSLRT	ADI-26950 LAD5227_P03_E10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 355	5680	AAGCAATCTTATTCTCTGAGAACT	ADI-26950 LAD5227_P03_E10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 356	5681	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATAATTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26954 LAD5227_P03_G12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 356	5682	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVTVSS	ADI-26954 LAD5227_P03_G12	Heavy chain variable region ("HC") amino acid sequence
Ab 356	5683	FNIKDYYMH	ADI-26954 LAD5227_P03_G12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 356	5684	TTCAACATCAAGGACTACTATATGCAC	ADI-26954 LAD5227_P03_G12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 356	5685	WIDLENANTIYDAKFQG	ADI-26954 LAD5227_P03_G12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 356	5686	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26954 LAD5227_P03_G12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 356	5687	ARDNYGGYFYDV	ADI-26954 LAD5227_P03_G12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 356	5688	GCGAGAGATAATTACGGGGGGTATTTTTACGACGTG	ADI-26954 LAD5227_P03_G12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 356	5689	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26954 LAD5227_P03_G12	Light chain variable region("LC") nucleic acid sequence
Ab 356	5690	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	ADI-26954 LAD5227_P03_G12	Light chain variable region ("LC") amino acid sequence
Ab 356	5691	KSSQSLLESRTGKNYLA	ADI-26954 LAD5227_P03_G12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 356	5692	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACTTAGCT	ADI-26954 LAD5227_P03_G12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 356	5693	WASTRES	ADI-26954 LAD5227_P03_G12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 356	5694	TGGGCATCTACCCGGGAATCC	ADI-26954 LAD5227_P03_G12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 356	5695	KQSYSLRT	ADI-26954 LAD5227_P03_G12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 356	5696	AAGCAATCTTATTCTCTGAGAACT	ADI-26954 LAD5227_P03_G12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 357	5697	GAAGTGAAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAGGCCAGGGGCCTTAGTCAAGTTGTCCTGCAAAGCTTCTGACTTCAACATTAAAGACTACTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGATGGATTGATCCTGAGAATGGTAATACTATATATGACCCGAAGTTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGGTAGGGATGGTAACTACTTTTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29534 SAD4961_P03_C10	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 357	5698	EVKLQQSGAELVRPGALVKLSCKASDFNIKDYYMHWVKQRPEQGLEWIGWIDPENGNTIYDPKFQGKASITADTSSNTAYLQLSSLTSEDTAVYYCGRDGNYFFDYWGQGTTVTVSS	ADI-29534 SAD4961_P03_C10	Heavy chain variable region ("HC") amino acid sequence
Ab 357	5699	FNIKDYYMH	ADI-29534 SAD4961_P03_C10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 357	5700	TTCAACATTAAAGACTACTATATGCAC	ADI-29534 SAD4961_P03_C10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 357	5701	WIDPENGNTIYDPKFQG	ADI-29534 SAD4961_P03_C10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 357	5702	TGGATTGATCCTGAGAATGGTAATACTATATATGACCCGAAGTTCCAGGGC	ADI-29534 SAD4961_P03_C10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 357	5703	GRDGNYFFDY	ADI-29534 SAD4961_P03_C10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 357	5704	GGTAGGGATGGTAACTACTTTTTTGACTAC	ADI-29534 SAD4961_P03_C10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 357	5705	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-29534 SAD4961_P03_C10	Light chain variable region("LC") nucleic acid sequence
Ab 357	5706	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-29534 SAD4961_P03_C10	Light chain variable region ("LC") amino acid sequence
Ab 357	5707	KSSQSLLNSRTRKNYLA	ADI-29534 SAD4961_P03_C10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 357	5708	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-29534 SAD4961_P03_C10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 357	5709	WASTRES	ADI-29534 SAD4961_P03_C10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 357	5710	TGGGCATCCACTAGGGAATCT	ADI-29534 SAD4961_P03_C10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 357	5711	KQSYNLRT	ADI-29534 SAD4961_P03_C10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 357	5712	AAGCAATCTTATAATCTTCGGACG	ADI-29534 SAD4961_P03_C10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 358	5713	GAAGTGCAGCTGCAGCAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATCTCCTGCAAGGCTTCTGACTACACCTTCACAAGCTACTATATTCACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAATTTCAAGGACAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCACCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGATGGTTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29535 SAD4961_P03_B08	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 358	5714	EVQLQQSGPELVKPGASVRISCKASDYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNENFKDKATLTADKSSSTAYMHLSSLTSEDSAVYFCARDDGYYFDYWGQGTTVTVSS	ADI-29535 SAD4961_P03_B08	Heavy chain variable region ("HC") amino acid sequence
Ab 358	5715	YTFTSYYIH	ADI-29535 SAD4961_P03_B08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 358	5716	TACACCTTCACAAGCTACTATATTCAC	ADI-29535 SAD4961_P03_B08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 358	5717	WIYPGNVNTKYNENFKD	ADI-29535 SAD4961_P03_B08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 358	5718	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAATTTCAAGGAC	ADI-29535 SAD4961_P03_B08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 358	5719	ARDDGYYFDY	ADI-29535 SAD4961_P03_B08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 358	5720	GCAAGAGATGATGGTTACTACTTTGACTAC	ADI-29535 SAD4961_P03_B08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 358	5721	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGCACAAAGCTGGAAATCAAA	ADI-29535 SAD4961_P03_B08	Light chain variable region("LC") nucleic acid sequence
Ab 358	5722	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	ADI-29535 SAD4961_P03_B08	Light chain variable region ("LC") amino acid sequence
Ab 358	5723	KSSQSLLNSRTRKNYLA	ADI-29535 SAD4961_P03_B08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 358	5724	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-29535 SAD4961_P03_B08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 358	5725	WASTRES	ADI-29535 SAD4961_P03_B08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 358	5726	TGGGCATCCACTAGGGAATCT	ADI-29535 SAD4961_P03_B08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 358	5727	KQSYNLRT	ADI-29535 SAD4961_P03_B08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 358	5728	AAGCAATCTTATAATCTTCGGACG	ADI-29535 SAD4961_P03_B08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 359	5729	CAAGTCAAGCTGGAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTCACAAACTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGAAGATGGTAATACTAAATACAATGAGAAATTCAAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGACTCTGCGATCTATTTCTGTGCAAGGAATAACGGTAGTAGCTATGCTATGGACTACTGGGGCCAAGGCACCACGGTCA	ADI-29536 SAD4961_P03_G07	Heavy chain variable region ("HC") nucleic acid sequence

		CCGTCTCCTCA		
Ab 359	5730	QVKLEQSGPELVKPGASVKMSCKASGYTFTNYYIHWVKQRPGQGLEWIGWIYPEDGNTKYNEKFKGKTTLTADKSSSTAYMLLSSLTSEDSAIYFCARNNGSSYAMDYWGQGTTVTVSS	ADI-29536 SAD4961_P03_G07	Heavy chain variable region ("HC") amino acid sequence
Ab 359	5731	YTFTNYYIH	ADI-29536 SAD4961_P03_G07	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 359	5732	TACACCTTCACAAACTACTATATACAC	ADI-29536 SAD4961_P03_G07	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 359	5733	WIYPEDGNTKYNEKFKG	ADI-29536 SAD4961_P03_G07	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 359	5734	TGGATTTATCCTGAAGATGGTAATACTAAATACAATGAGAAATTCAAGGGC	ADI-29536 SAD4961_P03_G07	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 359	5735	ARNNGSSYAMDY	ADI-29536 SAD4961_P03_G07	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 359	5736	GCAAGGAATAACGGTAGTAGCTATGCTATGGACTAC	ADI-29536 SAD4961_P03_G07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 359	5737	GGCATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAGTCTTATAATCTTCGGACGTTCGGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-29536 SAD4961_P03_G07	Light chain variable region("LC") nucleic acid sequence
Ab 359	5738	GIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLELK	ADI-29536 SAD4961_P03_G07	Light chain variable region ("LC") amino acid sequence
Ab 359	5739	KSSQSLLNSRTRKNYLA	ADI-29536 SAD4961_P03_G07	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 359	5740	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-29536 SAD4961_P03_G07	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 359	5741	WASTRES	ADI-29536 SAD4961_P03_G07	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 359	5742	TGGGCATCCACTAGGGAATCT	ADI-29536 SAD4961_P03_G07	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 359	5743	KQSYNLRT	ADI-29536 SAD4961_P03_G07	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 359	5744	AAGCAGTCTTATAATCTTCGGACG	ADI-29536 SAD4961_P03_G07	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 360	5745	CAAGTACAGCTGGAGCAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAGGCAGAGGCCTGGTCAGGGACTTGAGTGGATTGGATGGATTTTTCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGGTAACTACTCCTTTGCTTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29537 SAD4961_P03_A06	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 360	5746	QVQLEQSGPELVKPGASVRISCKASGYTFTSYYIHWVRQRPGQGLEWIGWIFPGNVNTKYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDGNYSFAYWGQGTTVTVSS	ADI-29537 SAD4961_P03_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 360	5747	YTFTSYYIH	ADI-29537 SAD4961_P03_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 360	5748	TACACCTTCACAAGCTACTATATACAC	ADI-29537 SAD4961_P03_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 360	5749	WIFPGNVNTKYNEKFKG	ADI-29537 SAD4961_P03_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 360	5750	TGGATTTTTCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-29537 SAD4961_P03_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 360	5751	ARDGNYSFAY	ADI-29537 SAD4961_P03_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 360	5752	GCAAGAGATGGTAACTACTCCTTTGCTTAC	ADI-29537 SAD4961_P03_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 360	5753	GACATTCAGCTCACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAAAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGGACAAAGCTGGAAATAAAA	ADI-29537 SAD4961_P03_A06	Light chain variable region("LC") nucleic acid sequence
Ab 360	5754	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	ADI-29537 SAD4961_P03_A06	Light chain variable region ("LC") amino acid sequence
Ab 360	5755	KSSQSLLNSRTRKNYLA	ADI-29537 SAD4961_P03_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 360	5756	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-29537 SAD4961_P03_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 360	5757	WASTRES	ADI-29537 SAD4961_P03_A06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 360	5758	TGGGCATCCACTAGGGAATCT	ADI-29537 SAD4961_P03_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 360	5759	KQSYNLRT	ADI-29537 SAD4961_P03_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 360	5760	AAGCAATCTTATAATCTTCGGACG	ADI-29537 SAD4961_P03_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 361	5761	CAGGTGAAGCTGGAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAACCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATGCTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGATGGGTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29538 SAD4961_P03_A05	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 361	5762	QVKLEQSGPELVKPGASVRISCKASGYTFTTYYIHWVKQRPGQGLEWIGWIYPGNVNAKYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDDGYYFDYWGQGTTVTVSS	ADI-29538 SAD4961_P03_A05	Heavy chain variable region ("HC") amino acid sequence
Ab 361	5763	YTFTTYYIH	ADI-29538 SAD4961_P03_A05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 361	5764	TACACCTTCACAACCTACTATATACAC	ADI-29538 SAD4961_P03_A05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 361	5765	WIYPGNVNAKYNEKFKG	ADI-29538 SAD4961_P03_A05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 361	5766	TGGATTTATCCTGGAAATGTTAATGCTAAGTACAATGAGAAGTTCAAGGGC	ADI-29538 SAD4961_P03_A05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 361	5767	ARDDGYYFDY	ADI-29538 SAD4961_P03_A05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 361	5768	GCAAGAGATGATGGGTACTACTTTGACTAC	ADI-29538 SAD4961_P03_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 361	5769	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGCACAAAGCTGGAAAATAAA	ADI-29538 SAD4961_P03_A05	Light chain variable region("LC") nucleic acid sequence
Ab 361	5770	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLENK	ADI-29538 SAD4961_P03_A05	Light chain variable region ("LC") amino acid sequence
Ab 361	5771	KSSQSLLNSRTRKNYLA	ADI-29538 SAD4961_P03_A05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 361	5772	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-29538 SAD4961_P03_A05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 361	5773	WASTRES	ADI-29538 SAD4961_P03_A05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 361	5774	TGGGCATCCACTAGGGAATCT	ADI-29538 SAD4961_P03_A05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 361	5775	KQSYNLRT	ADI-29538 SAD4961_P03_A05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 361	5776	AAGCAATCTTATAATCTTCGGACG	ADI-29538 SAD4961_P03_A05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 362	5777	GAGGTCCAGCTGCAACAATCAGGACCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAGGGTATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTCAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAACCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTACTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29539 SAD4961_P03_B04	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 362	5778	EVQLQQSGPELVKPGASVRVSCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTQYNEKFKGKATLTADKSSSTTYMQLSSLTSEDSAVYFCARDGDYYFDYWGQGTTVTVSS	ADI-29539 SAD4961_P03_B04	Heavy chain variable region ("HC") amino acid sequence
Ab 362	5779	YTFTSYYIH	ADI-29539 SAD4961_P03_B04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 362	5780	TACACCTTCACAAGCTACTATATACAC	ADI-29539 SAD4961_P03_B04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 362	5781	WIYPGNVNTQYNEKFKG	ADI-29539 SAD4961_P03_B04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 362	5782	TGGATTTATCCTGGAAATGTTAATACTCAGTACAATGAGAAGTTCAAGGGC	ADI-29539 SAD4961_P03_B04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 362	5783	ARDGDYYFDY	ADI-29539 SAD4961_P03_B04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 362	5784	GCAAGAGATGGTGATTACTACTTTGACTAC	ADI-29539 SAD4961_P03_B04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 362	5785	GGCATTCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGACCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGCACAAAGTTGGAAATAAAA	ADI-29539 SAD4961_P03_B04	Light chain variable region("LC") nucleic acid sequence
Ab 362	5786	GIQLTQSPSSLAVSAGEKVTMTCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	ADI-29539 SAD4961_P03_B04	Light chain variable region ("LC") amino acid sequence
Ab 362	5787	KSSQSLLNSRTRKNYLA	ADI-29539 SAD4961_P03_B04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 362	5788	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCT	ADI-29539 SAD4961_P03_B04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 362	5789	WASTRES	ADI-29539 SAD4961_P03_B04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 362	5790	TGGGCATCCACTAGGGAATCT	ADI-29539 SAD4961_P03_B04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 362	5791	KQSYNLRT	ADI-29539 SAD4961_P03_B04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 362	5792	AAGCAATCTTATAATCTTCGGACG	ADI-29539 SAD4961_P03_B04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 363	5793	GAGGTCAAGCTGCAGGAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTACTATATACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTACTTCTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29540 SAD4961_P03_E01	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 363	5794	EVKLQESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDGDYFFDYWGQGTTVTVSS	ADI-29540 SAD4961_P03_E01	Heavy chain variable region ("HC") amino acid sequence
Ab 363	5795	YTFTSYYIH	ADI-29540 SAD4961_P03_E01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 363	5796	TACACCTTCACAAGCTACTATATACAC	ADI-29540 SAD4961_P03_E01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 363	5797	WIYPGNVNTKYNEKFKG	ADI-29540 SAD4961_P03_E01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 363	5798	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTCAAGGGC	ADI-29540 SAD4961_P03_E01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 363	5799	ARDGDYFFDY	ADI-29540 SAD4961_P03_E01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 363	5800	GCAAGAGATGGTGATTACTTCTTTGACTAC	ADI-29540 SAD4961_P03_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 363	5801	GACATCCAGCTCACCCAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCAAAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCGGTGGAGGCACCAAGCTGAAAATCAAA	ADI-29540 SAD4961_P03_E01	Light chain variable region("LC") nucleic acid sequence
Ab 363	5802	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLKIK	ADI-29540 SAD4961_P03_E01	Light chain variable region ("LC") amino acid sequence
Ab 363	5803	KSSQSLLNSRTQKNYLA	ADI-29540 SAD4961_P03_E01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 363	5804	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCAAAAGAACTACTTGGCT	ADI-29540 SAD4961_P03_E01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 363	5805	WASTRES	ADI-29540 SAD4961_P03_E01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 363	5806	TGGGCATCCACTAGGGAATCT	ADI-29540 SAD4961_P03_E01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 363	5807	KQSYNLRT	ADI-29540 SAD4961_P03_E01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 363	5808	AAGCAATCTTATAATCTTCGGACG	ADI-29540 SAD4961_P03_E01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 364	5809	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACCTTCAATAAATACGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCCCGTATTAGAAGCAAATATAACAATTACGCCACATACTACGCCGACTCTGTGAAAGACAGATTCACCATCTCAAGAGATGATTCAAAGAACACAGCGTATCTGCAAATGAACAACCTGAAAACCGAGGACACGGCGGTGTACTACTGCGTGAGGCACGGCAACTTCGGGAATTCCTATATTTCATACTGGGCCTACTGGG	CTL-19613 LAD3583_P02_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 364	5810	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS	CTL-19613 LAD3583_P02_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 364	5811	FTFNKYAMN	CTL-19613 LAD3583_P02_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 364	5812	TTCACCTTCAATAAATACGCCATGAAC	CTL-19613 LAD3583_P02_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 364	5813	RIRSKYNNYATYYADSVKD	CTL-19613 LAD3583_P02_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 364	5814	CGTATTAGAAGCAAATATAACAATTACGCCACATACTACGCCGACTCTGTGAAAGAC	CTL-19613 LAD3583_P02_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 364	5815	VRHGNFGNSYISYWAY	CTL-19613 LAD3583_P02_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 364	5816	GTGAGGCACGGCAACTTCGGGAATTCCTATATTTCATACTGGGCCTAC	CTL-19613 LAD3583_P02_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 364	5817	CAGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGACAGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCAGTGGTAATTATCCCAACTGGGTCCAGCAGAAGCCTGGCCAAGCCCCCAGGGGACTGATTGGTGGTACAAAATTCCTGGCCCCCGGGACACCTGCCCGGTTCTCAGGCTCCCTCCTTGGGGGCAAAGCTGCCCTGACCCTTTCGGGTGTGCAGCCTGAGGATGAGGCTGAGTATTACTGCGTGCTCTGGTATAGTAATCGGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	CTL-19613 LAD3583_P02_A09	Light chain variable region("LC") nucleic acid sequence
Ab 364	5818	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	CTL-19613 LAD3583_P02_A09	Light chain variable region ("LC") amino acid sequence
Ab 364	5819	GSSTGAVTSGNYPN	CTL-19613 LAD3583_P02_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 364	5820	GGCTCCAGCACTGGAGCTGTCACCAGTGGTAATTATCCCAAC	CTL-19613 LAD3583_P02_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 364	5821	GTKFLAP	CTL-19613 LAD3583_P02_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 364	5822	GGTACAAAATTCCTGGCCCCC	CTL-19613 LAD3583_P02_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 364	5823	VLWYSNRWV	CTL-19613 LAD3583_P02_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 364	5824	GTGCTCTGGTATAGTAATCGGTGGGTG	CTL-19613 LAD3583_P02_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 365	5825	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACCTTCAATAAATACGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCCCGTATTAGAAGCAAATATAACAATTACGCCACATACTACGCCGACTCTGTGAAAGACAGATTCACCATCTCAAGAGATGATTCAAAGAACACAGCGTATCTGCAAATGAACAACCTGAAAACCGAGGACACGGCGGTGTACTACTGCGTGAGGCACGGCAACTTCGGGAATTCCTATATTTCATACTGGGCCTACTGGG	CTL-19669 LAD3584_P02_H12	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 365	5826	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS	CTL-19669 LAD3584_P02_H12	Heavy chain variable region ("HC") amino acid sequence
Ab 365	5827	FTFNKYAMN	CTL-19669 LAD3584_P02_H12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 365	5828	TTCACCTTCAATAAATACGCCATGAAC	CTL-19669 LAD3584_P02_H12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 365	5829	RIRSKYNNYATYYADSVKD	CTL-19669 LAD3584_P02_H12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 365	5830	CGTATTAGAAGCAAATATAACAATTACGCCACATACTACGCCGACTCTGTGAAAGAC	CTL-19669 LAD3584_P02_H12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 365	5831	VRHGNFGNSYISYWAY	CTL-19669 LAD3584_P02_H12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 365	5832	GTGAGGCACGGCAACTTCGGGAATTCCTATATTTCATACTGGGCCTAC	CTL-19669 LAD3584_P02_H12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 365	5833	CAGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCCCCAGGAGGGACAGTCACTCTCACCTGTGGCTCCAGCACTGGAGCTGTCACCAGTGGTAATTATCCCAACTGGGTCCAGCAGAAGCCTGGCCAAGCCCCCAGGGGACTGATTGGTGGTACAAAATTCCTGGCCCCCGGGACACCTGCCCGGTTCTCAGGCTCCCTCCTTGGGGGCAAAGCTGCCCTGACCCTTTCGGGTGTGCAGCCTGAGGATGAGGCTGAGTATTACTGCGTGCTCTGGTATAGTAATCGGTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	CTL-19669 LAD3584_P02_H12	Light chain variable region("LC") nucleic acid sequence
Ab 365	5834	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	CTL-19669 LAD3584_P02_H12	Light chain variable region ("LC") amino acid sequence
Ab 365	5835	GSSTGAVTSGNYPN	CTL-19669 LAD3584_P02_H12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 365	5836	GGCTCCAGCACTGGAGCTGTCACCAGTGGTAATTATCCCAAC	CTL-19669 LAD3584_P02_H12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 365	5837	GTKFLAP	CTL-19669 LAD3584_P02_H12	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 365	5838	GGTACAAAATTCCTGGCCCCC	CTL-19669 LAD3584_P02_H12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 365	5839	VLWYSNRWV	CTL-19669 LAD3584_P02_H12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 365	5840	GTGCTCTGGTATAGTAATCGGTGGGTG	CTL-19669 LAD3584_P02_H12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 366	5841	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATTCACCTTCACCAGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATCTACCCTGAAAATGATAACACAAAGTACAACGAGAAGTTCAAGGACAGAGTCACCATAACCGCGGACACGTCCACGAGCACAGCCTACCTGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGGGACGGATATTCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	CTL-19672 SAD5477_P02_H03	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 366	5842	EVQLVQSGAEVKKPGASVKVSCKASGFTFTSYYIHWVRQAPGQGLEWIGWIYPENDNTKYNEKFKDRVTITADTSTSTAYLELSSLRSEDTAVYYCARDGYSRYYFDYWGQGTLVTVSS	CTL-19672 SAD5477_P02_H03	Heavy chain variable region ("HC") amino acid sequence
Ab 366	5843	FTFTSYYIH	CTL-19672 SAD5477_P02_H03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 366	5844	TTCACCTTCACCAGCTACTATATACAC	CTL-19672 SAD5477_P02_H03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 366	5845	WIYPENDNTKYNEKFKD	CTL-19672 SAD5477_P02_H03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 366	5846	TGGATCTACCCTGAAAATGATAACACAAAGTACAACGAGAAGTTCAAGGAC	CTL-19672 SAD5477_P02_H03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 366	5847	ARDGYSRYYFDY	CTL-19672 SAD5477_P02_H03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 366	5848	GCCAGGGACGGATATTCTAGATATTACTTTGACTAC	CTL-19672 SAD5477_P02_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 366	5849	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGTCTCCTAAGCTGCTCATTTACTGGACATCTACCCGGAAGTCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAAAGCTTCATCCTTAGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA	CTL-19672 SAD5477_P02_H03	Light chain variable region("LC") nucleic acid sequence
Ab 366	5850	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWTSTRKSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSFILRTFGQGTKVEIK	CTL-19672 SAD5477_P02_H03	Light chain variable region ("LC") amino acid sequence
Ab 366	5851	KSSQSLLNSRTRKNYLA	CTL-19672 SAD5477_P02_H03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 366	5852	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTTAGCT	CTL-19672 SAD5477_P02_H03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 366	5853	WTSTRKS	CTL-19672 SAD5477_P02_H03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 366	5854	TGGACATCTACCCGGAAGTCC	CTL-19672 SAD5477_P02_H03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 366	5855	KQSFILRT	CTL-19672 SAD5477_P02_H03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 366	5856	AAGCAAAGCTTCATCCTTAGGACG	CTL-19672 SAD5477_P02_H03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 367	5857	GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATACCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGGGTCTCAGGTATTAGTTGGAATAGTGGTAGCATAGGCTATGCGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAGTCCCTGTATCTGCAAATGAACAGTCTGAGAGCTGAGGACACGGCGTTGTACTACTGCGCCAAGGACAATTCCGGATACGGCCACTACTACTACGGTATGGACGTCTGGGGGC	CAB21609_A01	Heavy chain variable region ("HC") nucleic acid sequence

		AAGGGACCACGGTCACCGTCGCCTCA		
Ab 367	5858	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYTMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKKSLYLQMNSLRAEDTALYYCAKDNSGYGHYYYGMDVWGQGTTVTVAS	CAB21609_A01	Heavy chain variable region ("HC") amino acid sequence
Ab 367	5859	FTFDDYTMH	CAB21609_A01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 367	5860	TTCACCTTTGATGATTATACCATGCAC	CAB21609_A01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 367	5861	GISWNSGSIGYADSVKG	CAB21609_A01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 367	5862	GGTATTAGTTGGAATAGTGGTAGCATAGGCTATGCGGACTCTGTGAAGGGC	CAB21609_A01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 367	5863	AKDNSGYGHYYYGMDV	CAB21609_A01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 367	5864	GCCAAGGACAATTCCGGATACGGCCACTACTACTACGGTATGGACGTC	CAB21609_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 367	5865	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAACATTACATCAATTGGCCTCTCACTTTCGGCGGAGGGACCAAG	CAB21609_A01	Light chain variable region("LC") nucleic acid sequence

		GTGGAGATCAAA		
Ab 367	5866	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQHYINWPLTFGGGTKVEIK	CAB21609_A01	Light chain variable region ("LC") amino acid sequence
Ab 367	5867	RASQSVSSNLA	CAB21609_A01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 367	5868	AGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC	CAB21609_A01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 367	5869	GASTRAT	CAB21609_A01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 367	5870	GGTGCATCCACCAGGGCCACT	CAB21609_A01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 367	5871	QHYINWPLT	CAB21609_A01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 367	5872	CAACATTACATCAATTGGCCTCTCACT	CAB21609_A01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 368	5873	GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCGGATCCCTGAGACTCTCCTGTGCAGCCACTGGATTCACCTTTGATGATTTCACCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGGGTCTCAGGTATTAGTTGGAATAGTGGTAGCATAGGCTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCTGAGGACACGGCGTTGTACTACTGCGCCAAGGACAACAGCGGATACGGCTACTACTACTACGGTATGGACGTCTGGGGGCAAGGGACCACGGTCACCGTCTCCTCA	CAB21609_B01	Heavy chain variable region ("HC") nucleic acid sequence

Ab 368	5874	EVQLVESGGGLVQPGGSLRLSCAATGFTFDDFTMHWVRQAPGKGLEWVSGISWNSGSIGYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDNSGYGYYYYGMDVWGQGTTVTVSS	CAB21609_B01	Heavy chain variable region ("HC") amino acid sequence
Ab 368	5875	FTFDDFTMH	CAB21609_B01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 368	5876	TTCACCTTTGATGATTTCACCATGCAC	CAB21609_B01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 368	5877	GISWNSGSIGYVDSVKG	CAB21609_B01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 368	5878	GGTATTAGTTGGAATAGTGGTAGCATAGGCTATGTGGACTCTGTGAAGGGC	CAB21609_B01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 368	5879	AKDNSGYGYYYYGMDV	CAB21609_B01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 368	5880	GCCAAGGACAACAGCGGATACGGCTACTACTACTACGGTATGGACGTC	CAB21609_B01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 368	5881	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCACAGTGTTAGCAGAAACTCAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAATTTATTACTGTCAACAGTATAATAATTGGCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	CAB21609_B01	Light chain variable region("LC") nucleic acid sequence
Ab 368	5882	EIVMTQSPATLSVSPGERATLSCRASHSVSRNSAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAIYYCQQYNNWPLTFGGGTKVEIK	CAB21609_B01	Light chain variable region ("LC") amino acid sequence
Ab 368	5883	RASHSVSRNSA	CAB21609_B01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 368	5884	AGGGCCAGTCACAGTGTTAGCAGAAACTCAGCC	CAB21609_B01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 368	5885	GASTRAT	CAB21609_B01	Light chain variable region CDR L2 ("L2")

				amino acid sequence
Ab 368	5886	GGTGCATCCACCAGGGCCACT	CAB21609_B01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 368	5887	QQYNNWPLT	CAB21609_B01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 368	5888	CAACAGTATAATAATTGGCCGCTCACT	CAB21609_B01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 369	5889	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGAAGCTATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATGGTATACTATGATGGAAATAATCAATACTATGCAGACTCCGTGAGGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGACGACACGGCGGTGTACTTCTGCGCTAGAGGTCCTGGCTATAACTGGTTGGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA	CAB21609_C01	Heavy chain variable region ("HC") nucleic acid sequence
Ab 369	5890	QVQLVESGGGVVQPGRSLRLSCAASGFTFRSYAMHWVRQAPGKGLEWVAMVYYDGNNQYYADSVRGRFTISRDNSKNTLYLQMNSLRADDTAVYFCARGPGYNWLDPWGQGTLVTVSS	CAB21609_C01	Heavy chain variable region ("HC") amino acid sequence
Ab 369	5891	FTFRSYAMH	CAB21609_C01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 369	5892	TTCACCTTCAGAAGCTATGCCATGCAC	CAB21609_C01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 369	5893	MVYYDGNNQYYADSVRG	CAB21609_C01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 369	5894	ATGGTATACTATGATGGAAATAATCAATACTATGCAGACTCCGTGAGGGGC	CAB21609_C01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 369	5895	ARGPGYNWLDP	CAB21609_C01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 369	5896	GCTAGAGGTCCTGGCTATAACTGGTTGGACCCC	CAB21609_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 369	5897	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGAAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAACAGTACAACAATTGGCCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAAA	CAB21609_C01	Light chain variable region("LC") nucleic acid sequence
Ab 369	5898	EIVMTQSPATLSVSPGERATLSCRASQSVSRNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVVIK	CAB21609_C01	Light chain variable region ("LC") amino acid sequence
Ab 369	5899	RASQSVSRNLA	CAB21609_C01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 369	5900	AGGGCCAGTCAGAGTGTTAGCAGAAACTTAGCC	CAB21609_C01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 369	5901	GASTRAT	CAB21609_C01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 369	5902	GGTGCATCCACCAGGGCCACT	CAB21609_C01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 369	5903	QQYNNWPLT	CAB21609_C01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 369	5904	CAACAGTACAACAATTGGCCTCTCACT	CAB21609_C01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 370	5905	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCGCCTGTGTAGCGTCTGGATTCACCTTCAGAAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGCAGTGGGTGGCAATGATATACTATGATGGAAAGAATAAATACTATGCAGACTCCGTGAGGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAACCTGAGAGTCGAGGACACGGCGATGTACTTCTGCGCCAGAGGTCCAGGCTATAACTGGTTGGACCCCTGGGGCCAGGGAACCCTGGTC	CAB21609_D01	Heavy chain variable region ("HC") nucleic acid sequence

		ACCGTCTCCTCA		
Ab 370	5906	QVQLVESGGGVVQPGRSLRLACVASGFTFRSYGMHWVRQAPGKGLQWVAMIYYDGKNKYYADSVRGRFTISRDNSKNTLYLQMNNLRVEDTAMYFCARGPGYNWLDPWGQGTLVTVSS	CAB21609_D01	Heavy chain variable region ("HC") amino acid sequence
Ab 370	5907	FTFRSYGMH	CAB21609_D01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 370	5908	TTCACCTTCAGAAGCTATGGCATGCAC	CAB21609_D01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 370	5909	MIYYDGKNKYYADSVRG	CAB21609_D01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 370	5910	ATGATATACTATGATGGAAAGAATAAATACTATGCAGACTCCGTGAGGGGC	CAB21609_D01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 370	5911	ARGPGYNWLDP	CAB21609_D01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 370	5912	GCCAGAGGTCCAGGCTATAACTGGTTGGACCCC	CAB21609_D01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 370	5913	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGAATTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTAGCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATGTTGCAGTTTATTACTGTCAGCAGCATCATAACTGGCCTCTCACTTTCGGCGGAGGGACCAAG	CAB21609_D01	Light chain variable region("LC") nucleic acid sequence

		GTGGAGATCAAA		
Ab 370	5914	EIVMTQSPATLSVSPGERATLSCRASQRISSNLAWYQQKPGQAPRLLIYGASTRATGSPARFSGSGSGTDFTLTISSLQSEDVAVYYCQQHHNWPLTFGGGTKVEIK	CAB21609_D01	Light chain variable region ("LC") amino acid sequence
Ab 370	5915	RASQRISSNLA	CAB21609_D01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 370	5916	AGGGCCAGTCAGAGAATTAGCAGCAACTTAGCC	CAB21609_D01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 370	5917	GASTRAT	CAB21609_D01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 370	5918	GGTGCATCCACCAGGGCCACT	CAB21609_D01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 370	5919	QQHHNWPLT	CAB21609_D01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 370	5920	CAGCAGCATCATAACTGGCCTCTCACT	CAB21609_D01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 371	5921	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-16606 LAD2189_P03_F02	Heavy chain variable region ("HC") nucleic acid sequence

Ab 371	5922	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS	ADI-16606 LAD2189_P03_F02	Heavy chain variable region ("HC") amino acid sequence
Ab 371	5923	FTFNTYAMN	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 371	5924	TTCACCTTTAACACATATGCCATGAAT	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 371	5925	RIRSKYNNYATYYADSVKD	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 371	5926	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 371	5927	VRHGNFGNSYVSWFAY	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 371	5928	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTAT	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 371	5929	CAGACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-16606 LAD2189_P03_F02	Light chain variable region("LC") nucleic acid sequence
Ab 371	5930	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL	ADI-16606 LAD2189_P03_F02	Light chain variable region ("LC") amino acid sequence
Ab 371	5931	RSSTGAVTTSNYAN	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 371	5932	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 371	5933	GTNKRAP	ADI-16606	Light chain variable region CDR L2 ("L2")

			LAD2189_P03_F02	amino acid sequence
Ab 371	5934	GGCACAAACAAGCGCGCTCCT	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 371	5935	ALWYSNLWV	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 371	5936	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-16606 LAD2189_P03_F02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 372	5937	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTTTGATGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-21960 SAD5837_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence
Ab 372	5938	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYFDVWGQGTLVTVSS	ADI-21960 SAD5837_P01_A04	Heavy chain variable region ("HC") amino acid sequence
Ab 372	5939	FNIKDYYMH	ADI-21960 SAD5837_P01_A04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 372	5940	TTCAACATCAAGGACTACTATATGCAC	ADI-21960 SAD5837_P01_A04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 372	5941	WIDLENGNTIYDPKFQG	ADI-21960 SAD5837_P01_A04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 372	5942	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21960 SAD5837_P01_A04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 372	5943	ARDGYARYYFDV	ADI-21960 SAD5837_P01_A04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 372	5944	GCGAGAGATGGATACGCTAGATATTACTTTGATGTG	ADI-21960 SAD5837_P01_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 372	5945	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21960 SAD5837_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 372	5946	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21960 SAD5837_P01_A04	Light chain variable region ("LC") amino acid sequence
Ab 372	5947	KSSQSLLNSRTGKNYLA	ADI-21960 SAD5837_P01_A04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 372	5948	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21960 SAD5837_P01_A04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 372	5949	WASTRES	ADI-21960 SAD5837_P01_A04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 372	5950	TGGGCATCTACCCGGGAATCC	ADI-21960 SAD5837_P01_A04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 372	5951	KQSYSRRT	ADI-21960 SAD5837_P01_A04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 372	5952	AAGCAATCTTATTCTCGGAGAACT	ADI-21960 SAD5837_P01_A04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 373	5953	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTACTATGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-21961 SAD5837_P01_C05	Heavy chain variable region ("HC") nucleic acid sequence

Ab 373	5954	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYYYDYWGQGTLVTVSS	ADI-21961 SAD5837_P01_C05	Heavy chain variable region ("HC") amino acid sequence
Ab 373	5955	FNIKDYYMH	ADI-21961 SAD5837_P01_C05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 373	5956	TTCAACATCAAGGACTACTATATGCAC	ADI-21961 SAD5837_P01_C05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 373	5957	WIDLENGNTIYDPKFQG	ADI-21961 SAD5837_P01_C05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 373	5958	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21961 SAD5837_P01_C05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 373	5959	ARDGYARYYYDY	ADI-21961 SAD5837_P01_C05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 373	5960	GCGAGAGATGGATACGCTAGATATTACTATGACTAC	ADI-21961 SAD5837_P01_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 373	5961	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21961 SAD5837_P01_C05	Light chain variable region("LC") nucleic acid sequence
Ab 373	5962	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21961 SAD5837_P01_C05	Light chain variable region ("LC") amino acid sequence
Ab 373	5963	KSSQSLLNSRTGKNYLA	ADI-21961 SAD5837_P01_C05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 373	5964	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21961 SAD5837_P01_C05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 373	5965	WASTRES	ADI-21961 SAD5837_P01_C05	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 373	5966	TGGGCATCTACCCGGGAATCC	ADI-21961 SAD5837_P01_C05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 373	5967	KQSYSRRT	ADI-21961 SAD5837_P01_C05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 373	5968	AAGCAATCTTATTCTCGGAGAACT	ADI-21961 SAD5837_P01_C05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 374	5969	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCAGTAGAGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-21962 SAD5837_P01_B06	Heavy chain variable region ("HC") nucleic acid sequence
Ab 374	5970	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCSRDGYARYYFDYWGQGTLVTVSS	ADI-21962 SAD5837_P01_B06	Heavy chain variable region ("HC") amino acid sequence
Ab 374	5971	FNIKDYYMH	ADI-21962 SAD5837_P01_B06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 374	5972	TTCAACATCAAGGACTACTATATGCAC	ADI-21962 SAD5837_P01_B06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 374	5973	WIDLENGNTIYDPKFQG	ADI-21962 SAD5837_P01_B06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 374	5974	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21962 SAD5837_P01_B06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 374	5975	SRDGYARYYFDY	ADI-21962 SAD5837_P01_B06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 374	5976	AGTAGAGATGGATACGCTAGATATTACTTTGACTAC	ADI-21962 SAD5837_P01_B06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 374	5977	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21962 SAD5837_P01_B06	Light chain variable region("LC") nucleic acid sequence
Ab 374	5978	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21962 SAD5837_P01_B06	Light chain variable region ("LC") amino acid sequence
Ab 374	5979	KSSQSLLNSRTGKNYLA	ADI-21962 SAD5837_P01_B06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 374	5980	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21962 SAD5837_P01_B06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 374	5981	WASTRES	ADI-21962 SAD5837_P01_B06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 374	5982	TGGGCATCTACCCGGGAATCC	ADI-21962 SAD5837_P01_B06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 374	5983	KQSYSRRT	ADI-21962 SAD5837_P01_B06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 374	5984	AAGCAATCTTATTCTCGGAGAACT	ADI-21962 SAD5837_P01_B06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 375	5985	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCAATAGAGATGGATACGCTAGATATTACTATGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-21964 SAD5837_P01_B08	Heavy chain variable region ("HC") nucleic acid sequence

Ab 375	5986	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCNRDGYARYYYDYWGQGTLVTVSS	ADI-21964 SAD5837_P01_B08	Heavy chain variable region ("HC") amino acid sequence
Ab 375	5987	FNIKDYYMH	ADI-21964 SAD5837_P01_B08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 375	5988	TTCAACATCAAGGACTACTATATGCAC	ADI-21964 SAD5837_P01_B08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 375	5989	WIDLENGNTIYDPKFQG	ADI-21964 SAD5837_P01_B08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 375	5990	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21964 SAD5837_P01_B08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 375	5991	NRDGYARYYYDY	ADI-21964 SAD5837_P01_B08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 375	5992	AATAGAGATGGATACGCTAGATATTACTATGACTAC	ADI-21964 SAD5837_P01_B08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 375	5993	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21964 SAD5837_P01_B08	Light chain variable region("LC") nucleic acid sequence
Ab 375	5994	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21964 SAD5837_P01_B08	Light chain variable region ("LC") amino acid sequence
Ab 375	5995	KSSQSLLNSRTGKNYLA	ADI-21964 SAD5837_P01_B08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 375	5996	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21964 SAD5837_P01_B08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 375	5997	WASTRES	ADI-21964 SAD5837_P01_B08	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 375	5998	TGGGCATCTACCCGGGAATCC	ADI-21964 SAD5837_P01_B08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 375	5999	KQSYSRRT	ADI-21964 SAD5837_P01_B08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 375	6000	AAGCAATCTTATTCTCGGAGAACT	ADI-21964 SAD5837_P01_B08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 376	6001	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATACGCTAGATATTTTTTTGACAATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-21966 SAD5837_P01_G10	Heavy chain variable region ("HC") nucleic acid sequence
Ab 376	6002	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYARYFFDNWGQGTLVTVSS	ADI-21966 SAD5837_P01_G10	Heavy chain variable region ("HC") amino acid sequence
Ab 376	6003	FNIKDYYMH	ADI-21966 SAD5837_P01_G10	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 376	6004	TTCAACATCAAGGACTACTATATGCAC	ADI-21966 SAD5837_P01_G10	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 376	6005	WIDLENGNTIYDPKFQG	ADI-21966 SAD5837_P01_G10	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 376	6006	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21966 SAD5837_P01_G10	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 376	6007	ARDGYARYFFDN	ADI-21966 SAD5837_P01_G10	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 376	6008	GCGAGAGATGGATACGCTAGATATTTTTTTGACAAT	ADI-21966 SAD5837_P01_G10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 376	6009	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21966 SAD5837_P01_G10	Light chain variable region("LC") nucleic acid sequence
Ab 376	6010	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21966 SAD5837_P01_G10	Light chain variable region ("LC") amino acid sequence
Ab 376	6011	KSSQSLLNSRTGKNYLA	ADI-21966 SAD5837_P01_G10	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 376	6012	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21966 SAD5837_P01_G10	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 376	6013	WASTRES	ADI-21966 SAD5837_P01_G10	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 376	6014	TGGGCATCTACCCGGGAATCC	ADI-21966 SAD5837_P01_G10	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 376	6015	KQSYSRRT	ADI-21966 SAD5837_P01_G10	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 376	6016	AAGCAATCTTATTCTCGGAGAACT	ADI-21966 SAD5837_P01_G10	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 377	6017	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGGGTACGGGAGATATTACTTTGACCGTTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-21968 SAD5837_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

Ab 377	6018	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYYFDRWGQGTLVTVSS	ADI-21968 SAD5837_P01_A12	Heavy chain variable region ("HC") amino acid sequence
Ab 377	6019	FNIKDYYMH	ADI-21968 SAD5837_P01_A12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 377	6020	TTCAACATCAAGGACTACTATATGCAC	ADI-21968 SAD5837_P01_A12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 377	6021	WIDLENGNTIYDPKFQG	ADI-21968 SAD5837_P01_A12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 377	6022	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21968 SAD5837_P01_A12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 377	6023	ARDGYGRYYFDR	ADI-21968 SAD5837_P01_A12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 377	6024	GCGAGAGATGGGTACGGGAGATATTACTTTGACCGT	ADI-21968 SAD5837_P01_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 377	6025	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCCCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21968 SAD5837_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 377	6026	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21968 SAD5837_P01_A12	Light chain variable region ("LC") amino acid sequence
Ab 377	6027	KSSQSLLNSRTGKNYLA	ADI-21968 SAD5837_P01_A12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 377	6028	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21968 SAD5837_P01_A12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 377	6029	WASTRES	ADI-21968 SAD5837_P01_A12	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 377	6030	TGGGCATCTACCCGGGAATCC	ADI-21968 SAD5837_P01_A12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 377	6031	KQSYSRRT	ADI-21968 SAD5837_P01_A12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 377	6032	AAGCAATCTTATTCTCGGAGAACT	ADI-21968 SAD5837_P01_A12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 378	6033	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGGTCGGATGGATACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-21969 SAD5837_P02_C01	Heavy chain variable region ("HC") nucleic acid sequence
Ab 378	6034	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGSDGYARYYFDYWGQGTLVTVSS	ADI-21969 SAD5837_P02_C01	Heavy chain variable region ("HC") amino acid sequence
Ab 378	6035	FNIKDYYMH	ADI-21969 SAD5837_P02_C01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 378	6036	TTCAACATCAAGGACTACTATATGCAC	ADI-21969 SAD5837_P02_C01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 378	6037	WIDLENGNTIYDPKFQG	ADI-21969 SAD5837_P02_C01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 378	6038	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGTTTCAGGGC	ADI-21969 SAD5837_P02_C01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 378	6039	GSDGYARYYFDY	ADI-21969 SAD5837_P02_C01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 378	6040	GGGTCGGATGGATACGCTAGATATTACTTTGACTAC	ADI-21969 SAD5837_P02_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 378	6041	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-21969 SAD5837_P02_C01	Light chain variable region("LC") nucleic acid sequence
Ab 378	6042	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-21969 SAD5837_P02_C01	Light chain variable region ("LC") amino acid sequence
Ab 378	6043	KSSQSLLNSRTGKNYLA	ADI-21969 SAD5837_P02_C01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 378	6044	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTTAGCT	ADI-21969 SAD5837_P02_C01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 378	6045	WASTRES	ADI-21969 SAD5837_P02_C01	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 378	6046	TGGGCATCTACCCGGGAATCC	ADI-21969 SAD5837_P02_C01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 378	6047	KQSYSRRT	ADI-21969 SAD5837_P02_C01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 378	6048	AAGCAATCTTATTCTCGGAGAACT	ADI-21969 SAD5837_P02_C01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 379	6049	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-26907 LAD5224_P03_D02	Heavy chain variable region ("HC") nucleic acid sequence

Ab 379	6050	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVTVSS	ADI-26907 LAD5224_P03_D02	Heavy chain variable region ("HC") amino acid sequence
Ab 379	6051	FNIKDYYMH	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 379	6052	TTCAACATCAAGGACTACTATATGCAC	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 379	6053	WIDLENANTIYDAKFQG	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 379	6054	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 379	6055	GRDAYGRYFYDV	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 379	6056	GGTAGAGATGCGTACGGGAGATATTTTTACGACGTG	ADI-26907 LAD5224_P03_D02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 379	6057	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26907 LAD5224_P03_D02	Light chain variable region("LC") nucleic acid sequence
Ab 379	6058	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26907 LAD5224_P03_D02	Light chain variable region ("LC") amino acid sequence
Ab 379	6059	KSSQSLLNARTGKNYLA	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 379	6060	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 379	6061	WASTRES	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 379	6062	TGGGCATCTACCCGGGAATCC	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 379	6063	KQSYSRRT	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 379	6064	AAGCAATCTTATTCTCGGAGAACT	ADI-26907 LAD5224_P03_D02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 380	6065	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-26912 LAD5224_P03_E05	Heavy chain variable region ("HC") nucleic acid sequence
Ab 380	6066	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTVSS	ADI-26912 LAD5224_P03_E05	Heavy chain variable region ("HC") amino acid sequence
Ab 380	6067	FNIKDYYMH	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 380	6068	TTCAACATCAAGGACTACTATATGCAC	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 380	6069	WIDLENANTIYDAKFQG	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 380	6070	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 380	6071	ARDVLGRYFYDV	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 380	6072	GCGAGAGATGTGTTGGGGAGATATTTTTACGACGTG	ADI-26912 LAD5224_P03_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 380	6073	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26912 LAD5224_P03_E05	Light chain variable region("LC") nucleic acid sequence
Ab 380	6074	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26912 LAD5224_P03_E05	Light chain variable region ("LC") amino acid sequence
Ab 380	6075	KSSQSLLNARTGKNYLA	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 380	6076	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 380	6077	WASTRES	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 380	6078	TGGGCATCTACCCGGGAATCC	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 380	6079	KQSYSRRT	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 380	6080	AAGCAATCTTATTCTCGGAGAACT	ADI-26912 LAD5224_P03_E05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 381	6081	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCAGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-26913 LAD5224_P03_A06	Heavy chain variable region ("HC") nucleic acid sequence

Ab 381	6082	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVTVSS	ADI-26913 LAD5224_P03_A06	Heavy chain variable region ("HC") amino acid sequence
Ab 381	6083	FNIKDYYMH	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 381	6084	TTCAACATCAAGGACTACTATATGCAC	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 381	6085	WIDLENANTIYDAKFQG	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 381	6086	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 381	6087	ARDQYGRYFYDV	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 381	6088	GCGAGAGATCAGTACGGGAGATATTTTTACGACGTG	ADI-26913 LAD5224_P03_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 381	6089	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26913 LAD5224_P03_A06	Light chain variable region("LC") nucleic acid sequence
Ab 381	6090	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26913 LAD5224_P03_A06	Light chain variable region ("LC") amino acid sequence
Ab 381	6091	KSSQSLLNARTGKNYLA	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 381	6092	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 381	6093	WASTRES	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 381	6094	TGGGCATCTACCCGGGAATCC	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 381	6095	KQSYSRRT	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 381	6096	AAGCAATCTTATTCTCGGAGAACT	ADI-26913 LAD5224_P03_A06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 382	6097	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACGGGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-26916 LAD5224_P03_F08	Heavy chain variable region ("HC") nucleic acid sequence
Ab 382	6098	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTVSS	ADI-26916 LAD5224_P03_F08	Heavy chain variable region ("HC") amino acid sequence
Ab 382	6099	FNIKDYYMH	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 382	6100	TTCAACATCAAGGACTACTATATGCAC	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 382	6101	WIDLENANTIYDAKFQG	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 382	6102	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 382	6103	ARDVYGRYFYDL	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 382	6104	GCGAGAGATGTGTACGGGAGATATTTTTACGACCTT	ADI-26916 LAD5224_P03_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 382	6105	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26916 LAD5224_P03_F08	Light chain variable region("LC") nucleic acid sequence
Ab 382	6106	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26916 LAD5224_P03_F08	Light chain variable region ("LC") amino acid sequence
Ab 382	6107	KSSQSLLNARTGKNYLA	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 382	6108	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 382	6109	WASTRES	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 382	6110	TGGGCATCTACCCGGGAATCC	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 382	6111	KQSYSRRT	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 382	6112	AAGCAATCTTATTCTCGGAGAACT	ADI-26916 LAD5224_P03_F08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 383	6113	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-26917 LAD5224_P03_B09	Heavy chain variable region ("HC") nucleic acid sequence

Ab 383	6114	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGGYFYDVWGQGTLVTVSS	ADI-26917 LAD5224_P03_B09	Heavy chain variable region ("HC") amino acid sequence
Ab 383	6115	FNIKDYYMH	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 383	6116	TTCAACATCAAGGACTACTATATGCAC	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 383	6117	WIDLENANTIYDAKFQG	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 383	6118	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 383	6119	ARDAYGGYFYDV	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 383	6120	GCGAGAGATGCGTACGGGGGGTATTTTTACGACGTG	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 383	6121	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26917 LAD5224_P03_B09	Light chain variable region("LC") nucleic acid sequence
Ab 383	6122	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26917 LAD5224_P03_B09	Light chain variable region ("LC") amino acid sequence
Ab 383	6123	KSSQSLLNARTGKNYLA	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 383	6124	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 383	6125	WASTRES	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 383	6126	TGGGCATCTACCCGGGAATCC	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 383	6127	KQSYSRRT	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 383	6128	AAGCAATCTTATTCTCGGAGAACT	ADI-26917 LAD5224_P03_B09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 384	6129	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATAATTACGGGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-26918 LAD5224_P03_E09	Heavy chain variable region ("HC") nucleic acid sequence
Ab 384	6130	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVTVSS	ADI-26918 LAD5224_P03_E09	Heavy chain variable region ("HC") amino acid sequence
Ab 384	6131	FNIKDYYMH	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 384	6132	TTCAACATCAAGGACTACTATATGCAC	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 384	6133	WIDLENANTIYDAKFQG	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 384	6134	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 384	6135	ARDNYGGYFYDV	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 384	6136	GCGAGAGATAATTACGGGGGGTATTTTTACGACGTG	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 384	6137	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26918 LAD5224_P03_E09	Light chain variable region("LC") nucleic acid sequence
Ab 384	6138	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-26918 LAD5224_P03_E09	Light chain variable region ("LC") amino acid sequence
Ab 384	6139	KSSQSLLNARTGKNYLA	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 384	6140	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 384	6141	WASTRES	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 384	6142	TGGGCATCTACCCGGGAATCC	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 384	6143	KQSYSRRT	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 384	6144	AAGCAATCTTATTCTCGGAGAACT	ADI-26918 LAD5224_P03_E09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 385	6145	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29601 SAD5269_P02_H05	Heavy chain variable region ("HC") nucleic acid sequence

Ab 385	6146	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS	ADI-29601 SAD5269_P02_H05	Heavy chain variable region ("HC") amino acid sequence
Ab 385	6147	FTFNTYAMN	ADI-29601 SAD5269_P02_H05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 385	6148	TTCACCTTTAACACATATGCCATGAAT	ADI-29601 SAD5269_P02_H05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 385	6149	RIRSKYNNYATYYADSVKD	ADI-29601 SAD5269_P02_H05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 385	6150	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29601 SAD5269_P02_H05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 385	6151	VRHGNFGNSYVSWFAY	ADI-29601 SAD5269_P02_H05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 385	6152	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTAT	ADI-29601 SAD5269_P02_H05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 385	6153	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29601 SAD5269_P02_H05	Light chain variable region("LC") nucleic acid sequence
Ab 385	6154	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDESDYYCALWYSNLWVFGGGTKLTVL	ADI-29601 SAD5269_P02_H05	Light chain variable region ("LC") amino acid sequence
Ab 385	6155	RSSTGAVTTSNYAN	ADI-29601 SAD5269_P02_H05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 385	6156	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29601 SAD5269_P02_H05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 385	6157	GTDKRAP	ADI-29601	Light chain variable region CDR L2 ("L2")

			SAD5269_P02_H05	amino acid sequence
Ab 385	6158	GGCACAGACAAGCGCGCTCCC	ADI-29601 SAD5269_P02_H05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 385	6159	ALWYSNLWV	ADI-29601 SAD5269_P02_H05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 385	6160	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-29601 SAD5269_P02_H05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 386	6161	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29602 SAD5269_P02_G06	Heavy chain variable region ("HC") nucleic acid sequence
Ab 386	6162	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS	ADI-29602 SAD5269_P02_G06	Heavy chain variable region ("HC") amino acid sequence
Ab 386	6163	FTFNTYAMN	ADI-29602 SAD5269_P02_G06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 386	6164	TTCACCTTTAACACATATGCCATGAAT	ADI-29602 SAD5269_P02_G06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 386	6165	RIRSKYNNYATYYADSVKD	ADI-29602 SAD5269_P02_G06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 386	6166	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29602 SAD5269_P02_G06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 386	6167	VRHGNFGNSYVSWFAY	ADI-29602 SAD5269_P02_G06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 386	6168	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTGGTTTGCTTAT	ADI-29602 SAD5269_P02_G06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 386	6169	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29602 SAD5269_P02_G06	Light chain variable region("LC") nucleic acid sequence
Ab 386	6170	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	ADI-29602 SAD5269_P02_G06	Light chain variable region ("LC") amino acid sequence
Ab 386	6171	RSSTGAVTTSNYAN	ADI-29602 SAD5269_P02_G06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 386	6172	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29602 SAD5269_P02_G06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 386	6173	GTNKRAP	ADI-29602 SAD5269_P02_G06	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 386	6174	GGCACAAACAAGCGCGCTCCT	ADI-29602 SAD5269_P02_G06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 386	6175	ALWYSNLWV	ADI-29602 SAD5269_P02_G06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 386	6176	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-29602 SAD5269_P02_G06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 387	6177	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29603 SAD5268_P01_A09	Heavy chain variable region ("HC") nucleic acid sequence

Ab 387	6178	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-29603 SAD5268_P01_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 387	6179	FTFDTYAMN	ADI-29603 SAD5268_P01_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 387	6180	TTCACCTTTGACACATATGCCATGAAT	ADI-29603 SAD5268_P01_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 387	6181	RIRSKYNNYATYYADSVKD	ADI-29603 SAD5268_P01_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 387	6182	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29603 SAD5268_P01_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 387	6183	VRHGNFGNSYVSWFAH	ADI-29603 SAD5268_P01_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 387	6184	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTGGTTTGCTCAT	ADI-29603 SAD5268_P01_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 387	6185	CAGACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAATCTGATTATTACTGTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29603 SAD5268_P01_A09	Light chain variable region("LC") nucleic acid sequence
Ab 387	6186	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL	ADI-29603 SAD5268_P01_A09	Light chain variable region ("LC") amino acid sequence
Ab 387	6187	RSSTGAVTTSNYAN	ADI-29603 SAD5268_P01_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 387	6188	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29603 SAD5268_P01_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 387	6189	GTNKRAP	ADI-29603	Light chain variable region CDR L2 ("L2")

			SAD5268_P01_A09	amino acid sequence
Ab 387	6190	GGCACAAACAAGCGCGCTCCT	ADI-29603 SAD5268_P01_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 387	6191	ALWYSNLWV	ADI-29603 SAD5268_P01_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 387	6192	GCGCTGTGGTACAGTAACCTTTGGGTG	ADI-29603 SAD5268_P01_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 388	6193	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACGGGAGATATTTTTACAGGGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29607 SAD6444_P02_F05	Heavy chain variable region ("HC") nucleic acid sequence
Ab 388	6194	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYRVWGQGTLVTVSS	ADI-29607 SAD6444_P02_F05	Heavy chain variable region ("HC") amino acid sequence
Ab 388	6195	FNIKDYYMH	ADI-29607 SAD6444_P02_F05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 388	6196	TTCAACATCAAGGACTACTATATGCAC	ADI-29607 SAD6444_P02_F05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 388	6197	WIDLENANTIYDAKFQG	ADI-29607 SAD6444_P02_F05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 388	6198	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29607 SAD6444_P02_F05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 388	6199	ARDAYGRYFYRV	ADI-29607 SAD6444_P02_F05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 388	6200	GCGAGAGATGCGTACGGGAGATATTTTTACAGGGTG	ADI-29607 SAD6444_P02_F05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 388	6201	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29607 SAD6444_P02_F05	Light chain variable region("LC") nucleic acid sequence
Ab 388	6202	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29607 SAD6444_P02_F05	Light chain variable region ("LC") amino acid sequence
Ab 388	6203	KSSQSLLNARTGKNYLA	ADI-29607 SAD6444_P02_F05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 388	6204	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29607 SAD6444_P02_F05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 388	6205	WASTRES	ADI-29607 SAD6444_P02_F05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 388	6206	TGGGCATCTACCCGGGAATCC	ADI-29607 SAD6444_P02_F05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 388	6207	KQSYSRRT	ADI-29607 SAD6444_P02_F05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 388	6208	AAGCAATCTTATTCTCGGAGAACT	ADI-29607 SAD6444_P02_F05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 389	6209	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCCCGAGAGATGCTTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29608 SAD6444_P01_G02	Heavy chain variable region ("HC") nucleic acid sequence

Ab 389	6210	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCPRDAYGRYFYDVWGQGTLVTVSS	ADI-29608 SAD6444_P01_G02	Heavy chain variable region ("HC") amino acid sequence
Ab 389	6211	FNIKDYYMH	ADI-29608 SAD6444_P01_G02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 389	6212	TTCAACATCAAGGACTACTATATGCAC	ADI-29608 SAD6444_P01_G02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 389	6213	WIDLENANTIYDAKFQG	ADI-29608 SAD6444_P01_G02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 389	6214	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29608 SAD6444_P01_G02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 389	6215	PRDAYGRYFYDV	ADI-29608 SAD6444_P01_G02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 389	6216	CCGAGAGATGCTTACGGGAGATATTTTTACGACGTG	ADI-29608 SAD6444_P01_G02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 389	6217	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29608 SAD6444_P01_G02	Light chain variable region("LC") nucleic acid sequence
Ab 389	6218	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29608 SAD6444_P01_G02	Light chain variable region ("LC") amino acid sequence
Ab 389	6219	KSSQSLLNARTGKNYLA	ADI-29608 SAD6444_P01_G02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 389	6220	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29608 SAD6444_P01_G02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 389	6221	WASTRES	ADI-29608 SAD6444_P01_G02	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 389	6222	TGGGCATCTACCCGGGAATCC	ADI-29608 SAD6444_P01_G02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 389	6223	KQSYSRRT	ADI-29608 SAD6444_P01_G02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 389	6224	AAGCAATCTTATTCTCGGAGAACT	ADI-29608 SAD6444_P01_G02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 390	6225	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACGGGAGATATTTTTACGACGGGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29609 SAD6444_P02_C05	Heavy chain variable region ("HC") nucleic acid sequence
Ab 390	6226	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDGWGQGTLVTVSS	ADI-29609 SAD6444_P02_C05	Heavy chain variable region ("HC") amino acid sequence
Ab 390	6227	FNIKDYYMH	ADI-29609 SAD6444_P02_C05	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 390	6228	TTCAACATCAAGGACTACTATATGCAC	ADI-29609 SAD6444_P02_C05	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 390	6229	WIDLENANTIYDAKFQG	ADI-29609 SAD6444_P02_C05	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 390	6230	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29609 SAD6444_P02_C05	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 390	6231	ARDAYGRYFYDG	ADI-29609 SAD6444_P02_C05	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 390	6232	GCGAGAGATGCGTACGGGAGATATTTTTACGACGGG	ADI-29609 SAD6444_P02_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 390	6233	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29609 SAD6444_P02_C05	Light chain variable region("LC") nucleic acid sequence
Ab 390	6234	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29609 SAD6444_P02_C05	Light chain variable region ("LC") amino acid sequence
Ab 390	6235	KSSQSLLNARTGKNYLA	ADI-29609 SAD6444_P02_C05	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 390	6236	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29609 SAD6444_P02_C05	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 390	6237	WASTRES	ADI-29609 SAD6444_P02_C05	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 390	6238	TGGGCATCTACCCGGGAATCC	ADI-29609 SAD6444_P02_C05	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 390	6239	KQSYSRRT	ADI-29609 SAD6444_P02_C05	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 390	6240	AAGCAATCTTATTCTCGGAGAACT	ADI-29609 SAD6444_P02_C05	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 391	6241	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCGTTACGGGGCTTATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29610 SAD6444_P02_D06	Heavy chain variable region ("HC") nucleic acid sequence

Ab 391	6242	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTVSS	ADI-29610 SAD6444_P02_D06	Heavy chain variable region ("HC") amino acid sequence
Ab 391	6243	FNIKDYYMH	ADI-29610 SAD6444_P02_D06	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 391	6244	TTCAACATCAAGGACTACTATATGCAC	ADI-29610 SAD6444_P02_D06	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 391	6245	WIDLENANTIYDAKFQG	ADI-29610 SAD6444_P02_D06	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 391	6246	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29610 SAD6444_P02_D06	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 391	6247	ARDRYGAYFYDV	ADI-29610 SAD6444_P02_D06	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 391	6248	GCGAGAGATCGTTACGGGGCTTATTTTTACGACGTG	ADI-29610 SAD6444_P02_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 391	6249	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29610 SAD6444_P02_D06	Light chain variable region("LC") nucleic acid sequence
Ab 391	6250	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29610 SAD6444_P02_D06	Light chain variable region ("LC") amino acid sequence
Ab 391	6251	KSSQSLLNARTGKNYLA	ADI-29610 SAD6444_P02_D06	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 391	6252	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29610 SAD6444_P02_D06	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 391	6253	WASTRES	ADI-29610 SAD6444_P02_D06	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 391	6254	TGGGCATCTACCCGGGAATCC	ADI-29610 SAD6444_P02_D06	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 391	6255	KQSYSRRT	ADI-29610 SAD6444_P02_D06	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 391	6256	AAGCAATCTTATTCTCGGAGAACT	ADI-29610 SAD6444_P02_D06	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 392	6257	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATCGGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29611 SAD6444_P02_D04	Heavy chain variable region ("HC") nucleic acid sequence
Ab 392	6258	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDRYGRYFYDVWGQGTLVTVSS	ADI-29611 SAD6444_P02_D04	Heavy chain variable region ("HC") amino acid sequence
Ab 392	6259	FNIKDYYMH	ADI-29611 SAD6444_P02_D04	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 392	6260	TTCAACATCAAGGACTACTATATGCAC	ADI-29611 SAD6444_P02_D04	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 392	6261	WIDLENANTIYDAKFQG	ADI-29611 SAD6444_P02_D04	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 392	6262	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29611 SAD6444_P02_D04	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 392	6263	ARDRYGRYFYDV	ADI-29611 SAD6444_P02_D04	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 392	6264	GCGAGAGATCGGTACGGGAGATATTTTTACGACGTG	ADI-29611 SAD6444_P02_D04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 392	6265	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29611 SAD6444_P02_D04	Light chain variable region("LC") nucleic acid sequence
Ab 392	6266	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29611 SAD6444_P02_D04	Light chain variable region ("LC") amino acid sequence
Ab 392	6267	KSSQSLLNARTGKNYLA	ADI-29611 SAD6444_P02_D04	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 392	6268	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29611 SAD6444_P02_D04	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 392	6269	WASTRES	ADI-29611 SAD6444_P02_D04	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 392	6270	TGGGCATCTACCCGGGAATCC	ADI-29611 SAD6444_P02_D04	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 392	6271	KQSYSRRT	ADI-29611 SAD6444_P02_D04	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 392	6272	AAGCAATCTTATTCTCGGAGAACT	ADI-29611 SAD6444_P02_D04	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 393	6273	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATTCGTACGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29613 SAD6444_P01_C03	Heavy chain variable region ("HC") nucleic acid sequence

Ab 393	6274	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDSYGRYFYDVWGQGTLVTVSS	ADI-29613 SAD6444_P01_C03	Heavy chain variable region ("HC") amino acid sequence
Ab 393	6275	FNIKDYYMH	ADI-29613 SAD6444_P01_C03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 393	6276	TTCAACATCAAGGACTACTATATGCAC	ADI-29613 SAD6444_P01_C03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 393	6277	WIDLENANTIYDAKFQG	ADI-29613 SAD6444_P01_C03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 393	6278	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29613 SAD6444_P01_C03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 393	6279	ARDSYGRYFYDV	ADI-29613 SAD6444_P01_C03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 393	6280	GCGAGAGATTCGTACGGGAGATATTTTTACGACGTG	ADI-29613 SAD6444_P01_C03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 393	6281	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29613 SAD6444_P01_C03	Light chain variable region("LC") nucleic acid sequence
Ab 393	6282	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29613 SAD6444_P01_C03	Light chain variable region ("LC") amino acid sequence
Ab 393	6283	KSSQSLLNARTGKNYLA	ADI-29613 SAD6444_P01_C03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 393	6284	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29613 SAD6444_P01_C03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 393	6285	WASTRES	ADI-29613 SAD6444_P01_C03	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 393	6286	TGGGCATCTACCCGGGAATCC	ADI-29613 SAD6444_P01_C03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 393	6287	KQSYSRRT	ADI-29613 SAD6444_P01_C03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 393	6288	AAGCAATCTTATTCTCGGAGAACT	ADI-29613 SAD6444_P01_C03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 394	6289	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACGGGAGATATCTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29614 SAD6444_P01_G03	Heavy chain variable region ("HC") nucleic acid sequence
Ab 394	6290	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVYGRYLYDVWGQGTLVTVSS	ADI-29614 SAD6444_P01_G03	Heavy chain variable region ("HC") amino acid sequence
Ab 394	6291	FNIKDYYMH	ADI-29614 SAD6444_P01_G03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 394	6292	TTCAACATCAAGGACTACTATATGCAC	ADI-29614 SAD6444_P01_G03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 394	6293	WIDLENANTIYDAKFQG	ADI-29614 SAD6444_P01_G03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 394	6294	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29614 SAD6444_P01_G03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 394	6295	ARDVYGRYLYDV	ADI-29614 SAD6444_P01_G03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 394	6296	GCGAGAGATGTGTACGGGAGATATCTTTACGACGTG	ADI-29614 SAD6444_P01_G03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 394	6297	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29614 SAD6444_P01_G03	Light chain variable region("LC") nucleic acid sequence
Ab 394	6298	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29614 SAD6444_P01_G03	Light chain variable region ("LC") amino acid sequence
Ab 394	6299	KSSQSLLNARTGKNYLA	ADI-29614 SAD6444_P01_G03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 394	6300	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29614 SAD6444_P01_G03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 394	6301	WASTRES	ADI-29614 SAD6444_P01_G03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 394	6302	TGGGCATCTACCCGGGAATCC	ADI-29614 SAD6444_P01_G03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 394	6303	KQSYSRRT	ADI-29614 SAD6444_P01_G03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 394	6304	AAGCAATCTTATTCTCGGAGAACT	ADI-29614 SAD6444_P01_G03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 395	6305	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACAGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29617 SAD6444_P01_E01	Heavy chain variable region ("HC") nucleic acid sequence

Ab 395	6306	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDVYRRYFYDVWGQGTLVTVSS	ADI-29617 SAD6444_P01_E01	Heavy chain variable region ("HC") amino acid sequence
Ab 395	6307	FNIKDYYMH	ADI-29617 SAD6444_P01_E01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 395	6308	TTCAACATCAAGGACTACTATATGCAC	ADI-29617 SAD6444_P01_E01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 395	6309	WIDLENANTIYDAKFQG	ADI-29617 SAD6444_P01_E01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 395	6310	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29617 SAD6444_P01_E01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 395	6311	ARDVYRRYFYDV	ADI-29617 SAD6444_P01_E01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 395	6312	GCGAGAGATGTGTACAGGAGATATTTTTACGACGTG	ADI-29617 SAD6444_P01_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 395	6313	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29617 SAD6444_P01_E01	Light chain variable region("LC") nucleic acid sequence
Ab 395	6314	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29617 SAD6444_P01_E01	Light chain variable region ("LC") amino acid sequence
Ab 395	6315	KSSQSLLNARTGKNYLA	ADI-29617 SAD6444_P01_E01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 395	6316	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29617 SAD6444_P01_E01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 395	6317	WASTRES	ADI-29617 SAD6444_P01_E01	Light chain variable region CDR L2 ("L2") amino acid sequence

Ab 395	6318	TGGGCATCTACCCGGGAATCC	ADI-29617 SAD6444_P01_E01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 395	6319	KQSYSRRT	ADI-29617 SAD6444_P01_E01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 395	6320	AAGCAATCTTATTCTCGGAGAACT	ADI-29617 SAD6444_P01_E01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 396	6321	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATTCAACATCAAGGACTACTATATGCACTGGGTGCGACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCGGTGTACTACTGCGTGAGAGATCTTCGGGGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29618 SAD6444_P01_A03	Heavy chain variable region ("HC") nucleic acid sequence
Ab 396	6322	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCVRDLRGRYFYDVWGQGTLVTVSS	ADI-29618 SAD6444_P01_A03	Heavy chain variable region ("HC") amino acid sequence
Ab 396	6323	FNIKDYYMH	ADI-29618 SAD6444_P01_A03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 396	6324	TTCAACATCAAGGACTACTATATGCAC	ADI-29618 SAD6444_P01_A03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 396	6325	WIDLENANTIYDAKFQG	ADI-29618 SAD6444_P01_A03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 396	6326	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGTTTCAGGGC	ADI-29618 SAD6444_P01_A03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 396	6327	VRDLRGRYFYDV	ADI-29618 SAD6444_P01_A03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 396	6328	GTGAGAGATCTTCGGGGGAGATATTTTTACGACGTG	ADI-29618 SAD6444_P01_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 396	6329	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTCACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCGGCGGAGGGACCAAGGTCGAGATCAAA	ADI-29618 SAD6444_P01_A03	Light chain variable region("LC") nucleic acid sequence
Ab 396	6330	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-29618 SAD6444_P01_A03	Light chain variable region ("LC") amino acid sequence
Ab 396	6331	KSSQSLLNARTGKNYLA	ADI-29618 SAD6444_P01_A03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 396	6332	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTTAGCT	ADI-29618 SAD6444_P01_A03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 396	6333	WASTRES	ADI-29618 SAD6444_P01_A03	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 396	6334	TGGGCATCTACCCGGGAATCC	ADI-29618 SAD6444_P01_A03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 396	6335	KQSYSRRT	ADI-29618 SAD6444_P01_A03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 396	6336	AAGCAATCTTATTCTCGGAGAACT	ADI-29618 SAD6444_P01_A03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 397	6337	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCAAGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGGTGGTTACGTATCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29716 SAD6619_P01_B03	Heavy chain variable region ("HC") nucleic acid sequence

Ab 397	6338	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSKLYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFAHWGQGTLVTVSS	ADI-29716 SAD6619_P01_B03	Heavy chain variable region ("HC") amino acid sequence
Ab 397	6339	FTFDTYAMN	ADI-29716 SAD6619_P01_B03	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 397	6340	TTCACCTTTGACACATATGCCATGAAT	ADI-29716 SAD6619_P01_B03	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 397	6341	RIRSKYNNYATYYADSVKD	ADI-29716 SAD6619_P01_B03	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 397	6342	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29716 SAD6619_P01_B03	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 397	6343	VRHGNFGGGYVSWFAH	ADI-29716 SAD6619_P01_B03	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 397	6344	GTCAGGCACGGTAACTTCGGGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-29716 SAD6619_P01_B03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 397	6345	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29716 SAD6619_P01_B03	Light chain variable region("LC") nucleic acid sequence
Ab 397	6346	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29716 SAD6619_P01_B03	Light chain variable region ("LC") amino acid sequence
Ab 397	6347	GSSTGAVTTSNYAN	ADI-29716 SAD6619_P01_B03	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 397	6348	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29716 SAD6619_P01_B03	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 397	6349	GTDKRAP	ADI-29716	Light chain variable region CDR L2 ("L2")

			SAD6619_P01_B03	amino acid sequence
Ab 397	6350	GGCACAGACAAGCGCGCTCCT	ADI-29716 SAD6619_P01_B03	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 397	6351	ALWYSNHWV	ADI-29716 SAD6619_P01_B03	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 397	6352	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29716 SAD6619_P01_B03	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 398	6353	GAGGTGCAGCTGTTGGGGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACTCGTACGTTTCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29717 SAD6619_P01_B02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 398	6354	EVQLLGSGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGTLVTVSS	ADI-29717 SAD6619_P01_B02	Heavy chain variable region ("HC") amino acid sequence
Ab 398	6355	FTFDTYAMN	ADI-29717 SAD6619_P01_B02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 398	6356	TTCACCTTTGACACATATGCCATGAAT	ADI-29717 SAD6619_P01_B02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 398	6357	RIRSKYNNYATYYADSVKD	ADI-29717 SAD6619_P01_B02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 398	6358	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29717 SAD6619_P01_B02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 398	6359	VRHGNFGNSYVSWFAH	ADI-29717 SAD6619_P01_B02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 398	6360	GTCAGGCACGGTAACTTCGGGAACTCGTACGTTTCCTGGTTTGCTCAT	ADI-29717 SAD6619_P01_B02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 398	6361	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29717 SAD6619_P01_B02	Light chain variable region("LC") nucleic acid sequence
Ab 398	6362	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29717 SAD6619_P01_B02	Light chain variable region ("LC") amino acid sequence
Ab 398	6363	GSSTGAVTTSNYAN	ADI-29717 SAD6619_P01_B02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 398	6364	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29717 SAD6619_P01_B02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 398	6365	GTDKRAP	ADI-29717 SAD6619_P01_B02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 398	6366	GGCACAGACAAGCGCGCTCCT	ADI-29717 SAD6619_P01_B02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 398	6367	ALWYSNHWV	ADI-29717 SAD6619_P01_B02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 398	6368	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29717 SAD6619_P01_B02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 399	6369	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGTGGGGGTTACGTAGCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29718 SAD6619_P04_G09	Heavy chain variable region ("HC") nucleic acid sequence

Ab 399	6370	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGGYVAWFAHWGQGTLVTVSS	ADI-29718 SAD6619_P04_G09	Heavy chain variable region ("HC") amino acid sequence
Ab 399	6371	FTFDTYAMN	ADI-29718 SAD6619_P04_G09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 399	6372	TTCACCTTTGACACATATGCCATGAAT	ADI-29718 SAD6619_P04_G09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 399	6373	RIRSKYNNYATYYADSVKD	ADI-29718 SAD6619_P04_G09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 399	6374	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29718 SAD6619_P04_G09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 399	6375	VRHGNFGGGYVAWFAH	ADI-29718 SAD6619_P04_G09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 399	6376	GTCAGGCACGGTAACTTCGGTGGGGGTTACGTAGCCTGGTTTGCTCAT	ADI-29718 SAD6619_P04_G09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 399	6377	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29718 SAD6619_P04_G09	Light chain variable region("LC") nucleic acid sequence
Ab 399	6378	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29718 SAD6619_P04_G09	Light chain variable region ("LC") amino acid sequence
Ab 399	6379	GSSTGAVTTSNYAN	ADI-29718 SAD6619_P04_G09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 399	6380	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29718 SAD6619_P04_G09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 399	6381	GTDKRAP	ADI-29718	Light chain variable region CDR L2 ("L2")

			SAD6619_P04_G09	amino acid sequence
Ab 399	6382	GGCACAGACAAGCGCGCTCCT	ADI-29718 SAD6619_P04_G09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 399	6383	ALWYSNHWV	ADI-29718 SAD6619_P04_G09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 399	6384	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29718 SAD6619_P04_G09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 400	6385	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTTTAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29719 SAD6619_P04_A09	Heavy chain variable region ("HC") nucleic acid sequence
Ab 400	6386	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKFNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQGTLVTVSS	ADI-29719 SAD6619_P04_A09	Heavy chain variable region ("HC") amino acid sequence
Ab 400	6387	FTFDTYAMN	ADI-29719 SAD6619_P04_A09	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 400	6388	TTCACCTTTGACACATATGCCATGAAT	ADI-29719 SAD6619_P04_A09	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 400	6389	RIRSKFNNYATYYADSVKD	ADI-29719 SAD6619_P04_A09	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 400	6390	AGGATTAGATCCAAGTTTAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29719 SAD6619_P04_A09	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 400	6391	VRHGNFQGGYVSWFAH	ADI-29719 SAD6619_P04_A09	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 400	6392	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-29719 SAD6619_P04_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 400	6393	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29719 SAD6619_P04_A09	Light chain variable region("LC") nucleic acid sequence
Ab 400	6394	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29719 SAD6619_P04_A09	Light chain variable region ("LC") amino acid sequence
Ab 400	6395	GSSTGAVTTSNYAN	ADI-29719 SAD6619_P04_A09	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 400	6396	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29719 SAD6619_P04_A09	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 400	6397	GTDKRAP	ADI-29719 SAD6619_P04_A09	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 400	6398	GGCACAGACAAGCGCGCTCCT	ADI-29719 SAD6619_P04_A09	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 400	6399	ALWYSNHWV	ADI-29719 SAD6619_P04_A09	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 400	6400	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29719 SAD6619_P04_A09	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 401	6401	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29720 SAD6619_P02_F12	Heavy chain variable region ("HC") nucleic acid sequence

Ab 401	6402	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNVGGGYVSWFAHWGQGTLVTVSS	ADI-29720 SAD6619_P02_F12	Heavy chain variable region ("HC") amino acid sequence
Ab 401	6403	FTFDTYAMN	ADI-29720 SAD6619_P02_F12	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 401	6404	TTCACCTTTGACACATATGCCATGAAT	ADI-29720 SAD6619_P02_F12	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 401	6405	RIRSKYNNYATYYADSVKD	ADI-29720 SAD6619_P02_F12	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 401	6406	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29720 SAD6619_P02_F12	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 401	6407	VRHGNVGGGYVSWFAH	ADI-29720 SAD6619_P02_F12	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 401	6408	GTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTGGTTTGCTCAT	ADI-29720 SAD6619_P02_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 401	6409	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29720 SAD6619_P02_F12	Light chain variable region("LC") nucleic acid sequence
Ab 401	6410	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29720 SAD6619_P02_F12	Light chain variable region ("LC") amino acid sequence
Ab 401	6411	GSSTGAVTTSNYAN	ADI-29720 SAD6619_P02_F12	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 401	6412	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29720 SAD6619_P02_F12	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 401	6413	GTDKRAP	ADI-29720	Light chain variable region CDR L2 ("L2")

			SAD6619_P02_F12	amino acid sequence
Ab 401	6414	GGCACAGACAAGCGCGCTCCT	ADI-29720 SAD6619_P02_F12	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 401	6415	ALWYSNHWV	ADI-29720 SAD6619_P02_F12	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 401	6416	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29720 SAD6619_P02_F12	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 402	6417	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29721 SAD6619_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 402	6418	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQGTLVTVSS	ADI-29721 SAD6619_P01_A02	Heavy chain variable region ("HC") amino acid sequence
Ab 402	6419	FTFDTYAMN	ADI-29721 SAD6619_P01_A02	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 402	6420	TTCACCTTTGACACATATGCCATGAAT	ADI-29721 SAD6619_P01_A02	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 402	6421	RIRSKYNNYATYYADSVKD	ADI-29721 SAD6619_P01_A02	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 402	6422	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29721 SAD6619_P01_A02	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 402	6423	VRHDNFGAGYVSWFAH	ADI-29721 SAD6619_P01_A02	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 402	6424	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCAT	ADI-29721 SAD6619_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 402	6425	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29721 SAD6619_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 402	6426	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29721 SAD6619_P01_A02	Light chain variable region ("LC") amino acid sequence
Ab 402	6427	GSSTGAVTTSNYAN	ADI-29721 SAD6619_P01_A02	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 402	6428	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29721 SAD6619_P01_A02	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 402	6429	GTDKRAP	ADI-29721 SAD6619_P01_A02	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 402	6430	GGCACAGACAAGCGCGCTCCT	ADI-29721 SAD6619_P01_A02	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 402	6431	ALWYSNHWV	ADI-29721 SAD6619_P01_A02	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 402	6432	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29721 SAD6619_P01_A02	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 403	6433	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29722 SAD6619_P01_F01	Heavy chain variable region ("HC") nucleic acid sequence

Ab 403	6434	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQGTLVTVSS	ADI-29722 SAD6619_P01_F01	Heavy chain variable region ("HC") amino acid sequence
Ab 403	6435	FTFDTYAMN	ADI-29722 SAD6619_P01_F01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 403	6436	TTCACCTTTGACACATATGCCATGAAT	ADI-29722 SAD6619_P01_F01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 403	6437	RIRSKYNNYATYYADSVKD	ADI-29722 SAD6619_P01_F01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 403	6438	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29722 SAD6619_P01_F01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 403	6439	VRHGNFGVGYVSWFAS	ADI-29722 SAD6619_P01_F01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 403	6440	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCT	ADI-29722 SAD6619_P01_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 403	6441	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29722 SAD6619_P01_F01	Light chain variable region("LC") nucleic acid sequence
Ab 403	6442	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29722 SAD6619_P01_F01	Light chain variable region ("LC") amino acid sequence
Ab 403	6443	GSSTGAVTTSNYAN	ADI-29722 SAD6619_P01_F01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 403	6444	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29722 SAD6619_P01_F01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 403	6445	GTDKRAP	ADI-29722	Light chain variable region CDR L2 ("L2")

			SAD6619_P01_F01	amino acid sequence
Ab 403	6446	GGCACAGACAAGCGCGCTCCT	ADI-29722 SAD6619_P01_F01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 403	6447	ALWYSNHWV	ADI-29722 SAD6619_P01_F01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 403	6448	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29722 SAD6619_P01_F01	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 404	6449	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGTTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29723 SAD6619_P04_G08	Heavy chain variable region ("HC") nucleic acid sequence
Ab 404	6450	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQGTLVTVSS	ADI-29723 SAD6619_P04_G08	Heavy chain variable region ("HC") amino acid sequence
Ab 404	6451	FTFDTYAMN	ADI-29723 SAD6619_P04_G08	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 404	6452	TTCACCTTTGACACATATGCCATGAAT	ADI-29723 SAD6619_P04_G08	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 404	6453	RIRSKYNNYATYYADSVKD	ADI-29723 SAD6619_P04_G08	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 404	6454	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29723 SAD6619_P04_G08	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 404	6455	VRHGNFGNYAVSWFAH	ADI-29723 SAD6619_P04_G08	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 404	6456	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTGGTTTGCTCAT	ADI-29723 SAD6619_P04_G08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 404	6457	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29723 SAD6619_P04_G08	Light chain variable region("LC") nucleic acid sequence
Ab 404	6458	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29723 SAD6619_P04_G08	Light chain variable region ("LC") amino acid sequence
Ab 404	6459	GSSTGAVTTSNYAN	ADI-29723 SAD6619_P04_G08	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 404	6460	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29723 SAD6619_P04_G08	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 404	6461	GTDKRAP	ADI-29723 SAD6619_P04_G08	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 404	6462	GGCACAGACAAGCGCGCTCCT	ADI-29723 SAD6619_P04_G08	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 404	6463	ALWYSNHWV	ADI-29723 SAD6619_P04_G08	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 404	6464	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29723 SAD6619_P04_G08	Light chain variable region CDR L3 ("L3") nucleic acid sequence
Ab 405	6465	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACACATATGCCATGAATTGGGTTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCCAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTAGCTTCGGGAACCATATTGTATCCTGGTTTGCTCATTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29724 SAD6619_P03_H01	Heavy chain variable region ("HC") nucleic acid sequence

Ab 405	6466	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGSFGNHIVSWFAHWGQGTLVTVSS	ADI-29724 SAD6619_P03_H01	Heavy chain variable region ("HC") amino acid sequence
Ab 405	6467	FTFDTYAMN	ADI-29724 SAD6619_P03_H01	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 405	6468	TTCACCTTTGACACATATGCCATGAAT	ADI-29724 SAD6619_P03_H01	Heavy chain variable region CDR H1 ("H1") nucleic acid sequence
Ab 405	6469	RIRSKYNNYATYYADSVKD	ADI-29724 SAD6619_P03_H01	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 405	6470	AGGATTAGATCCAAGTATAACAATTACGCTACATACTACGCAGACTCCGTGAAGGAT	ADI-29724 SAD6619_P03_H01	Heavy chain variable region CDR H2 ("H2") nucleic acid sequence
Ab 405	6471	VRHGSFGNHIVSWFAH	ADI-29724 SAD6619_P03_H01	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 405	6472	GTCAGGCACGGTAGCTTCGGGAACCATATTGTATCCTGGTTTGCTCAT	ADI-29724 SAD6619_P03_H01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 405	6473	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCCCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCAGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCGGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGTGCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA	ADI-29724 SAD6619_P03_H01	Light chain variable region("LC") nucleic acid sequence
Ab 405	6474	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	ADI-29724 SAD6619_P03_H01	Light chain variable region ("LC") amino acid sequence
Ab 405	6475	GSSTGAVTTSNYAN	ADI-29724 SAD6619_P03_H01	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 405	6476	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCCAAC	ADI-29724 SAD6619_P03_H01	Light chain variable region CDR L1 ("L1") nucleic acid sequence
Ab 405	6477	GTDKRAP	ADI-29724	Light chain variable region CDR L2 ("L2")

			SAD6619_P03_H01	amino acid sequence
Ab 405	6478	GGCACAGACAAGCGCGCTCCT	ADI-29724 SAD6619_P03_H01	Light chain variable region CDR L2 ("L2") nucleic acid sequence
Ab 405	6479	ALWYSNHWV	ADI-29724 SAD6619_P03_H01	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 405	6480	GCGCTGTGGTACAGTAACCATTGGGTG	ADI-29724 SAD6619_P03_H01	Light chain variable region CDR L3 ("L3") nucleic acid sequence

Table 3. Antibody sequences

Ab 406	6481	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32238	Heavy chain variable region ("HC") amino acid sequence
Ab 406	6482	**FNIKD**Y**Y**MH	ADI-32238	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 406	6483	WI**DLE**N**A**NT**I**Y**DA**KFQG	ADI-32238	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 406	6484	ARDAYGRYFYDV	ADI-32238	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 406	6485	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32238	Light chain variable region ("LC") amino acid sequence
Ab 406	6486	KSSQS**L**L**NARTG**KNYLA	ADI-32238	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 406	6487	WASTRES	ADI-32238	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 406	6488	**K**Q**S**YS**RR**T	ADI-32238	Light chain variable region CDR L3 ("L3") amino acid sequence

Ab 407	6489	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32241	Heavy chain variable region ("HC") amino acid sequence
Ab 407	6490	**FNIKD**Y**Y**MH	ADI-32241	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 407	6491	WI**DLE**N**A**NT**I**Y**DA**KFQG	ADI-32241	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 407	6492	ARDAYGRYFYDV	ADI-32241	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 407	6493	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32241	Light chain variable region ("LC") amino acid sequence
Ab 407	6494	KSSQS**L**L**NARTG**KNYLA	ADI-32241	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 407	6495	WASTRES	ADI-32241	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 407	6496	**K**Q**S**YS**RR**T	ADI-32241	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 408	6497	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32244	Heavy chain variable region ("HC") amino acid sequence
Ab 408	6498	**FNIKD**Y**Y**MH	ADI-32244	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 408	6499	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32244	Heavy chain variable region CDR H2 ("H2") amino acid sequence

Ab 408	6500	ARDAYGRYFYDV	ADI-32244	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 408	6501	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32244	Light chain variable region ("LC") amino acid sequence
Ab 408	6502	KSSQS**L**L**NARTG**KNYLA	ADI-32244	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 408	6503	WASTRES	ADI-32244	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 408	6504	**K**Q**S**YS**RR**T	ADI-32244	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 409	6505	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32247	Heavy chain variable region ("HC") amino acid sequence
Ab 409	6506	**FNIKD**Y**Y**MH	ADI-32247	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 409	6507	WI**DLE**N**A**NT**I**Y**DA**KFQG	ADI-32247	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 409	6508	ARDAYGRYFYDV	ADI-32247	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 409	6509	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK	ADI-32247	Light chain variable region ("LC") amino acid sequence
Ab 409	6510	KSSQS**L**L**NARTG**KNYLA	ADI-32247	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 409	6511	WASTRES	ADI-32247	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 409	6512	**K**Q**S**Y**FRR**T	ADI-32247	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 410	6513	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR	ADI-32250	Heavy chain variable region ("HC") amino acid

		QAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS		sequence
Ab 410	6514	**FNIKD**Y**Y**MH	ADI-32250	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 410	6515	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32250	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 410	6516	ARDAYGRYFYDV	ADI-32250	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 410	6517	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK	ADI-32250	Light chain variable region ("LC") amino acid sequence
Ab 410	6518	KSSQS**L**L**NARTG**KNYLA	ADI-32250	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 410	6519	WASTRES	ADI-32250	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 410	6520	**K**Q**S**Y**FRR**T	ADI-32250	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 411	6521	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32253	Heavy chain variable region ("HC") amino acid sequence
Ab 411	6522	**FNIKD**Y**Y**MH	ADI-32253	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 411	6523	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32253	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 411	6524	ARDAYGRYFYDV	ADI-32253	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 411	6525	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT	ADI-32253	Light chain variable region ("LC") amino acid sequence

		ISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK		
Ab 411	6526	KSSQS**L**L**NARTG**KNYLA	ADI-32253	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 411	6527	WASTRES	ADI-32253	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 411	6528	**K**Q**S**Y**FRR**T	ADI-32253	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 412	6529	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32256	Heavy chain variable region ("HC") amino acid sequence
Ab 412	6530	**FNIKD**Y**Y**MH	ADI-32256	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 412	6531	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32256	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 412	6532	ARDAYGRYFYDV	ADI-32256	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 412	6533	DIVMTQSPDSLAVSLGERATINCKSSQNLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK	ADI-32256	Light chain variable region ("LC") amino acid sequence
Ab 412	6534	KSSQ**NL**L**NARTG**KNYLA	ADI-32256	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 412	6535	WASTRES	ADI-32256	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 412	6536	**K**Q**S**Y**FRR**T	ADI-32256	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 413	6537	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32259	Heavy chain variable region ("HC") amino acid sequence

Ab 413	6538	**FNIKD**Y**Y**MH	ADI-32259	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 413	6539	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32259	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 413	6540	ARDAYGRYFYDV	ADI-32259	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 413	6541	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32259	Light chain variable region ("LC") amino acid sequence
Ab 413	6542	KSSQS**L**L**NARTG**KNYLA	ADI-32259	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 413	6543	WASTRES	ADI-32259	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 413	6544	**K**Q**S**YS**RR**T	ADI-32259	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 414	6545	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32239	Heavy chain variable region ("HC") amino acid sequence
Ab 414	6546	**FNIKD**Y**Y**MH	ADI-32239	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 414	6547	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32239	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 414	6548	ARDAYGRYFYDV	ADI-32239	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 414	6549	DIVMTQSPDSLAVSLGERATINCRSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32239	Light chain variable region ("LC") amino acid sequence
Ab 414	6550	**R**SSQS**L**L**NARTG**KNYLA	ADI-32239	Light chain variable region CDR L1 ("L1") amino acid sequence

Ab 414	6551	WASTRES	ADI-32239	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 414	6552	**K**Q**S**YS**RR**T	ADI-32239	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 415	6553	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWIGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32242	Heavy chain variable region ("HC") amino acid sequence
Ab 415	6554	**FNIKD**Y**Y**MH	ADI-32242	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 415	6555	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32242	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 415	6556	ARDAYGRYFYDV	ADI-32242	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 415	6557	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK	ADI-32242	Light chain variable region ("LC") amino acid sequence
Ab 415	6558	KSSQS**L**L**NARTG**KNYLA	ADI-32242	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 415	6559	WASTRES	ADI-32242	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 415	6560	**K**Q**S**Y**FRR**T	ADI-32242	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 416	6561	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32245	Heavy chain variable region ("HC") amino acid sequence
Ab 416	6562	**FNIKD**Y**Y**MH	ADI-32245	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 416	6563	WI**DLE**N**A**NT**I**Y**DA**KFQG	ADI-32245	Heavy chain variable region CDR H2 ("H2") amino acid sequence

Ab 416	6564	ARDAYGRYFYDV	ADI-32245	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 416	6565	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYSRRTFGGGTKVEIK	ADI-32245	Light chain variable region ("LC") amino acid sequence
Ab 416	6566	KSSQS**L**L**NARTG**KNYLA	ADI-32245	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 416	6567	WASTRES	ADI-32245	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 416	6568	**T**Q**S**YS**RR**T	ADI-32245	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 417	6569	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32248	Heavy chain variable region ("HC") amino acid sequence
Ab 417	6570	**FNIKD**Y**Y**MH	ADI-32248	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 417	6571	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32248	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 417	6572	ARDAYGRYFYDV	ADI-32248	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 417	6573	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYSRRTFGGGTKVEIK	ADI-32248	Light chain variable region ("LC") amino acid sequence
Ab 417	6574	KSSQS**L**L**NARTG**KNYLA	ADI-32248	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 417	6575	WASTRES	ADI-32248	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 417	6576	**T**Q**S**YS**RR**T	ADI-32248	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 418	6577	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR	ADI-32251	Heavy chain variable region ("HC") amino acid

		QAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS		sequence
Ab 418	6578	**FNIKD**Y**Y**MH	ADI-32251	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 418	6579	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32251	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 418	6580	ARDAYGRYFYDV	ADI-32251	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 418	6581	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCTQSYFRRTFGGGTKVEIK	ADI-32251	Light chain variable region ("LC") amino acid sequence
Ab 418	6582	KSSQS**L**L**NARTG**KNYLA	ADI-32251	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 418	6583	WASTRES	ADI-32251	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 418	6584	**T**Q**S**Y**FRR**T	ADI-32251	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 419	6585	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	ADI-32254	Heavy chain variable region ("HC") amino acid sequence
Ab 419	6586	**FNIKD**Y**Y**MH	ADI-32254	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 419	6587	WI**DLE**N**A**NT**I**Y**DA**KFQG	ADI-32254	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 419	6588	ARDAYGRYFYDV	ADI-32254	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 419	6589	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT	ADI-32254	Light chain variable region ("LC") amino acid sequence

		ISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK		
Ab 419	6590	KSSQS**L**L**NARTG**KNYLA	ADI-32254	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 419	6591	WASTRES	ADI-32254	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 419	6592	**K**Q**S**YS**RR**T	ADI-32254	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 420	6593	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32257	Heavy chain variable region ("HC") amino acid sequence
Ab 420	6594	WI**DLE**N**A**NT**I**Y**DA**KFQG	ADI-32257	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 420	6595	ARDAYGRYFYDV	ADI-32257	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 420	6596	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32257	Light chain variable region ("LC") amino acid sequence
Ab 420	6597	KSSQS**L**L**NARTG**KNYLA	ADI-32257	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 420	6598	WASTRES	ADI-32257	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 420	6599	**K**Q**S**YS**RR**T	ADI-32257	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 421	6600	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32260	Heavy chain variable region ("HC") amino acid sequence
Ab 421	6601	**FNIKD**Y**Y**MH	ADI-32260	Heavy chain variable region CDR H1 ("H1") amino acid sequence

Ab 421	6602	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32260	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 421	6603	ARDAYGRYFYDV	ADI-32260	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 421	6604	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYSRRTFGCGTKVEIK	ADI-32260	Light chain variable region ("LC") amino acid sequence
Ab 421	6605	KSSQS**L**L**NARTG**KNYLA	ADI-32260	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 421	6606	WASTRES	ADI-32260	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 421	6607	**T**Q**S**YS**RR**T	ADI-32260	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 422	6608	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32240	Heavy chain variable region ("HC") amino acid sequence
Ab 422	6609	**FNIKD**Y**Y**MH	ADI-32240	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 422	6610	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32240	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 422	6611	ARDAYGRYFYDV	ADI-32240	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 422	6612	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRTFGCGTKVEIK	ADI-32240	Light chain variable region ("LC") amino acid sequence
Ab 422	6613	KSSQS**L**L**NARTG**KNYLA	ADI-32240	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 422	6614	WASTRES	ADI-32240	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 422	6615	**K**Q**S**Y**FRR**T	ADI-32240	Light chain variable region CDR L3 ("L3") amino acid sequence

Ab 423	6616	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32243	Heavy chain variable region ("HC") amino acid sequence
Ab 423	6617	**FNIKD**Y**Y**MH	ADI-32243	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 423	6618	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32243	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 423	6619	ARDAYGRYFYDV	ADI-32243	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 423	6620	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYFRRTFGCGTKVEIK	ADI-32243	Light chain variable region ("LC") amino acid sequence
Ab 423	6621	KSSQS**L**L**NARTG**KNYLA	ADI-32243	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 423	6622	WASTRES	ADI-32243	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 423	6623	**K**Q**S**Y**FRR**T	ADI-32243	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 424	6624	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWIGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32246	Heavy chain variable region ("HC") amino acid sequence
Ab 424	6625	**FNIKD**Y**Y**MH	ADI-32246	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 424	6626	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32246	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 424	6627	ARDAYGRYFYDV	ADI-32246	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 424	6628	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA	ADI-32246	Light chain variable region ("LC") amino acid

		WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYFRRTFGCGTKVEIK		sequence
Ab 424	6629	KSSQS**L**L**NARTG**KNYLA	ADI-32246	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 424	6630	WASTRES	ADI-32246	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 424	6631	**K**Q**S**Y**FRR**T	ADI-32246	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 425	6632	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTVYDAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS	ADI-32249	Heavy chain variable region ("HC") amino acid sequence
Ab 425	6633	**FNIKD**Y**Y**MH	ADI-32249	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 425	6634	WI**DLE**N**A**NT**V**Y**DA**KFQG	ADI-32249	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 425	6635	ARDAYGRYFYDV	ADI-32249	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 425	6636	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCTQSYFRRTFGCGTKVEIK	ADI-32249	Light chain variable region ("LC") amino acid sequence
Ab 425	6637	KSSQS**L**L**NARTG**KNYLA	ADI-32249	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 425	6638	WASTRES	ADI-32249	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 425	6639	**T**Q**S**Y**FRR**T	ADI-32249	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 426	6640	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTIYNAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV	ADI-32252	Heavy chain variable region ("HC") amino acid sequence

		SS		
Ab 426	6641	**FNIKD**Y**Y**MH	ADI-32252	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 426	6642	WI**DLE**N**A**NT**I**Y**NA**KFQG	ADI-32252	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 426	6643	ARDAYGRYFYDV	ADI-32252	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 426	6644	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32252	Light chain variable region ("LC") amino acid sequence
Ab 426	6645	KSSQS**L**L**NARTG**KNYLA	ADI-32252	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 426	6646	WASTRES	ADI-32252	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 426	6647	**K**Q**S**YS**RR**T	ADI-32252	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 427	6648	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYNAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32255	Heavy chain variable region ("HC") amino acid sequence
Ab 427	6649	**FNIKD**Y**Y**MH	ADI-32255	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 427	6650	WI**DLE**N**A**NT**I**Y**NA**KFQG	ADI-32255	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 427	6651	ARDAYGRYFYDV	ADI-32255	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 427	6652	DIVMTQSPDSLAVSLGERVTINCKSSQSLLNARTGKSYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32255	Light chain variable region ("LC") amino acid sequence
Ab 427	6653	KSSQS**L**L**NARTG**K**S**YLA	ADI-32255	Light chain variable region CDR L1 ("L1") amino acid sequence

Ab 427	6654	WASTRES	ADI-32255	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 427	6655	**K**Q**S**YS**RR**T	ADI-32255	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 428	6656	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTVYNAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32258	Heavy chain variable region ("HC") amino acid sequence
Ab 428	6657	**FNIKD**Y**Y**MH	ADI-32258	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 428	6658	WI**DLE**N**A**NT**V**Y**NA**KFQG	ADI-32258	Heavy chain variable region CDR H2 ("H2") amino acid sequence
Ab 428	6659	ARDAYGRYFYDV	ADI-32258	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 428	6660	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32258	Light chain variable region ("LC") amino acid sequence
Ab 428	6661	KSSQS**L**L**NARTG**KNYLA	ADI-32258	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 428	6662	WASTRES	ADI-32258	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 428	6663	**K**Q**S**YS**RR**T	ADI-32258	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 429	6664	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTVYNAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	ADI-32261	Heavy chain variable region ("HC") amino acid sequence
Ab 429	6665	**FNIKD**Y**Y**MH	ADI-32261	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 429	6666	WI**DLE**N**A**NT**V**Y**NA**KFQG	ADI-32261	Heavy chain variable region CDR H2 ("H2") amino acid sequence

Ab 429	6667	ARDAYGRYFYDV	ADI-32261	Heavy chain variable region CDR H3 ("H3") amino acid sequence
Ab 429	6668	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYFRRTFGCGTKVEIK	ADI-32261	Light chain variable region ("LC") amino acid sequence
Ab 429	6669	KSSQS**L**L**NARTG**KNYLA	ADI-32261	Light chain variable region CDR L1 ("L1") amino acid sequence
Ab 429	6670	WASTRES	ADI-32261	Light chain variable region CDR L2 ("L2") amino acid sequence
Ab 429	6671	**K**Q**S**Y**FRR**T	ADI-32261	Light chain variable region CDR L3 ("L3") amino acid sequence

Table 4. Additional bispecific CD3 antibody sequences

Ab 430	6672	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29291	Heavy chain HC1
Ab 430	6673	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYL AWYQQKPGQSPKLLIYWTSTRKSGVPDRFSGSGSGTDFT LTISSLQAEDVAVYYCKQSFILRTFGCGTKVEIKGGGGS GGGGSGGGGSGGGGSEVQLVQSGAEVKKPGASVKVSCKA SGFTFTSYYIHWVRQAPGQCLEWIGWIYPENDNTKYNEK FKDRVTITADTSTSTAYLELSSLRSEDTAVYYCARDGYS RYYFDYWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNY	ADI-29291	Heavy chain HC2 (CD3 binder as scFv)

		KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG		
Ab 430	6674	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29291	Light chain LC
Ab 431	6675	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29292	Heavy chain HC1
Ab 431	6676	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGCGTKLTVLGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29292	Heavy chain HC2 (CD3 binder as scFv)
Ab 431	6677	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29292	Light chain LC

Ab 432	6678	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29293	Heavy chain HC1
Ab 432	6679	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQADLPAFAFGCGTKVEIKGGGGSGGGGSGGGGSGGGGSEVRLLESGGGLVQPGGSLRLSCAASGFTFSNYAMGWVRQAPGKCLEWVSAISGSGGSTYYADSVKGRFTTSRDDSKNALYLQMNSLRAEDTAVYYCARGGPGWYAADVWGQGTTVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29293	Heavy chain HC2 (CD3 binder as scFv)
Ab 432	6680	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29293	Light chain LC
Ab 433	6681	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS	ADI-29294	Heavy chain HC1

		VMHEALHNHYTQKSLSLSPG		
Ab 433	6682	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29294	Heavy chain HC2 (CD3 binder as scFv)
Ab 433	6683	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29294	Light chain LC
Ab 434	6684	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29295	Heavy chain HC1
Ab 434	6685	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW	ADI-29295	Heavy chain HC2 (CD3 binder as scFv)

		LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG		
Ab 434	6686	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29295	Light chain LC
Ab 435	6687	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29297	Heavy chain HC1
Ab 435	6688	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29297	Heavy chain HC2 (CD3 binder as scFv)
Ab 435	6689	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE	ADI-29297	Light chain LC

		VTHQGLSSPVTKSFNRGEC		
Ab 436	6690	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29298	Heavy chain HC1
Ab 436	6691	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGCGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29298	Heavy chain HC2 (CD3 binder as scFv)
Ab 436	6692	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29298	Light chain LC
Ab 437	6693	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV	ADI-29300	Heavy chain HC1

		CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG		
Ab 437	6694	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSLRTFGCGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29300	Heavy chain HC2 (CD3 binder as scFv)
Ab 437	6695	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29300	Light chain LC
Ab 438	6696	EVRLLESGGGLVQPGGSLRLSCAASGFTFSNYAMGWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTTSRDDSKNALYLQMNSLRAEDTAVYYCARGGPGWYAADVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29301	Heavy chain HC1
Ab 438	6697	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA	ADI-29301	Heavy chain HC2 (CD3 binder as scFv)

		GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG		
Ab 438	6698	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQADLPAFAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29301	Light chain LC
AB 439	6699	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29302	Heavy chain HC1
Ab 439	6700	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVLGGGGSGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29302	Heavy chain HC2 (CD3 binder as scFv)
Ab 439	6701	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS	ADI-29302	Light chain LC

		GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC		
Ab 440	6702	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29303	Heavy chain HC1
Ab 440	6703	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVLGGGGSGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFAWWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29303	Heavy chain HC2 (CD3 binder as scFv)
Ab 440	6704	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29303	Light chain LC
Ab 441	6705	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL	ADI-29304	Heavy chain HC1

		HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG		
Ab 441	6706	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGCGTKLTVLGGGGSGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29304	Heavy chain HC2 (CD3 binder as scFv)
Ab 441	6707	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29304	Light chain LC
Ab 442	6708	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29305	Heavy chain HC1
Ab 442	6709	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSDLWVFGCGTKLTVLGGGGSGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQAPGKCLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNVG	ADI-29305	Heavy chain HC2 (CD3 binder as scFv)

		GGYVSWFAHWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG		
Ab 442	6710	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	ADI-29305	Light chain LC
Ab 443	6711	EVRLLESGGGLVQPGGSLRLSCAASGFTFSNYAMGWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTTSRDDSKNALYLQMNSLRAEDTAVYYCARGGPGWYAADVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	ADI-29306	Heavy chain HC1
Ab 443	6712	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGCGTKLTVLGGGGSGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFGGYVSWFAWWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG	ADI-29306	Heavy chain HC2 (CD3 binder as scFv)
Ab 443	6713	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQADLPAFAFGGGTKVEIKRTVAAPSVFI	ADI-29306	Light chain LC

		FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC		

Further embodiments are enumerated in clauses below.

1. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said antibody displays an enhanced developability profile relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

2. The antibody according to Clause 1, wherein the enhanced developability profile is obtained by performing a PSR assay; an SCP assay; AS-CINS; a BVP assay; an ELISA; a DSF assay; a Tm assay; a HIC assay; a CIC assay; or combinations thereof.

3. An antibody comprising a CD3 binding domain, wherein said antibody displays a developability score of: between about 0 MFI and about 500 MFI; between about 0 MFI and about 450 MFI; between about 0 MFI and about 400 MFI; between about 0 MFI and about 350 MFI; between about 0 MFI and about 300 MFI; between about 0 MFI and about 250 MFI; between about 0 MFI and about 200 MFI; between about 0 MFI and about 150 MFI; between about 0 MFI and about 100 MFI; between about 0 MFI and about 50 MFI; between about 200 MFI and 500 MFI; ; between about 200 MFI and about 450 MFI; between about 200 MFI and about 400 MFI; between about 200 MFI and about 350 MFI; between about 200 MFI and about 300 MFI; between about 200 MFI and about 250 MFI; between about 100 MFI and about 450 MFI; between about 100 MFI

and about 400 MFI; between about 100 MFI and about 350 MFI; between about 100 MFI and about 300 MFI; between about 100 MFI and about 250 MFI; between about 100 MFI and about 200 MFI; or between about 100 MFI and about 150 MFI.

4. The antibody according to Clause 3, wherein the developability score is obtained by performing a PSR assay, an SCP assay AS-CINS; a BVP assay; an ELISA; a DSF assay; a Tm assay; a HIC assay; a CIC assay; or combinations thereof.

5. An antibody comprising a CD3 binding domain, wherein said antibody displays a normalized developability score of between about 0.0 and about 0.6; between about 0.0 and about 0.57; between about 0.0 and about 0.55; between about 0.0 and about 0.53; between about 0.0 and about 0.51; between about 0.0 and about 0.49; between about 0.0 and about 0.47; between about 0.0 and about 0.45; between about 0.0 and about 0.43; between about 0.0 and about 0.41; between about 0.0 and about 0.39; between about 0.0 and about 0.37; between about 0.0 and about 0.35; between about 0.0 and about 0.33; between about 0.0 and about 0.31; between about 0.0 and about 0.29; between about 0.0 and about 0.27; between about 0.0 and about 0.25; between about 0.0 and about 0.23; between about 0.0 and about 0.21; between about 0.0 and about 0.19; between about 0.0 and about 0.17; between about 0.0 and about 0.15; between about 0.0 and about 0.13; between about 0.0 and about 0.11; between about 0.0 and about 0.09; between about 0.0 and about 0.07; or between about 0.0 and about 0.05.

6. An antibody comprising a CD3 binding domain, wherein said antibody elicits T cell activation or T cell killing while displaying a decreased propensity to elicit cytokine production to levels capable of inducing cytokine release syndrome.

7. An antibody comprising a CD3 binding domain, wherein said antibody elicits T cell activation or T cell killing while displaying a decreased propensity to elicit cytokine production to levels capable of inducing cytokine release relative to that observed one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

8. The antibody of Clause 6 or Clause 7, wherein the T cell activation, T cell killing, and/or cytokine production is assessed by performing a cell-based assay.

9. The antibody of Clause 8, wherein the T cell activation, T cell killing, and/or cytokine production is assessed by performing a T-cell activation assay, a T cell redirected target cell killing assay, and cytokine production level assay, wherein each assay comprises incubating PBMCs with the antibody.

10. The antibody of Clause 9, wherein the T cell redirected target cell killing assay further comprises incubating the PBMCs and the antibody with target cells expressing a target antigen other than CD3.

11. The antibody of any one of Clauses 6 through 10, wherein at least one cytokine for which cytokine production levels are measured is selected from the group consisting of: Interleukin 6 (IL-6); Interleukin 12 (IL-12); tumor necrosis factor alpha (TNFa); (TGFb); Interleukin-2 (IL-2); and Interferon gamma (IFNg).

12. The antibody of any one of Clauses 6 through 11, wherein IFNg production levels are measured.

13. The antibody of any one of Clauses 6 through 13, wherein the cytokine production levels constitute a cytokine release syndrome (CRS) risk profile.

14. The antibody of any one of Clauses 6 through 13 wherein the production levels constitute a cytokine release syndrome risk profile that is indicative of decreased risk of eliciting cytokine release syndrome (CRS).

15. The antibody of any one of Clauses 6 through 14 wherein the cytokine production levels constitute a cytokine release syndrome risk profile that is indicative of decreased risk of eliciting cytokine release syndrome (CRS) when compared to the cytokine release syndrome risk profile assessed for one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

16. An antibody comprising a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH3 is not 100% identical to the CDRH3 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

17. An antibody comprising a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH2 is not 100% identical to the CDRH2 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

18. An antibody comprising a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to;

at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRH1 is not 100% identical to the CDRH1 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

19. An antibody comprising a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL3 is not 100% identical to the CDRL3 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

20. An antibody comprising a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL2 is not 100% identical to the CDRL2 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

21. An antibody comprising a CDRL1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the CDRL1 is not 100% identical to the CDRL1 of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

22. An antibody comprising a heavy chain (HC) that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; an HC selected from the group consisting of the HCs of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the HC is not 100% identical to the HC of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

23. An antibody comprising a light chain (LC) that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; an LC selected from the group consisting of the LCs of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the LC is not 100% identical to the LC of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

24. An antibody comprising:

A) a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

B) a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and

C) a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; with the proviso that the neither the CDRH3, CDRH2, nor the CHRH1 is 100% identical to the CHRH3, CDRH2, or CDRH1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

25. An antibody comprising:

A) a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

B) a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and

C) a CDRL1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

with the proviso that the neither the CDRL3, CDRL2, nor the CHRL1 is 100% identical to the CHRL3, CDRL2, or CDRL1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

26. An antibody comprising:

A) a CDRH3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH3 selected from the group consisting of the CDRH3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

B) a CDRH2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH2 selected from the group consisting of the CDRH2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

C) a CDRH1 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRH1 selected from the group consisting of the CDRH1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

D) a CDRL3 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to;

at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL3 selected from the group consisting of the CDRL3s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

E) a CDRL2 that is: 100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL2 selected from the group consisting of the CDRL2s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2; and

F) a CDRL1 that is:100% identical to; at least 99% identical to; at least 98% identical to; at least 97% identical to; at least 96% identical to; at least 95% identical to; at least 94% identical to; at least 93% identical to; at least 92% identical to; at least 91% identical to; at least 90% identical to; at least 89% identical to; at least 88% identical to; at least 87% identical to; at least 86% identical to; at least 85% identical to; at least 84% identical to; at least 83% identical to; at least 82% identical to; or at least 80% identical to; a CDRL1 selected from the group consisting of the CDRL1s of Mabs 1 through 21, 23 through 222, 224 through 363, and 371 through 405 as provided in Table 2;

with the proviso that the neither the CDRH3, CDRH2, CDRH1, CDRL3, CDHL2, nor the CHRL1 is 100% identical to the CHRH3, CDRH2, CDRH1, CDRL3, CDHL2, or the CDRL1, respectively, of any of Mabs 223, 364, 365, 366, 367, 368, 369, or 370 as provided in Table 2.

27. An antibody according to any one of Clauses 16 through 26, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain.

28. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-15512; ADI-15516; and ADI-16513; as provided in Table 2.

29. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-18562; ADI-18564; ADI-18565; ADI-18566; ADI-18567; ADI-18568; ADI-18570; ADI-18571; ADI-18572; ADI-18573; ADI-18563; ADI-18569; ADI-18574; ADI-18575; ADI-18576; ADI-18578; ADI-18579; ADI-18580; ADI-18581; ADI-18582; ADI-18584; ADI-18585; ADI-18577; ADI-18583; ADI-18588; ADI-18589; ADI-18590; ADI-18591; ADI-18593; ADI-18594; ADI-18595; ADI-18596; ADI-18597; ADI-18592; ADI-18587; ADI-18586; and; ADI-16606; as provided in Table 2.

30. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-18576; ADI-20820; ADI-20578; ADI-20571; ADI-21097; ADI-20577; ADI-20576; ADI-20568; ADI-20582; ADI-20575; ADI-20567; ADI-20574; ADI-20573; ADI-20579; ADI-18565; ADI-20818; ADI-20587; ADI-20588; ADI-20589; ADI-20590; ADI-20594; ADI-20596; ADI-20599; ADI-20605; ADI-20607; ADI-20608; and ADI-20609; as provided in Table 2.

31. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-16606; ADI-20587; ADI-20607; ADI-20590; ADI-28708; ADI-28709; ADI-28710; ADI-21943; ADI-28711; ADI-28712; ADI-28713; ADI-28714; ADI-28715; ADI-21944; ADI-28716; ADI-21945; ADI-21946; ADI-28717; ADI-21947; ADI-28718; ADI-28719; ADI-28720; ADI-28721; ADI-28722; ADI-28723; ADI-28724; ADI-28725; ADI-28726; ADI-28727; ADI-28728; ADI-28729; ADI-28730; ADI-28731; ADI-28732; ADI-28733; ADI-28734; ADI-28735; ADI-28736; ADI-28737; ADI-28738;

ADI-28739; ADI-28740; ADI-28741; ADI-28742; ADI-28743; ADI-21948; ADI-21949; ADI-28744; ADI-21950; ADI-28745; ADI-28746; ADI-28747; ADI-28748; ADI-21951; ADI-21952; ADI-28749; ADI-28750; ADI-28751; ADI-21953; ADI-28752; ADI-21954; ADI-28753; ADI-28754; ADI-28755; ADI-28756; ADI-28757; ADI-28758; ADI-28759; ADI-28760; ADI-28761; ADI-28762; ADI-28763; ADI-28764; ADI-28765; ADI-28766; ADI-28767; ADI-28768; ADI-21955; ADI-28769; ADI-28770; ADI-21956; ADI-28771; ADI-28772; ADI-28773; ADI-28774; and ADI-28775; as provided in Table 2.

32. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-21959; ADI-21963; ADI-21965; ADI-21967; ADI-21970; ADI-21971; ADI-21972; ADI-21973; ADI-21974; ADI-21975; ADI-21976; ADI-21977; ADI-21978; ADI-21979; ADI-21943; ADI-21944; ADI-21945; ADI-21946; ADI-21947; ADI-21948; ADI-21949; ADI-21950; ADI-21951; ADI-21952; ADI-21953; ADI-21954; ADI-21955; and ADI-21956; as provided in Table 2.

33. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-21952; ADI-22523; ADI-24403; ADI-24404; ADI-24405; ADI-24407; ADI-24408; ADI-24409; ADI-24410; ADI-24411; ADI-24412; ADI-24413; ADI-24414; ADI-24415; ADI-24416; ADI-24417; ADI-24418; ADI-24434; ADI-24435; ADI-24436; ADI-24437; ADI-24438; ADI-24439; ADI-24440; ADI-24441; ADI-24442; ADI-24443; ADI-24444; ADI-24445; ADI-24446; ADI-24449; ADI-24388; ADI-24389; ADI-24390; ADI-24391; ADI-24392; ADI-24393; ADI-24394; ADI-24395; ADI-24396; ADI-24397; ADI-24398; ADI-24399; ADI-24400; ADI-24401; ADI-24402; ADI-24419; ADI-24420; ADI-24421; ADI-24422; ADI-24423; ADI-24424; ADI-24425; ADI-24426; ADI-24427; ADI-24428; ADI-24429; ADI-24430; ADI-24431; ADI-24432; ADI-24433; ADI-24447; and ADI-24448; as provided in Table 2.

34. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-23652; ADI-23653; ADI-23654; ADI-23655; ADI-23656; ADI-23657; ADI-23658; ADI-23651; ADI-23644; ADI-23645; ADI-23646; ADI-23647; ADI-23648; ADI-23649; ADI-23650; ADI-23667; ADI-23668; ADI-23669; ADI-23670; ADI-23671; ADI-23672; ADI-23673; ADI-23659; ADI-23660; ADI-23661; ADI-23663; ADI-23664; ADI-23639; ADI-23641; ADI-23642; ADI-23640; ADI-23643; ADI-21952; ADI-23633; ADI-23634; ADI-23635; ADI-23636; ADI-23637; ADI-23638; ADI-23632; and ADI-23629; as provided in Table 2.

35. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26909; ADI-26910; ADI-26912; ADI-26913; ADI-26915; ADI-26916; ADI-26917; ADI-26918; ADI-26919; ADI-26920; ADI-26921; ADI-26924; ADI-26925; ADI-26927; ADI-26928; ADI-26929; ADI-26930; ADI-26932; ADI-26933; ADI-26938; ADI-26939; ADI-26940; ADI-26941; ADI-26942; ADI-26943; ADI-26944; ADI-26945; ADI-26950; ADI-26954; ADI-23672; ADI-23673; ADI-23664; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26968; ADI-26969; ADI-26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; ADI-26994; and ADI-26995; as provided in Table 2.

36. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26910; ADI-26913; ADI-26915; ADI-26919; ADI-26920; ADI-26921;

ADI-26943; ADI-26954; ADI-21952; ADI-26955; ADI-26956; ADI-26962; ADI-26978; ADI-26983; and ADI-26994; as provided in Table 2.

37. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: ADI-15512; ADI-16513; ADI-15516; ADI-18565; ADI-18589; ADI-18585; ADI-18590; ADI-18576; ADI-20568; ADI-20580; ADI-21978; ADI-22523; ADI-25133; and ADI-26906.

38. An antibody according to any one of Clauses 16 through 27, wherein the antibody comprises an anti-cluster of differentiation three (CD3) binding domain that is selected from the group consisting of: ADI-16606; ADI-29601; ADI-29602; ADI-29603; ADI-20587; ADI-20607; ADI-20590; ADI-21952; ADI-23633; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26961; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26967; ADI-26968; ADI-26969; ADI-26970; ADI-26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; and ADI-26994.

39. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-15512; ADI-15516; and ADI-16513; as provided in Table 2.

40. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-18562; ADI-18564; ADI-18565; ADI-18566; ADI-18567; ADI-18568; ADI-18570; ADI-18571; ADI-18572; ADI-18573; ADI-18563; ADI-18569; ADI-18574;

ADI-18575; ADI-18576; ADI-18578; ADI-18579; ADI-18580; ADI-18581; ADI-18582; ADI-18584; ADI-18585; ADI-18577; ADI-18583; ADI-18588; ADI-18589; ADI-18590; ADI-18591; ADI-18593; ADI-18594; ADI-18595; ADI-18596; ADI-18597; ADI-18592; ADI-18587; ADI-18586; and; ADI-16606; as provided in Table 2.

41. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-18576; ADI-20820; ADI-20578; ADI-20571; ADI-21097; ADI-20577; ADI-20576; ADI-20568; ADI-20582; ADI-20575; ADI-20567; ADI-20574; ADI-20573; ADI-20579; ADI-18565; ADI-20818; ADI-20587; ADI-20588; ADI-20589; ADI-20590; ADI-20594; ADI-20596; ADI-20599; ADI-20605; ADI-20607; ADI-20608; and ADI-20609; as provided in Table 2.

42. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-16606; ADI-20587; ADI-20607; ADI-20590; ADI-28708; ADI-28709; ADI-28710; ADI-21943; ADI-28711; ADI-28712; ADI-28713; ADI-28714; ADI-28715; ADI-21944; ADI-28716; ADI-21945; ADI-21946; ADI-28717; ADI-21947; ADI-28718; ADI-28719; ADI-28720; ADI-28721; ADI-28722; ADI-28723; ADI-28724; ADI-28725; ADI-28726; ADI-28727; ADI-28728; ADI-28729; ADI-28730; ADI-28731; ADI-28732; ADI-28733; ADI-28734; ADI-28735; ADI-28736; ADI-28737; ADI-28738; ADI-28739; ADI-28740; ADI-28741; ADI-28742; ADI-28743; ADI-21948; ADI-21949; ADI-28744; ADI-21950; ADI-28745; ADI-28746; ADI-28747; ADI-28748; ADI-21951; ADI-21952; ADI-28749; ADI-28750; ADI-28751; ADI-21953; ADI-28752; ADI-21954; ADI-28753; ADI-28754; ADI-28755; ADI-28756; ADI-28757; ADI-28758; ADI-28759; ADI-28760; ADI-28761; ADI-28762; ADI-28763; ADI-28764; ADI-28765; ADI-28766; ADI-28767; ADI-28768; ADI-21955; ADI-28769; ADI-28770; ADI-21956; ADI-28771; ADI-28772; ADI-28773; ADI-28774; and ADI-28775; as provided in Table 2.

43. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-21959; ADI-21963; ADI-21965; ADI-21967; ADI-21970; ADI-21971; ADI-21972; ADI-21973; ADI-21974; ADI-21975; ADI-21976; ADI-21977; ADI-21978; ADI-21979; ADI-21943; ADI-21944; ADI-21945; ADI-21946; ADI-21947; ADI-21948; ADI-21949; ADI-21950; ADI-21951; ADI-21952; ADI-21953; ADI-21954; ADI-21955; and ADI-21956; as provided in Table 2.

44. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-21952; ADI-22523; ADI-24403; ADI-24404; ADI-24405; ADI-24407; ADI-24408; ADI-24409; ADI-24410; ADI-24411; ADI-24412; ADI-24413; ADI-24414; ADI-24415; ADI-24416; ADI-24417; ADI-24418; ADI-24434; ADI-24435; ADI-24436; ADI-24437; ADI-24438; ADI-24439; ADI-24440; ADI-24441; ADI-24442; ADI-24443; ADI-24444; ADI-24445; ADI-24446; ADI-24449; ADI-24388; ADI-24389; ADI-24390; ADI-24391; ADI-24392; ADI-24393; ADI-24394; ADI-24395; ADI-24396; ADI-24397; ADI-24398; ADI-24399; ADI-24400; ADI-24401; ADI-24402; ADI-24419; ADI-24420; ADI-24421; ADI-24422; ADI-24423; ADI-24424; ADI-24425; ADI-24426; ADI-24427; ADI-24428; ADI-24429; ADI-24430; ADI-24431; ADI-24432; ADI-24433; ADI-24447; and ADI-24448; as provided in Table 2.

45. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-23652; ADI-23653; ADI-23654; ADI-23655; ADI-23656; ADI-23657; ADI-23658; ADI-23651; ADI-23644; ADI-23645; ADI-23646; ADI-23647; ADI-23648; ADI-23649; ADI-23650; ADI-23667; ADI-23668; ADI-23669; ADI-23670; ADI-23671; ADI-23672; ADI-23673; ADI-23659; ADI-23660; ADI-23661; ADI-23663; ADI-23664; ADI-23639; ADI-23641; ADI-23642; ADI-23640; ADI-23643; ADI-21952; ADI-23633; ADI-23634; ADI-23635; ADI-23636; ADI-23637; ADI-23638; ADI-23632; and ADI-23629; as provided in Table 2.

46. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26909; ADI-26910; ADI-26912; ADI-26913; ADI-26915; ADI-26916; ADI-26917; ADI-26918; ADI-26919; ADI-26920; ADI-26921; ADI-26924; ADI-26925; ADI-26927; ADI-26928; ADI-26929; ADI-26930; ADI-26932; ADI-26933; ADI-26938; ADI-26939; ADI-26940; ADI-26941; ADI-26942; ADI-26943; ADI-26944; ADI-26945; ADI-26950; ADI-26954; ADI-23672; ADI-23673; ADI-23664; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26968; ADI-26969; ADI-26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; ADI-26994; and ADI-26995; as provided in Table 2.

47. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: the CD3 binding domains of ADI-22523; ADI-26906; ADI-26907; ADI-26908; ADI-26910; ADI-26913; ADI-26915; ADI-26919; ADI-26920; ADI-26921; ADI-26943; ADI-26954; ADI-21952; ADI-26955; ADI-26956; ADI-26962; ADI-26978; ADI-26983; and ADI-26994; as provided in Table 2.

48. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: ADI-15512; ADI-16513; ADI-15516; ADI-18565; ADI-18589; ADI-18585; ADI-18590; ADI-18576; ADI-20568; ADI-20580; ADI-21978; ADI-22523; ADI-25133; and ADI-26906.

49. An antibody comprising an anti-cluster of differentiation three (CD3) binding domain, wherein said CD3 binding domain is selected from the group consisting of: ADI-16606; ADI-29601; ADI-29602; ADI-29603; ADI-20587; ADI-20607;

ADI-20590; ADI-21952; ADI-23633; ADI-26955; ADI-26956; ADI-26957; ADI-26958; ADI-26959; ADI-26960; ADI-26961; ADI-26962; ADI-26963; ADI-26964; ADI-26965; ADI-26966; ADI-26967; ADI-26968; ADI-26969; ADI-26970; ADI-26971; ADI-26972; ADI-26973; ADI-26974; ADI-26975; ADI-26976; ADI-26977; ADI-26978; ADI-26979; ADI-26980; ADI-26981; ADI-26982; ADI-26983; ADI-26984; ADI-26985; ADI-26986; ADI-26987; ADI-26988; ADI-26989; ADI-26990; ADI-26991; ADI-26992; ADI-26993; and ADI-26994.

50. An antibody according to any one of Clauses 1 through 49, wherein the antibody displays a decreased propensity for degradation relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

51. An antibody according to any one of Clauses 16 through 49, wherein the antibody displays a decreased CRS risk profile relative to one or more of: trastuzumab; (Herceptin®); lintuzumab; blinatumomab (Blincyto®); and Mab 364, Mab366, Mab 367, Mab 368, Mab 369, Mab 370, or Mab 22, as provided in Table 2.

52. An antibody according to any one of Clauses 1 through 51, wherein the antibody comprises a multispecific antibody.

53. An antibody according to any one of Clauses 1 through 52, wherein the antibody comprises a bispecific antibody.

54. An antibody according to any one of Clauses 1 through 53, wherein the antibody comprises at least a second antigen binding domain that specifically binds to an oncology target; an immune-oncology target; a neurodegenerative disease targets; an autoimmune disorder target; an infectious disease target; a metabolic disease target; a cognitive disorder target; a blood-brain barrier target; or a blood disease target.

55. An antibody according to any one of Clauses 1 through 54, wherein the antibody comprises at least a second antigen binding domain that specifically binds to an antigen selected from the group consisting of: 17-IA, 4-1BB, 4Dc, 6- keto-PGFla, 8-iso-PGF2a, 8-oxo-dG, Al Adenosine Receptor, A33, ACE, ACE-2, Activin, Activin A, Activin AB, Activin B, Activin C, Activin RIA, Activin RIA ALK-2, Activin RIB ALK-4, Activin RIIA, Activin RUB, ADAM, ADAM10, ADAM12, ADAM15, ADAM17/TACE, ADAM8, ADAM9, ADAMTS, ADAMTS4, ADAMTS5, Addressins, aFGF, ALCAM, ALK, ALK-1, ALK-7, alpha-l-antitrypsin, alpha-V/beta-1 antagonist, ANG, Ang, APAF-1, APE, APJ, APP, APRIL, AR, ARC, ART, Artemin, anti-Id, ASPARTIC, Atrial natriuretic factor, av/b3 integrin, Axl, b2M, B7-1, B7-2, B7-H, B-lymphocyte Stimulator (BlyS), BACE, BACE-1, Bad, BAFF, BAFF-R, Bag-1, BAK, Bax, BCA-1, BCAM, Bel, BCMA, BDNF, b-ECGF, bFGF, BID, Bik, BIM, BLC, BL-CAM, BLK, BMP, BMP-2 BMP-2a, BMP-3 Osteogenin, BMP-4 BMP-2b, BMP-5, BMP-6 Vgr-1, BMP-7 (OP-1), BMP-8 (BMP-8a, OP-2), BMPR, BMPR-IA (ALK-3), BMPR-IB (ALK-6), BRK-2, RPK-1, BMPR-II (BRK-3), BMPs, b- NGF, BOK, Bombesin, Bone-derived neurotrophic factor, BPDE, BPDE-DNA, BTC, complement factor 3 (C3), C3a, C4, C5, C5a, CIO, CA125, CAD-8, Calcitonin, cAMP, carcinoembryonic antigen (CEA), carcinoma-associated antigen, Cathepsin A, Cathepsin B, Cathepsin C/DPPI, Cathepsin D, Cathepsin E, Cathepsin H, Cathepsin L, Cathepsin O, Cathepsin S, Cathepsin V, Cathepsin X/Z/P, CBL, CCI, CCK2, CCL, CCLl, CCLll, CCL12, CCL13, CCL 14, CCL15, CCL16, CCLl 7, CCL18, CCL19, CCL2, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CCL3, CCL4, CCL5, CCL6, CCL7, CCL8, CCL9/10, CCR, CCR1, CCR10, CCR10, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CD1, CD2, CD4, CD5, CD6, CD7, CD8, CD10, CDlla, CDllb, CDllc, CD13, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD27L, CD28, CD29, CD30, CD30L, CD32, CD33 (p67 proteins), CD34, CD38, CD40, CD40L, CD44, CD45, CD46, CD49a, CD52, CD54, CD55, CD56, CD61, CD64, CD66e, CD74, CD80 (B7-1), CD89, CD95, CD123, CD137, CD138, CD140a, CD146, CD147, CD148, CD152, CD164, CEACAM5, CFTR, cGMP, CINC, Clostridium botulinum toxin, Clostridium perfringens toxin, CKb8-l, CLC, CMV, CMV UL, CNTF, CNTN-1, COX, C-Ret, CRG-2, CT-1, CTACK, CTGF, CTLA-4, CX3CL1, CX3CR1, CXCL, CXCLl, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9,

CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CXCR, CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, cytokeratin tumor-associated antigen, DAN, DCC, DcR3, DC-SIGN, Decay accelerating factor, des(l-3)-IGF-I (brain IGF-1), Dhh, digoxin, DNAM-1, Dnase, Dpp, DPPIV/CD26, Dtk, ECAD, EDA, EDA-A1, EDA-A2, EDAR, EGF, EGFR (ErbB-1), EMA, EMMPRIN, EN A, endothelin receptor, Enkephalinase, eNOS, Eot, eotaxinl, EpCAM, Ephrin B2/ EphB4, EPO, ERCC, E-selectin, ET-1, Factor Ila, Factor VII, Factor VIIIc, Factor IX, fibroblast activation protein (FAP), Fas, FcRl, FEN-1, Ferritin, FGF, FGF-19, FGF-2, FGF3, FGF-8, FGFR, FGFR-3, Fibrin, FL, FLIP, Flt-3, Flt-4, Follicle stimulating hormone, Fractalkine, FZD1, FZD2, FZD3, FZD4, FZD5, FZD6, FZD7, FZD8, FZD9, FZD10, G250, Gas 6, GCP-2, GCSF, GD2, GD3, GDF, GDF-1, GDF-3 (Vgr-2), GDF-5 (BMP-14, CDMP- 1), GDF-6 (BMP-13, CDMP-2), GDF-7 (BMP-12, CDMP-3), GDF-8 (Myostatin), GDF-9, GDF- 15 (MIC-1), GDNF, GFAP, GFRa-1, GFR-alphal, GFR-alpha2, GFR-alpha3, GITR, Glucagon, Glut 4, glycoprotein Ilb/IIIa (GP Ilb/IIIa), GM-CSF, gpl30, gp72, GRO, Growth hormone releasing factor, Hapten (NP-cap or NIP-cap), HB-EGF, HCC, HCMV gB envelope glycoprotein, HCMV) gH envelope glycoprotein, HCMV UL, Hemopoietic growth factor (HGF), Hep B gpl20, heparanase, Her2, Her2/neu (ErbB-2), Her3 (ErbB-3), Her4 (ErbB-4), herpes simplex virus (HSV) gB glycoprotein, HSV gD glycoprotein, HGFA, High molecular weight melanoma-associated antigen (HMW-MAA), HIV gpl20, HIV IIIB gp 120 V3 loop, HLA, HLA-DR, HM1.24, HMFG PEM, HRG, Hrk, human cardiac myosin, human cytomegalovirus (HCMV), human growth hormone (HGH), HVEM, 1-309, IAP, ICAM, ICAM-1, ICAM-3, ICE, ICOS, IFNg, Ig, IgA receptor, IgE, IGF, IGF binding proteins, IGF-1R, IGFBP, IGF-I, IGF-II, IL, IL-1, IL-1R, IL-2, IL-2R, IL-4, IL-4R, IL-5, IL-5R, IL-6, IL-6R, IL-8, IL- 9, IL-10, IL-12, IL-13, IL-15, IL-18, IL-18R, IL-23, interferon (INF)-alpha, INF-beta, INF- gamma, Inhibin, iNOS, Insulin A-chain, Insulin B-chain, Insulin-like growth factor 1, integrin alpha2, integrin alpha3, integrin alpha4, integrin alpha4/betal, integrin, alpha4/beta7, integrin alpha5 (alphaV), integrin alpha5/betal, integrin alpha5/beta3, integrin alpha6, integrin betal, integrin beta2, interferon gamma, IP-10, 1-TAC, JE, Kallikrein 2, Kallikrein 5, Kallikrein 6, , Kallikrein 11, Kallikrein 12, Kallikrein 14, Kallikrein 15, Kallikrein LI, Kallikrein L2, Kallikrein L3, Kallikrein L4, KC, KDR, Keratinocyte Growth Factor (KGF), laminin 5, LAMP, LAP, LAP (TGF- 1), Latent

TGF-1, Latent TGF-1 bpl, LBP, LDGF, LECT2, Lefty, Lewis-Y antigen, Lewis-Y related antigen, LFA-1, LFA-3, Lfo, LIF, LIGHT, lipoproteins, LIX, LKN, Lptn, L-Selectin, LT-a, LT-b, LTB4, LTBP-1, Lung surfactant, Luteinizing hormone, Lymphotoxin Beta Receptor, Mac-1, MAdCAM, MAG, MAP2, MARC, MCAM, MCAM, MCK-2, MCP, M-CSF, MDC, Mer, METALLOPROTEASES, MGDF receptor, MGMT, MHC (HLA-DR), MIF, MIG, MIP, MIP-1-alpha, MK, MMAC1, MMP, MMP-1, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-2, MMP-24, MMP- 3, MMP-7, MMP-8, MMP-9, MPIF, Mpo, MSK, MSP, mucin (Mucl), MUC18, Muellerian- inhibiting substance, Mug, MuSK, NAIP, NAP, NCAD, N-Cadherin, NCA 90, NCAM, NCAM, Neprilysin, Neurotrophin-3,-4, or -6, Neurturin, Neuronal growth factor (NGF), NGFR, NGF-beta, nNOS, NO, NOS, Npn, NRG-3, NT, NTN, OB, OGG1, OPG, OPN, OSM, OX40L, OX40R, pl50, p95, PADPr, Parathyroid hormone, PARC, PARP, PBR, PBSF, PCAD, P-Cadherin, PCNA, PDGF, PDGF, PDK-1, PECAM, PEM, PF4, PGE, PGF, PGI2, PGJ2, PIN, PLA2, placental alkaline phosphatase (PLAP), P1GF, PLP, PP14, Proinsulin, Prorelaxin, Protein C, PS, PSA, PSCA, prostate specific membrane antigen (PSMA), PTEN, PTHrp, Ptk, PTN, R51, RANK, RANKL, RANTES, Relaxin A-chain, Relaxin B-chain, renin, respiratory syncytial virus (RSV) F, RSV Fgp, Ret, Rheumatoid factors, RLIP76, RPA2, RSK, S100, SCF/KL, SDF-1, SERINE, Serum albumin, sFRP-3, Shh, SIGIRR, SK-1, SLAM, SLPI, SMAC, SMDF, SMOH, SOD, SPARC, Stat, STEAP, STEAP-II, TACE, TACI, TAG-72 (tumor- associated glycoprotein-72), TARC, TCA-3, T-cell receptors (e.g., T-cell receptor alpha/beta), TdT, TECK, TEM1, TEM5, TEM7, TEM8, TERT, testicular PLAP-like alkaline phosphatase, TfR, TGF, TGF-alpha, TGF-beta, TGF-beta Pan Specific, TGF-beta RI (ALK-5), TGF-beta RII, TGF-beta Rllb, TGF-beta RIII, TGF-betal, TGF-beta2, TGF-beta3, TGF-beta4, TGF-beta5, Thrombin, Thymus Ck-1, Thyroid stimulating hormone, Tie, TIMP, TIQ, Tissue Factor, TMEFF2, Tmpo, TMPRSS2, TNF, TNF-alpha, TNF-alpha beta, TNF-beta2, TNFc, TNF-RI, TNF-RII, TNFRSF10A (TRAIL Rl Apo-2, DR4), TNFRSFIOB (TRAIL R2 DR5, KILLER, TRICK-2A, TRICK-B), TNFRSF10C (TRAIL R3 DcRl, LIT, TRID), TNFRSF10D (TRAIL R4 DcR2, TRUNDD), TNFRSF11A (RANK ODF R, TRANCE R), TNFRSFllB (OPG OCIF, TR1), TNFRSF12 (TWEAK R FN14), TNFRSF13B (TACI), TNFRSF13C (BAFF R), TNFRSF14 (HVEM ATAR, HveA, LIGHT R, TR2), TNFRSF16 (NGFR p75NTR), TNFRSF17 (BCMA),

TNFRSF18 (GITR AITR), TNFRSF19 (TROY TAJ, TRADE), TNFRSF19L (RELT), TNFRSFIA (TNF RI CD120a, p55-60), TNFRSFIB (TNF RII CD120b, p75-80), TNFRSF26 (TNFRH3), TNFRSF3 (LTbR TNF RIII, TNFC R), TNFRSF4 (OX40 ACT35, TXGP1 R), TNFRSF5 (CD40 p50), TNFRSF6 (Fas Apo-1, APT1, CD95), TNFRSF6B (DcR3 M68, TR6), TNFRSF7 (CD27), TNFRSF8 (CD30), TNFRSF9 (4-lBB CD137, ILA), TNFRSF21 (DR6), TNFRSF22 (DcTRAIL R2 TNFRH2), TNFRST23 (DcTRAIL Rl TNFRH1), TNFRSF25 (DR3 Apo-3, LARD, TR-3, TRAMP, WSL-1), TNFSF10 (TRAIL Apo-2 Ligand, TL2), TNFSF11 (TRANCE/RANK Ligand ODF, OPG Ligand), TNFSF12 (TWEAK Apo-3 Ligand, DR3 Ligand), TNFSF13 (APRIL TALL2), TNFSF13B (BAFF BLYS, TALL1, THANK, TNFSF20), TNFSF14 (LIGHT HVEM Ligand, LTg), TNFSF15 (TL1A/VEGI), TNFSF18 (GITR Ligand AITR Ligand, TL6), TNFSFIA (TNF-a Conectin, DIF, TNFSF2), TNFSF1B (TNF-b LTa, TNFSF1), TNFSF3 (LTb TNFC, p33), TNFSF4 (OX40 Ligand gp34, TXGP1), TNFSF5 (CD40 Ligand CD154, gp39, HIGM1, IMD3, TRAP), TNFSF6 (Fas Ligand Apo-1 Ligand, APT1 Ligand), TNFSF7 (CD27 Ligand CD70), TNFSF8 (CD30 Ligand CD153), TNFSF9 (4-lBB Ligand CD137 Ligand), TP-1, t-PA, Tpo, TRAIL, TRAIL R, TRAIL-R1, TRAIL-R2, TRANCE, transferring receptor, TRF, Trk, TROP-2, TSG, TSLP, tumor-associated antigen CA 125, tumor-associated antigen expressing Lewis Y related carbohydrate, TWEAK, TXB2, Ung, uPAR, uPAR-1, Urokinase, VCAM, VCAM-1, VECAD, VE-Cadherin, VE-cadherin-2, VEFGR-1 (flt-1), VEGF, VEGFR, VEGFR-3 (flt-4), VEGI, VIM, Viral antigens, VLA, VLA-1, VLA-4, VNR integrin, von Willebrands factor, WIF- 1, WNT1, WNT2, WNT2B/13, WNT3, WNT3A, WNT4, WNT5A, WNT5B, WNT6, WNT7A, WNT7B, WNT8A, WNT8B, WNT9A, WNT9A, WNT9B, WNT10A, WNT10B, WNT11, WNT16, XCL1, XCL2, XCR1, XCR1, XEDAR, XIAP, XPD, CTLA4 (cytotoxic T lymphocyte antigen-4), PD1 (programmed cell death protein 1), PD-L1 (programmed cell death ligand 1), LAG-3 (lymphocyte activation gene-3), TIM-3 (T cell immunoglobulin and mucin protein-3), receptors for hormones, and growth factors.

56. An antibody according to any one of Clauses 1 through 55, wherein the antibody comprises at least a second antigen binding domain that specifically binds to an antigen selected from the group consisting of: BCMA, CTLA4 (cytotoxic T

lymphocyte antigen-4), PD1 (programmed cell death protein 1), PD-L1 (programmed cell death ligand 1), LAG-3 (lymphocyte activation gene-3), TIM-3, CD20, CD2, CD19, Her2, EGFR, EpCAM, FcyRIIIa (CD16), FcyRIIa (CD32a), FcyRIIb (CD32b), FcyRI (CD64), Toll-like receptors (TLRs), TLR4, TLR9, cytokines, IL-2, IL-5, IL-13, IL-6, IL-17, IL-12, IL-23, TNFa, TGFb, cytokine receptors, IL-2R, chemokines, chemokine receptors, growth factors, VEGF, and HGF.

57. An antibody according to any one of Clauses 1 through 56, wherein the antibody comprises at least a second antigen binding domain that specifically binds to an antigen, wherein said antibody comprises a multispecific format selected from the group consisting of: Fab-Fc-scFv, “bottle-opener, Mab-scFv, Mab-Fv, Dual scFv, central Fv, central scFv, one-arm central scFv, Fab-Fab, Fab-Fv, mAb-Fv, mAb-Fab, DART, BiTE, common light chain-IgG, TandAb, Cross-Mab, SEED, BEAT, TrioMab, and DuetMab.

58. An isolated nucleic acid sequence encoding an antibody according to any one of Clauses 1 through 57.

59. An expression vector comprising the isolated nucleic acid sequence according to Clause 58.

60. A host cell transfected, transformed, or transduced with a nucleic acid sequence according to Clause 58 or an expression vector according to Clause 59.

61. A pharmaceutical composition comprising: one or more of an antibody according to any one of Clauses 1 through 57; and a pharmaceutically acceptable carrier and/or excipient.

62. A pharmaceutical composition comprising: one or more nucleic acid sequences according to Clause 58; or one or more the expression vectors according to Clause 59; and a pharmaceutically acceptable carrier and/or excipient.

63. A method of treating or delaying the progression of a disorder in a mammal in need of such treating, the method comprising adimistering one or more antibodies according to any one of Clauses 1 through 57, wherein the disorder is decreased or ameliorated as a result of said administering.

64. A method of preventing or decreasing risk of developing a disorder in a mammal by administering an antibody according any one of Clauses 1 through 57, wherein the disorder is prevented as a result of said administering.

65. A method of treating a disorder in a mammal in need of such treating, wherein the disorder comprises a proliferative disorder, an oncological disorder, an immuno-oncological disorder, a neurological disorder, a neurodegenerative disorder, or an autoimmune disorder, comprising administering one or more antibodies according to any one of Clauses 1 through 57, wherein the disorder is decreased or ameliorated as a result of said administering.

66. The method according to any one of Clauses 63 through 65, wherein the method further comprises administering to the mammal an additional therapeutic agent.

67. The method according to any one of Clauses 63 through 66, wherein the mammal is a human.

68. A heterodimeric CD3 fusion protein comprising: a first polypeptide chain comprising a CD3 epsilon polypeptide fused to a first Fc region; and a second polypeptide chain comprising CD3 delta polypeptide fused to a second Fc region.

69. The heterodimeric CD3 fusion protein according to Clause 68, wherein the CD3 epsilon polypeptide comprises a human CD3 epsilon polypeptide and the CD3 delta polypeptide comprises a human CD3 delta polypeptide.

70. The heterodimeric CD3 fusion protein according to Clause 68, wherein the CD3 epsilon polypeptide is a human CD3 epsilon polypeptide and the CD3 delta polypeptide is a human CD3 delta polypeptide.

71. The heterodimeric CD3 fusion protein according to Clause 69, wherein the CD3 epsilon polypeptide comprises a cynomolgus CD3 epsilon polypeptide and the CD3 delta polypeptide comprises a cyno CD3 delta polypeptide.

72. The heterodimeric CD3 fusion protein according to Clause 69, wherein the CD3 epsilon polypeptide is a cynomolgus CD3 epsilon polypeptide and the CD3 delta polypeptide is a cyno CD3 delta polypeptide.

73. The heterodimeric fusion protein according to any one of Clauses 68 through 70, wherein the first polypeptide chain comprises the following amino acid sequence:
QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK;

and the second polypeptide chain comprises the following amino acid sequence:
FKIPIEELEDRVFVNCNTSITWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRMCQSCVELDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK.

74. The heterodimeric fusion protein according to any one of Clauses 68, 71, and 72, wherein the first polypeptide chain comprises the following amino acid sequence:

QDGNEEMGSITQTPYQVSISGTTVILTCSQHLGSEAQWQHNGKNKEDSGDRLFLPEFSEMEQSGYYVCYPRGSNPEDASHHLYLKARVCENCMEMDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK;

and the second polypeptide chain comprises the following amino acid sequence:

FKIPVEELEDRVFVKCNTSVTWVEGTVGTLLTNNTRLDLGKRILDPRGIYRCNGTDIYKDKESAVQVHYRMCQNCVELDPGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK.

75. An antibody or antigen-binding polypeptide comprising a CDRH1 comprising an amino acid sequence of FNIKDYYMH (SEQ ID NO: 6720), YTFTSYTIH (SEQ ID NO: 6721), or FTFX_1TYAMN (SEQ ID NO: 6722), wherein X_1 is any amino acid.

76. The antibody or antigen-binding polypeptide according to Clause 75, wherein X_1 is N or D.

77. An antibody or antigen-binding polypeptide comprising a CDRH2 comprising an amino acid sequence of WIDLENX_1NTX_2YDX_3KFOG (SEQ ID NO: 6723), wherein X_1, X_2, and X_3 independently are any amino acid.

78. The antibody or antigen-binding polypeptide according to Clause 77, wherein X_1 is not G.

79. The antibody or antigen binding polypeptide of any of Clauses 77-78, wherein X_2 is V or I.

80. The antibody or antigen binding polypeptide of any of Clauses 77-79, wherein X_3 is not G.

81. An antibody or antigen-binding polypeptide comprising a CDRH3 comprising an amino acid sequence of X_1QSYSX_2RT (SEQ ID NO: 6724) or X_3RDX_4YGX_5YFYDV (SEQ ID NO: 6725), wherein X_1, X_2, X_3, X_4, and X_5 are independently are any amino acid.

82. The antibody or antigen-binding polypeptide of Clause 81, wherein X_1 is K or T.

83. The antibody or antigen-binding polypeptide of Clause 81, wherein X_1 is T.

84. The antibody or antigen-binding polypeptide of any of Clauses 81-83, wherein X_2 is R or L.

85. The antibody or antigen-binding polypeptide of any of Clauses 81-83, wherein X_3 is A or G.

86. The antibody or antigen-binding polypeptide of any of Clause 81-83, wherein X_4 is not G.

87. The antibody or antigen-binding polypeptide of any of Clauses 81-86, wherein X_5 is R, A, G, or L.

88. An antibody or antigen-binding polypeptide comprising a CDRL1 comprising an amino acid sequence of X_1KSSQX_2LLX_3X_4RTGKX_5YLA (SEQ ID NO: 6726), wherein X_1, X_2, X_3, X_4, and X_5 independently are any amino acid.

89. The antibody or antigen-binding polypeptide according to Clause 88, whrein X_1 is K or R.

90. The antibody or antigen-binding polypeptide according to Clause 88, wherein X_2 is S or N

91. The antibody or antigen-binding polypeptide according to Clause 88, wherein X_3 is E or N.

92. The antibody or antigen-binding polypeptide according to Clause 88, wherein X_4 is A or S.

93. The antibody or antigen-binding polypeptide according to Clause 88, wherein X_5 is N or S.

94. An antibody or antigen-binding polypeptide comprising a CDRL2 comprising an amino acid sequence of WASTRES (SEQ ID NO: 6727) or GTX_1KRAP (SEQ ID NO: 6728), wherein X_1 is any amino acid.

95. The antibody or antigen-binding polypeptide according to Clause 94, wherein X_1 is N or D.

96. An antibody or antigen-binding polypeptide comprising a CDRL3 comprising an amino acid sequence of KQSYSX_1RT (SEQ ID NO: 6729), wherein X_1 is any amino acid.

97. The antibody or antigen-binding polypeptide according to Clause 96, wherein X_1 is R.

98. The antibody or antigen binding polypeptide according to Clause 96, wherein X_1 is L or I.

99. An antibody or antigen binding polypeptide comprising one or more of a CDRH1 according to any of Clauses 75-76, a CDRH2 according to any of Clauses 77-81, and a CDRH3 according to any of Clauses 84-90.

100. An antibody or antigen-binding polypeptide comprising one or more of a CDRL1 according to any of Clauses 88-91, a CDRL2 according to any of Clauses 94-95, and a CDRL3 according to any of Clauses 96-98.

101. An antibody or antigen-binding polypeptide comprising a CDRH1 according to any of Clauses 75-76, a CDRH2 according to any of Clauses 77-81, a CDRH3 according to any of Clauses 84-90, and a CDRL1 according to any of Clauses 88-91, a CDRL2 according to any of Clauses 94-95, and a CDRL3 according to any of Clauses 96-98.

CLAIMS

What Is Claimed Is:

1. An antibody or antigen-binding polypeptide comprising a CDRH1 comprising an amino acid sequence of FNIKDYYMH (SEQ ID NO: 6720), YTFTSYTIH (SEQ ID NO: 6721), or FTFX_1TYAMN (SEQ ID NO: 6722), wherein X_1 is any amino acid.

2. The antibody or antigen-binding polypeptide according to Claim 1, wherein X_1 is N or D.

3. An antibody or antigen-binding polypeptide comprising a CDRH2 comprising an amino acid sequence of WIDLENX_1NTX_2YDX_3KFOG (SEQ ID NO: 6723), wherein X_1, X_2, and X_3 independently are any amino acid.

4. The antibody or antigen-binding polypeptide according to Claim 3, wherein X_1 is not G.

5. The antibody or antigen binding polypeptide of any of Claims 3-4, wherein X_2 is V or I.

6. The antibody or antigen binding polypeptide of any of Claims 3-5, wherein X_3 is not G.

7. An antibody or antigen-binding polypeptide comprising a CDRH3 comprising an amino acid sequence of X_1QSYSX_2RT (SEQ ID NO: 6724) or X_3RDX_4YGX_5YFYDV (SEQ ID NO: 6725), wherein X_1, X_2, X_3, X_4, and X_5 are independently are any amino acid.

8. The antibody or antigen-binding polypeptide of Claim 7, wherein X_1 is K or T.

9. The antibody or antigen-binding polypeptide of Claim 7, wherein X_1 is T.

10. The antibody or antigen-binding polypeptide of any of Claims 7-9, wherein X_2 is R or L.

11. The antibody or antigen-binding polypeptide of any of Claims 7-9, wherein X_3 is A or G.

12. The antibody or antigen-binding polypeptide of any of Claim 7-11, wherein X_4 is not G.

13. The antibody or antigen-binding polypeptide of any of Claims 7-12, wherein X_5 is R, A, G, or L.

14. An antibody or antigen-binding polypeptide comprising a CDRL1 comprising an amino acid sequence of X_1KSSQX_2LLX_3X_4RTGKX_5YLA (SEQ ID NO: 6726), wherein X_1, X_2, X_3, X_4, and X_5 independently are any amino acid.

15. The antibody or antigen-binding polypeptide according to Claim 14, whrein X_1 is K or R.

16. The antibody or antigen-binding polypeptide according to Claim 14, wherein X_2 is S or N

17. The antibody or antigen-binding polypeptide according to Claim 14, wherein X_3 is E or N.

18. The antibody or antigen-binding polypeptide according to Claim 14, wherein X_4 is A or S.

19. The antibody or antigen-binding polypeptide according to Claim 14, wherein X_5 is N or S.

20. An antibody or antigen-binding polypeptide comprising a CDRL2 comprising an amino acid sequence of WASTRES (SEQ ID NO: 6727) or GTX_1KRAP (SEQ ID NO: 6728), wherein X_1 is any amino acid.

21. The antibody or antigen-binding polypeptide according to Claim 20, wherein X_1 is N or D.

22. An antibody or antigen-binding polypeptide comprising a CDRL3 comprising an amino acid sequence of KQSYSX_1RT (SEQ ID NO: 6729), wherein X_1 is any amino acid.

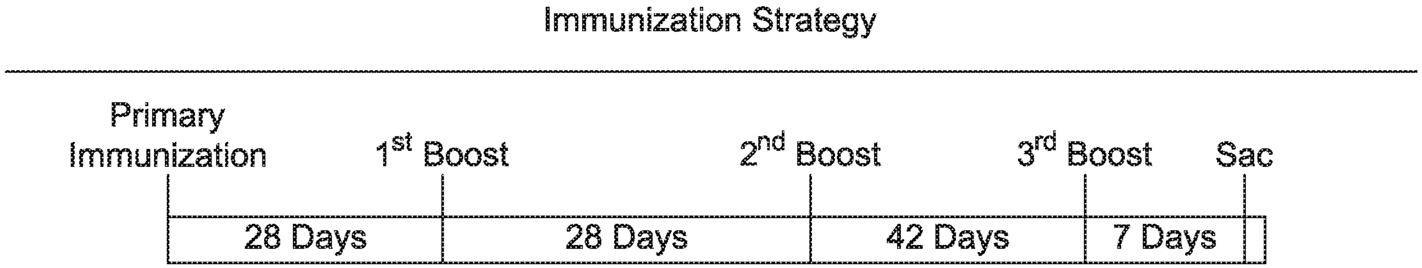
23. The antibody or antigen-binding polypeptide according to Claim 22, wherein X_1 is R.

24. The antibody or antigen binding polypeptide according to Claim 22, wherein X_1 is L or I.

25. An antibody or antigen binding polypeptide comprising one or more of a CDRH1 according to any of Claims 1-2, a CDRH2 according to any of Claims 3-6, and a CDRH3 according to any of Claims 7-13.

26. An antibody or antigen-binding polypeptide comprising one or more of a CDRL1 according to any of Claims 14-17, a CDRL2 according to any of Claims 20-21, and a CDRL3 according to any of Claims 22-24.

27. An antibody or antigen-binding polypeptide comprising a CDRH1 according to any of Claims 1-2, a CDRH2 according to any of Claims 3-6, a CDRH3 according to any of Claims 7-13, and a CDRL1 according to any of Claims 14-17, a CDRL2 according to any of Claims 20-21, and a CDRL3 according to any of Claims 22-24.



Primary Immunization: 1.0x10^6 Purified Human T Cells with Sigma Adjuvant in Each of 10 mice

1st Boost: 1.0x10^6 Purified Human T Cells with Sigma Adjuvant in Each of 10 Mice

2nd Boost: 1.5x10^6 Purified T Cells with Sigma Adjuvant; 5 of the Mice with Human T Cells, the other 5 Mice with Cynomolgus T-Cells

3rd Boost: 50 ug Denatured Cyno CD3 Protein Mixed with 7 ug N-terminal Peptide-BSA

Figure 1

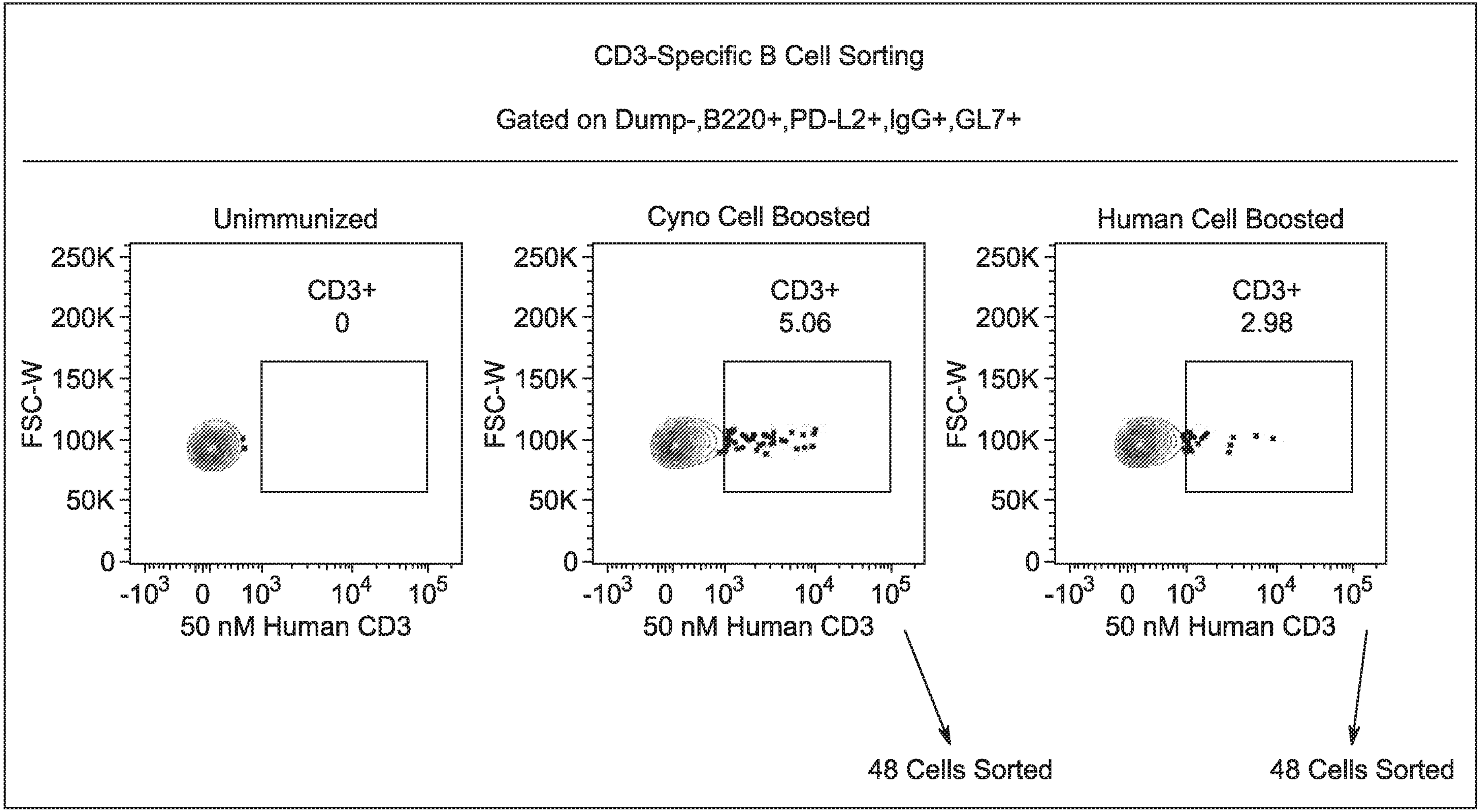

CD3-Specific B Cell Sorting
Gated on Dump-,B220+,PD-L2+,IgG+,GL7+
Unimmunized
Cyno Cell Boosted
Human Cell Boosted
FSC-W
250K
200K
150K
100K
50K
0
CD3+
0
CD3+
5.06
CD3+
2.98
-10^3
0
10^3
10^4
10^5
50 nM Human CD3
48 Cells Sorted
48 Cells Sorted

Figure 2

Efficient Amplification of Murine Heavy Chain and Light Chain Variable Genes

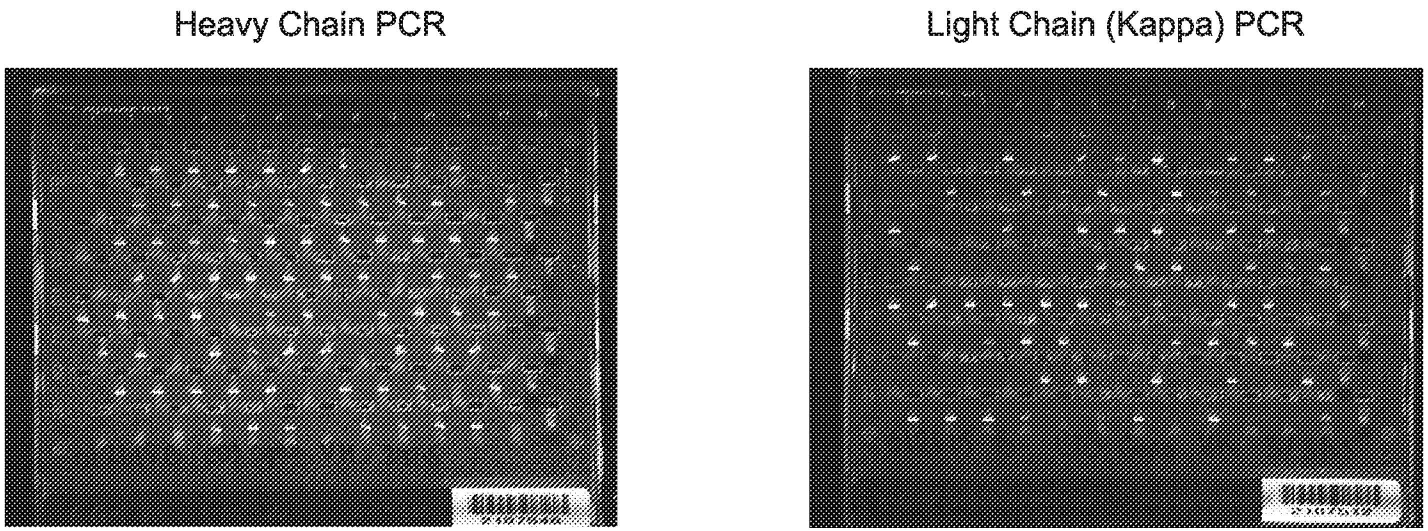


Figure 3

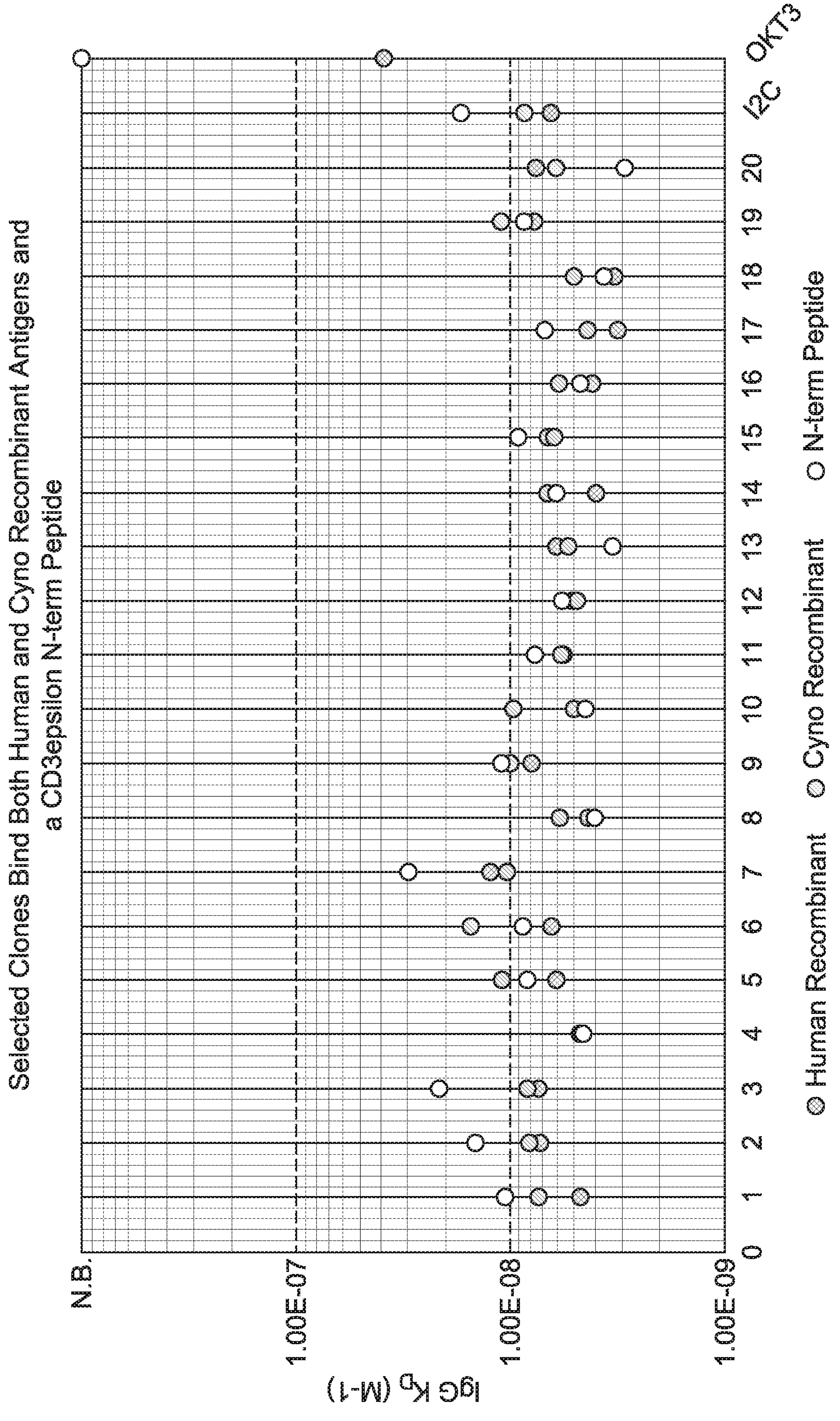

Selected Clones Bind Both Human and Cyno Recombinant Antigens and a CD3epsilon N-term Peptide
IgG K_D (M-1)
N.B.
1.00E-07
1.00E-08
1.00E-09
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
I2C
OKT3
▨ Human Recombinant
▨ Cyno Recombinant
○ N-term Peptide

Figure 4A

Clones with Related Sequences Comprise ~85% of the Binding Response

Clone ID	VH Germ line	VH CDR1	VH CDR2	VH FR3	VH CDR3	VL Germ line	VL CDR3
ADI-29538	V1-125B	YTFTTYYIH	WIYPGNVNAKYNEKFKG	KATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARDDGYYFDY	VK08-021	KQSYNLRT
ADI-29535	V1-125B	YTFTSYYIH	WIYPGNVNTKYNENFKD	KATLTADKSSSTAYMHLSSLTSEDSAVYFC	ARDDGYYFDY	VK08-021	KQSYNLRT
ADI-15505	V1-125B	YTFISYYIH	WIYPGNVNTKYNEKFKA	KATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARDDNYSFAY	VK08-021	KQSYNLRT
ADI-15506	V1-125E	YAFTSYYIH	WIYLGDGSTNYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSATYFC	ARDDSYYFDY	VK08-021	KQSYSLRT
ADI-29540	V1-125B	YTFTSYYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARDGDYFFDY	VK08-021	KQSYNLRT
ADI-29539	V1-125B	YTFTSYYIH	WIYPGNVNTQYNEKFKG	KATLTADKSSSTTYMQLSSLTSEDSAVYFC	ARDGDYYFDY	VK08-021	KQSYNLRT
ADI-15507	V1-125B	YTFTRYYIH	WIYPGNVNTKYNEKFKG	KATLSADKSSSTAYMQLSSLTSEDSAVYFC	ARDGDYYFDY	VK08-021	KQSYNLRT
ADI-15508	V1-125B	YTFTSYYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARDGDYYFDY	VK08-021	KQSYNLRT
ADI-15509	V1-125B	YTFTSYYIH	WIYPGNVNTKYNEKFKG	KATLTADTSSSTAYMQLSSLTSEDSAVYFC	ARDGNYFFDV	VK08-021	KQSYNLRT
ADI-15510	V1-125B	YTFTSYYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMQLSSLTSEDSAIYFC	ARDGNYFFDV	VK08-021	KQSYNLRT
ADI-29537	V1-125B	YTFTSYYIH	WIFPGNVNTKYNEKFKG	KATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARDGNYSFAY	VK08-021	KQSYNLRT
ADI-15511	V1-125B	NTFTSSYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTVYMQLSSLTSEDSAVYFC	ARDGSSYYFDY	VK08-021	KQSYNLRT
ADI-15512	V1-125E	YTFTSYYIH	WIYPGDGSTKYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSAIYFC	ARDGSYYFDY	VK08-021	KQSYSLRT
ADI-15515	V1-125B	YTFTSYYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTVYMQLSSLTSEDSAVYFC	ARDYGYYFDY	VK08-021	KQSYNLRT
ADI-15514	V1-125E	YTFTSYYIH	WIYPGDGSTKYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSAIYFC	ARDYGYYFDY	VK08-021	KQSYNLRT
ADI-15516	V1-125B	YTFTSSYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMHLSSLTSEDSAVYFC	ARDYGYYFDY	VK08-021	KQSYNLRT
ADI-15517	V1-125B	YTFTSYYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARDYGYYFGS	VK08-021	KQSYNLRT
ADI-16513	VH14-1	FNIKDYYMH	WIDPENGNTIYDPKFQG	KASITADTSSNTAYLQLSSLTSEDTAVYYC	ARDGYARYYFDY	VK08-021	KQSYNLRT
ADI-29536	V1-125E	YTFTNYYIH	WIYPEDGNTKYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSAIYFC	ARNNGSSYAMDY	VK08-021	KQSYNLRT
ADI-29534	V1-039A	FNIKDYYMH	WIDPENGNTIYDPKFQG	KASITADTSSNTAYLQLSSLTSEDTAVYYC	GRDGNYFFDY	VK08-021	KQSYNLRT
ADI-15518	V1-125B	YTFTSYYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTVYMQLSSLTSEDSAVYFC	GRDYYGSYYFDN	VK08-021	KQSYNLRT

Figure 4B

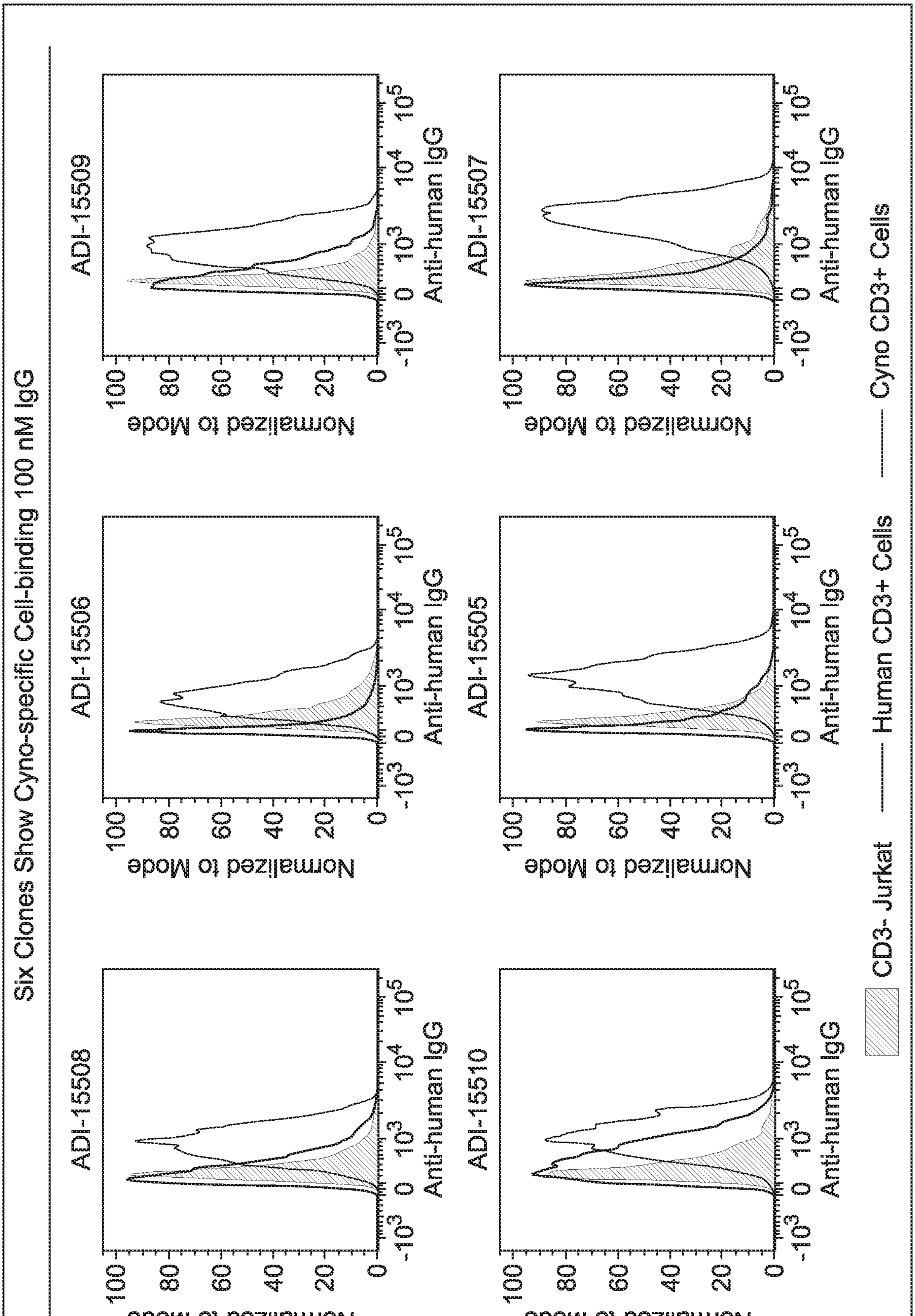

Six Clones Show Cyno-specific Cell-binding 100 nM IgG
ADI-15508
ADI-15506
ADI-15509
ADI-15510
ADI-15505
ADI-15507
Normalized to Mode
100
80
60
40
20
0
-10³
0
10³
10⁴
10⁵
Anti-human IgG
CD3- Jurkat
Human CD3+ Cells
Cyno CD3+ Cells

Figure 5

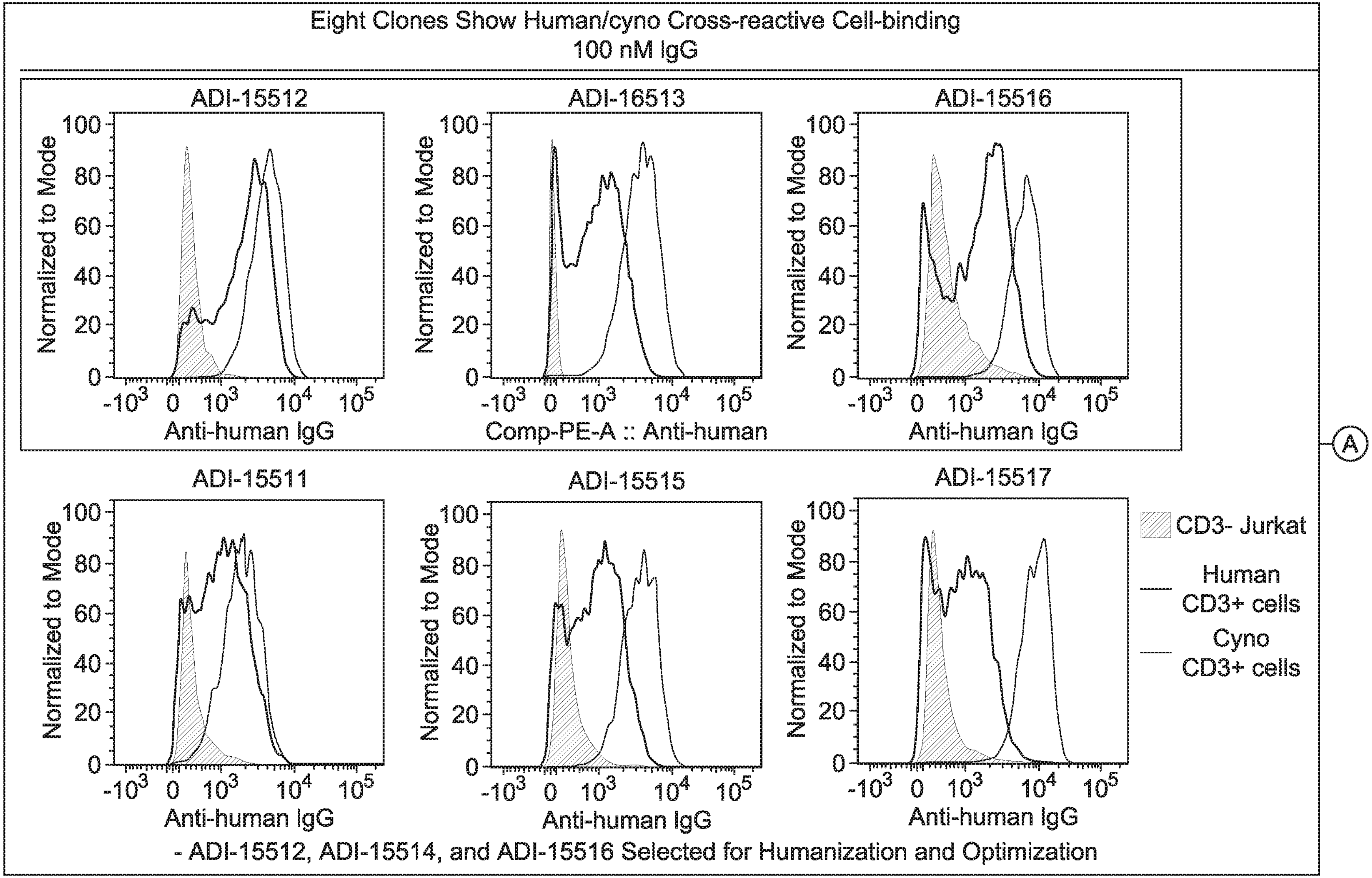
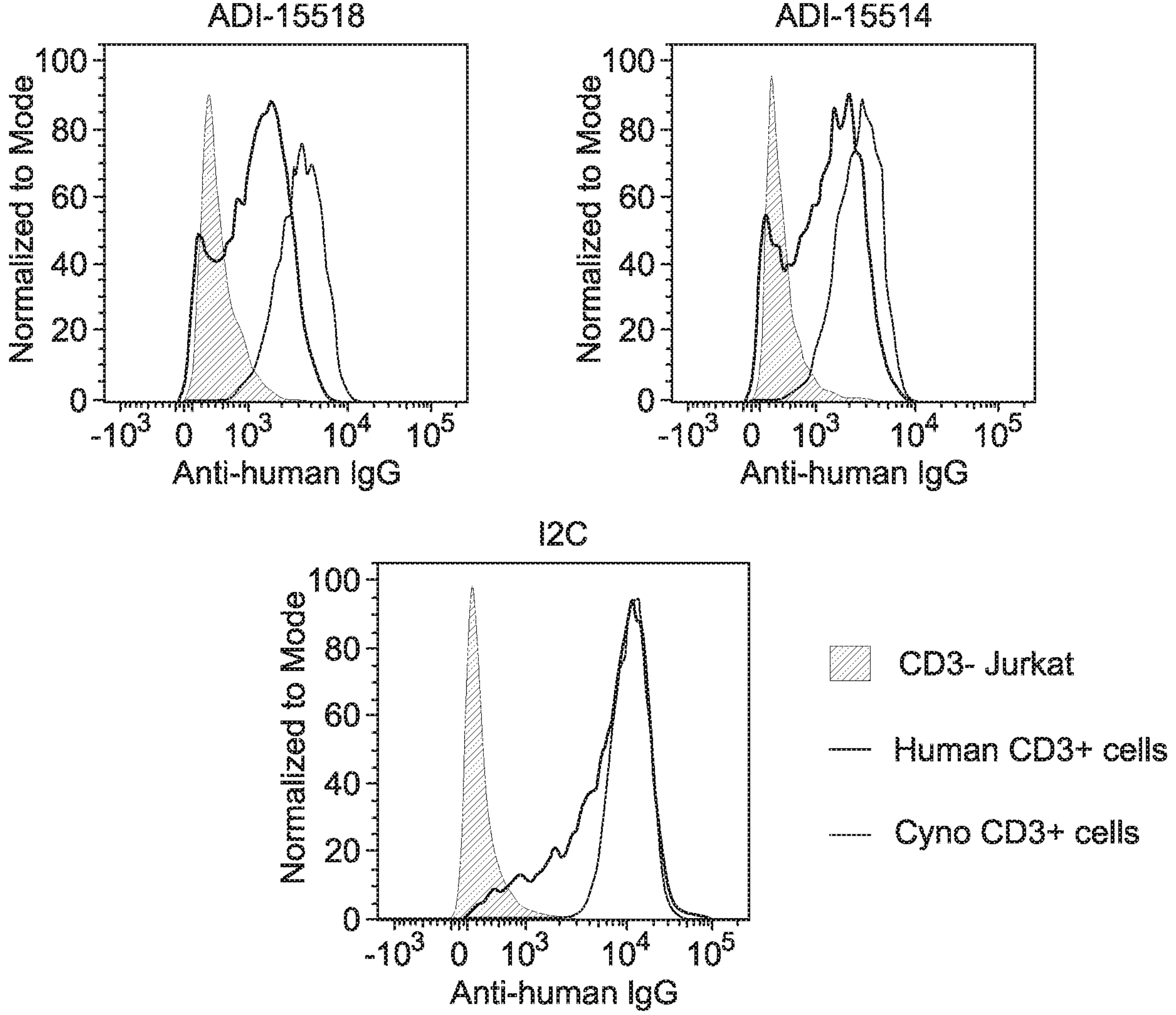

Eight Clones Show Human/cyno Cross-reactive Cell-binding
100 nM IgG
ADI-15512
ADI-16513
ADI-15516
ADI-15511
ADI-15515
ADI-15517
Normalized to Mode
0
20
40
60
80
100
-10³
0
10³
10⁴
10⁵
Anti-human IgG
Comp-PE-A :: Anti-human
▨ CD3- Jurkat
Human CD3+ cells
Cyno CD3+ cells
A
- ADI-15512, ADI-15514, and ADI-15516 Selected for Humanization and Optimization

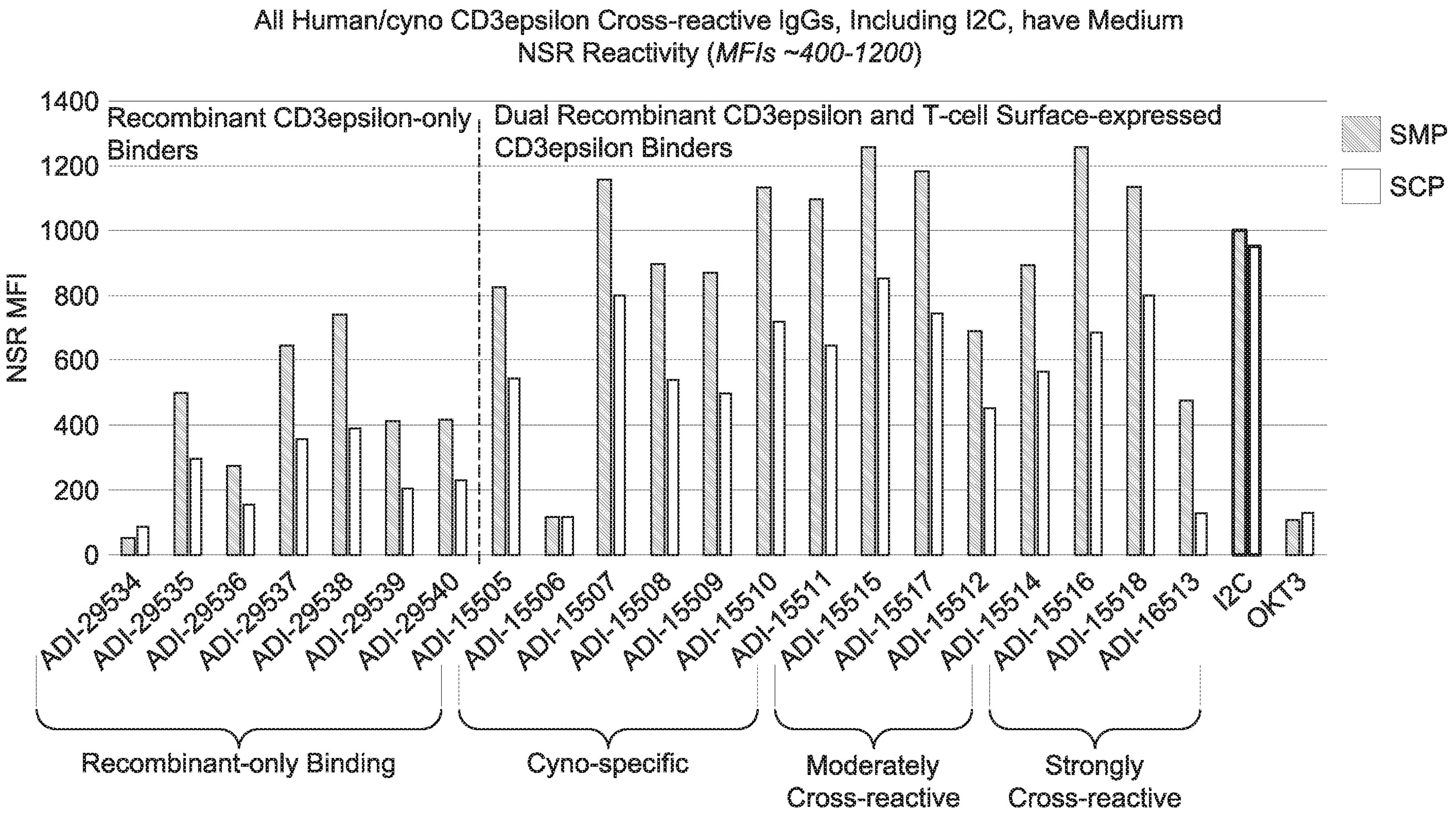
Figure 6

Eight Clones Show Human/cyno Cross-reactive Cell-binding
100 nM IgG



- ADI-15512, ADI-15514, and ADI-15516 Selected for Humanization and Optimization

Figure 6 (Continued)



All Human/cyno CD3epsilon Cross-reactive IgGs, Including I2C, have Medium NSR Reactivity (*MFIs ~400-1200*)

Figure 7

All Cell Binders Strongly Compete with I2C

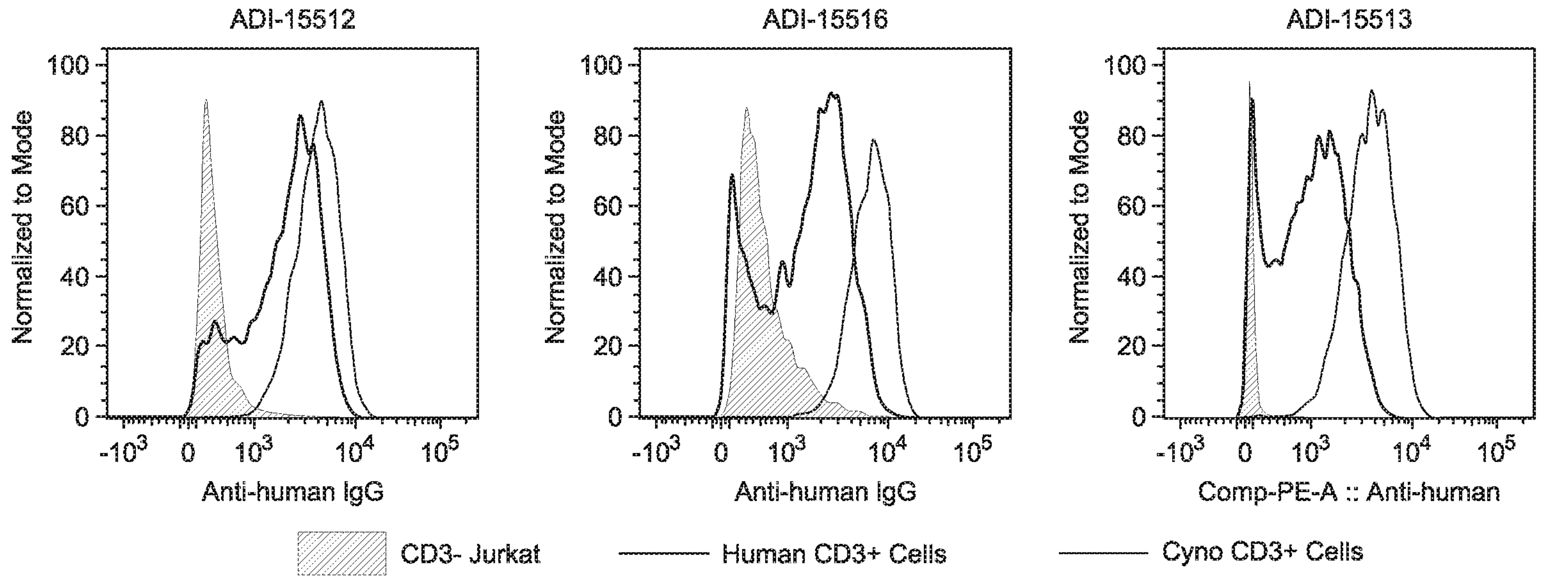
	% Reduction in Antigen Binding Relative to Antigen-only Control	
Clone	OKT3 Competition*	I2C Competition*
ADI-15505	-15	96
ADI-15506	-50	99
ADI-15507	-22	98
ADI-15508	-18	99
ADI-15509	-21	99
ADI-15510	-9	98
ADI-15511	-1	93
ADI-15515	-1	93
ADI-15517	-12	94
ADI-15512	0	98
ADI-15514	-5	97
ADI-15516	0	94
ADI-15518	-2	96
ADI-15513	-2	97
I2C	-31	92
OKT3	60	25

*Competition Performed on the Surface of Yeast

Figure 8

Three CD3epsilon-binding Clones Selected for Humanization

30 nM IgG Used for Cell Staining



Clone ID	VH Germline	VH CDR1	VH CDR2	VH FR3	VH CDR3	VL Germ line	VL CDR3
ADI-16513	V1-039A	FNIKDYYMH	WIDPENGNTIYDPKFQG	KASITADTSSNTAYLQLSSLTSEDTAVYYC	ARDGYARYYFDY	VK08-021	KQSYNLRT
ADI-15512	V1-125E	YTFTSYYIH	WIYPGDGSTKYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSAIYFC	ARDGSYYFDY	VK08-021	KQSYSLRT
ADI-15516	V1-125B	YTFTSSYIH	WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMHLSSLTSEDSAVYFC	ARDYGYYFDY	VK08-021	KQSYNLRT

Figure 9

Notes	Clone ID	VH Germline	VH FR1	VH CDR1	VH FR2	VH CDR2	VH FR3
	ADI-18562	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWMG	WIYPGDGSTKYNEKFKG	RVTMTRDTSTSTVYMELSSLRSEDTAVYYC
	ADI-18564	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWIG	WIYPGDGSTKYNEKFKG	RVTMTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18565	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWMG	WIYPGDGSTKYNEKFKG	RVTMTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18566	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWIG	WIYPGDGSTKYNEKFKG	RTTLTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18567	VH1-46	QVQLVQSGAEVKKPGSSVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWIG	WIYPGDGSTKYNEKFKG	RTTLTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18568	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWMG	WIYPGDGSTKYNEKFKG	RVTMTRDTSTSTVYMELSSLRSEDTAVYYC
	ADI-18570	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWIG	WIYPGDGSTKYNEKFKG	RVTMTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18571	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWMG	WIYPGDGSTKYNEKFKG	RVTMTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18572	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWIG	WIYPGDGSTKYNEKFKG	RTTLTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18573	VH1-46	QVQLVQSGAEVKKPGSSVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWIG	WIYPGDGSTKYNEKFKG	RTTLTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18563	VH1-69	QVQLVQSGAEVKKPGSSVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWMG	WIYPGDGSTKYNEKFKG	RVTITADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18569	VH1-69	QVQLVQSGAEVKKPGSSVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWMG	WIYPGDGSTKYNEKFKG	RVTITADKSTSTAYMELSSLRSEDTAVYYC
Chimeric	ADI-15512	V1-125E	EVQLEQSGPELVKPGASVKMSCKASG	YTFTSYYIH	WVKQRPGQGLEWIG	WIYPGDGSTKYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSAIYFC
	ADI-18574	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQRLEWMG	WIYPGNVNTKYNEKFKG	RVTITRDTSASTAYMELSSLRSEDTAVYYC
	ADI-18575	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWIG	WIYPGNVNTKYNEKFKG	RATLTADKSASTAYMHLSSLRSEDTAVYYC
	ADI-18576	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQRLEWIG	WIYPGNVNTKYNEKFKG	RVTITADKSASTAYMELSSLRSEDTAVYYC
	ADI-18578	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWIG	WIYPGNVNTKYNEKFKG	RVTMTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18579	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWIG	WIYPGNVNTKYNEKFKG	RATLTADKSTSTAYMHLSSLRSEDTAVYYC
	ADI-18580	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQRLEWMG	WIYPGNVNTKYNEKFKG	RVTITRDTSASTAYMELSSLRSEDTAVYYC
	ADI-18581	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWIG	WIYPGNVNTKYNEKFKG	RATLTADKSASTAYMHLSSLRSEDTAVYYC
	ADI-18582	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQRLEWIG	WIYPGNVNTKYNEKFKG	RVTITADKSASTAYMELSSLRSEDTAVYYC
	ADI-18584	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWIG	WIYPGNVNTKYNEKFKG	RVTMTADKSTSTAYMELSSLRSEDTAVYYC
	ADI-18585	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWIG	WIYPGNVNTKYNEKFKG	RATLTADKSTSTAYMHLSSLRSEDTAVYYC
	ADI-18577	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWMG	WIYPGNVNTKYNEKFKG	RVTMTRDTSTSTVYMELSSLRSEDTAVYYC
	ADI-18583	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWMG	WIYPGNVNTKYNEKFKG	RVTMTRDTSTSTVYMELSSLRSEDTAVYYC
Chimeric	ADI-15516	V1-125B	EVQLEESGPELVRPGASVRISCKASG	YTFTSSYIH	WVKQRPGQGLEWIG	WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMHLSSLTSEDSAVYFC
	ADI-18588	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQGLEWIG	WIDPENGNTIYDPKFQG	RATITADTSTNTAYMELSSLRSEDTAVYYC
	ADI-18589	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWMG	WIDPENGNTIYDPKFQG	RVTITRDTSASTAYMELSSLRSEDTAVYYC
	ADI-18590	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWIG	WIDPENGNTIYDPKFQG	RVTITADTSASTAYMELSSLRSEDTAVYYC
	ADI-18591	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWIG	WIDPENGNTIYDPKFQG	RATITADTSANTAYMELSSLRSEDTAVYYC
	ADI-18593	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQGLEWIG	WIDPENGNTIYDPKFQG	RATITADTSTNTAYMELSSLRSEDTAVYYC
	ADI-18594	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWMG	WIDPENGNTIYDPKFQG	RVTITRDTSASTAYMELSSLRSEDTAVYYC
	ADI-18595	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWIG	WIDPENGNTIYDPKFQG	RVTITADTSASTAYMELSSLRSEDTAVYYC
	ADI-18596	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWIG	WIDPENGNTIYDPKFQG	RATITADTSANTAYMELSSLRSEDTAVYYC
	ADI-18597	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQGLEWIG	WIDPENGNTIYDPKFQG	RVTMTADTSTSTAYMELSSLRSEDTAVYYC
	ADI-18592	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQGLEWMG	WIDPENGNTIYDPKFQG	RVTMTRDTSTSTVYMELSSLRSEDTAVYYC
	ADI-18587	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQGLEWIG	WIDPENGNTIYDPKFQG	RVTMTADTSTSTAYMELSSLRSEDTAVYYC
	ADI-18586	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQGLEWMG	WIDPENGNTIYDPKFQG	RVTMTRDTSTSTVYMELSSLRSEDTAVYYC
Chimeric	ADI-16513	V1-039A	QVQLEQSGAELVRPGALVKLSCKASG	FNIKDYYMH	WVKQRPEQGLEWIG	WIDPENGNTIYDPKFQG	KASITADTSSNTAYLQLSSLTSEDTAVYYC

Ⓐ

Figure 10A

Ⓐ

VH CDR3	VL Germline	VL CDR3
ARDGSYYFDY	VK4-1	KQSYSLRT
ARDGSYYFDY	VK4-1	KQSYSLRT
ARDGSYYFDY	VK4-1	KQSYSLRT
ARDGSYYFDY	VK4-1	KQSYSLRT
ARDGSYYFDY	VK4-1	KQSYSLRT
ARDGSYYFDY	VK4-1	KQSYNLRT
ARDGSYYFDY	VK4-1	KQSYNLRT
ARDGSYYFDY	VK4-1	KQSYNLRT
ARDGSYYFDY	VK4-1	KQSYNLRT
ARDGSYYFDY	VK4-1	KQSYNLRT
ARDGSYYFDY	VK4-1	KQSYSLRT
ARDGSYYFDY	VK4-1	KQSYNLRT
ARDGSYYFDY	VK08-021	KQSYSLRT
ARDYGYYFDY	VK4-1	KQSYSLRT
ARDYGYYFDY	VK4-1	KQSYSLRT
ARDYGYYFDY	VK4-1	KQSYSLRT
ARDYGYYFDY	VK4-1	KQSYSLRT
ARDYGYYFDY	VK4-1	KQSYSLRT
ARDYGYYFDY	VK4-1	KQSYNLRT
ARDYGYYFDY	VK4-1	KQSYNLRT
ARDYGYYFDY	VK4-1	KQSYNLRT
ARDYGYYFDY	VK4-1	KQSYNLRT
ARDYGYYFDY	VK4-1	KQSYNLRT
ARDYGYYFDY	VK4-1	KQSYSLRT
ARDYGYYFDY	VK4-1	KQSYNLRT
ARDYGYYFDY	VK08-021	KQSYNLRT
ARDGYARYYFDY	VK4-1	KQSYSLRT
ARDGYARYYFDY	VK4-1	KQSYSLRT
ARDGYARYYFDY	VK4-1	KQSYSLRT
ARDGYARYYFDY	VK4-1	KQSYSLRT
ARDGYARYYFDY	VK4-1	KQSYNLRT
ARDGYARYYFDY	VK4-1	KQSYNLRT
ARDGYARYYFDY	VK4-1	KQSYNLRT
ARDGYARYYFDY	VK4-1	KQSYNLRT
ARDGYARYYFDY	VK4-1	KQSYNLRT
ARDGYARYYFDY	VK4-1	KQSYNLRT
ARDGYARYYFDY	VK4-1	KQSYSLRT
ARDGYARYYFDY	VK4-1	KQSYSLRT
ARDGYARYYFDY	VK08-021	KQSYNLRT

Figure 10A (Continued)

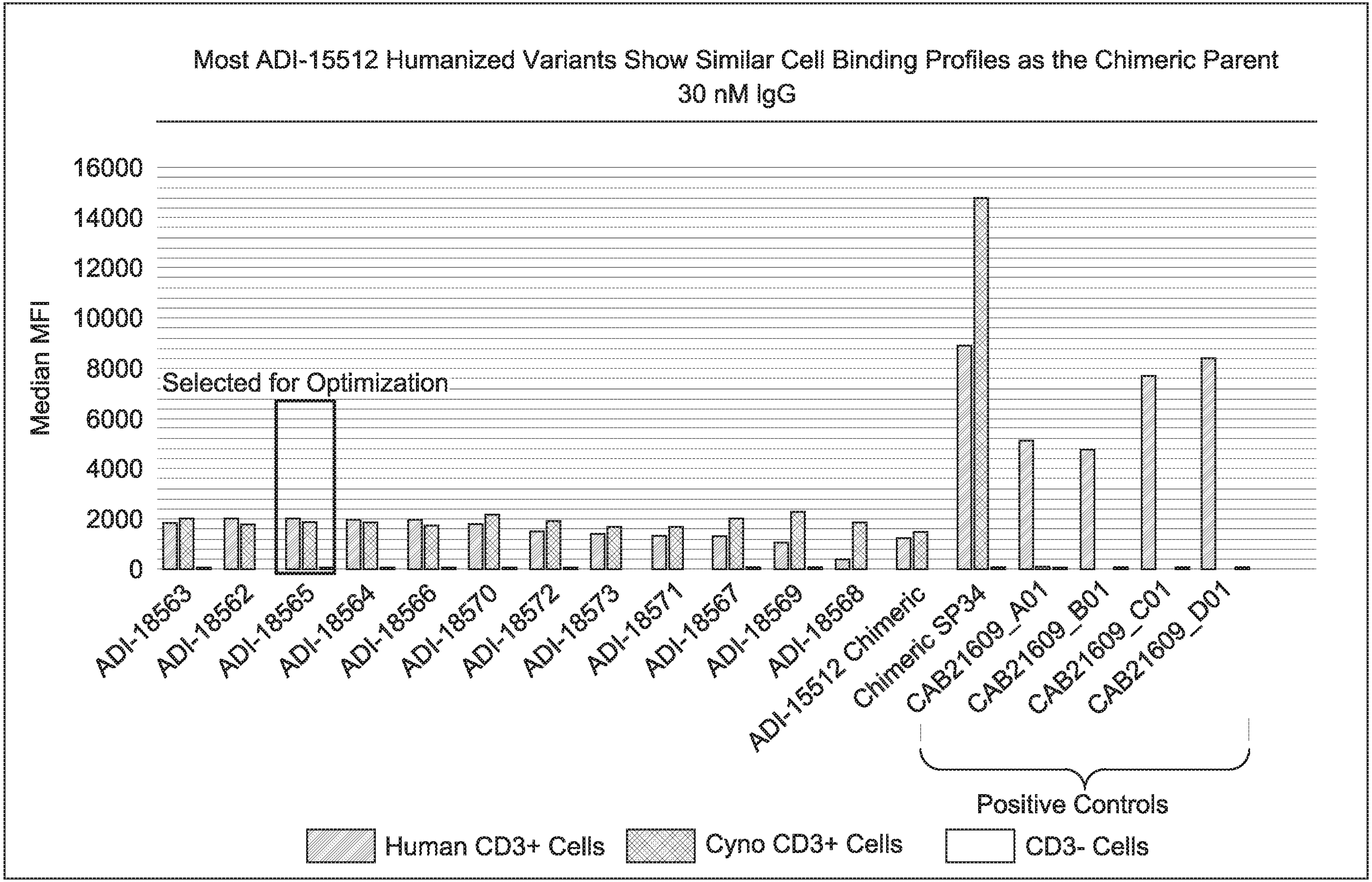

Most ADI-15512 Humanized Variants Show Similar Cell Binding Profiles as the Chimeric Parent
30 nM IgG
Median MFI
16000
14000
12000
10000
8000
6000
4000
2000
0
Selected for Optimization
ADI-18563
ADI-18562
ADI-18565
ADI-18564
ADI-18566
ADI-18570
ADI-18572
ADI-18573
ADI-18571
ADI-18567
ADI-18569
ADI-18568
ADI-15512 Chimeric
Chimeric SP34
CAB21609_A01
CAB21609_B01
CAB21609_C01
CAB21609_D01
Positive Controls
Human CD3+ Cells
Cyno CD3+ Cells
CD3- Cells

Figure 10B

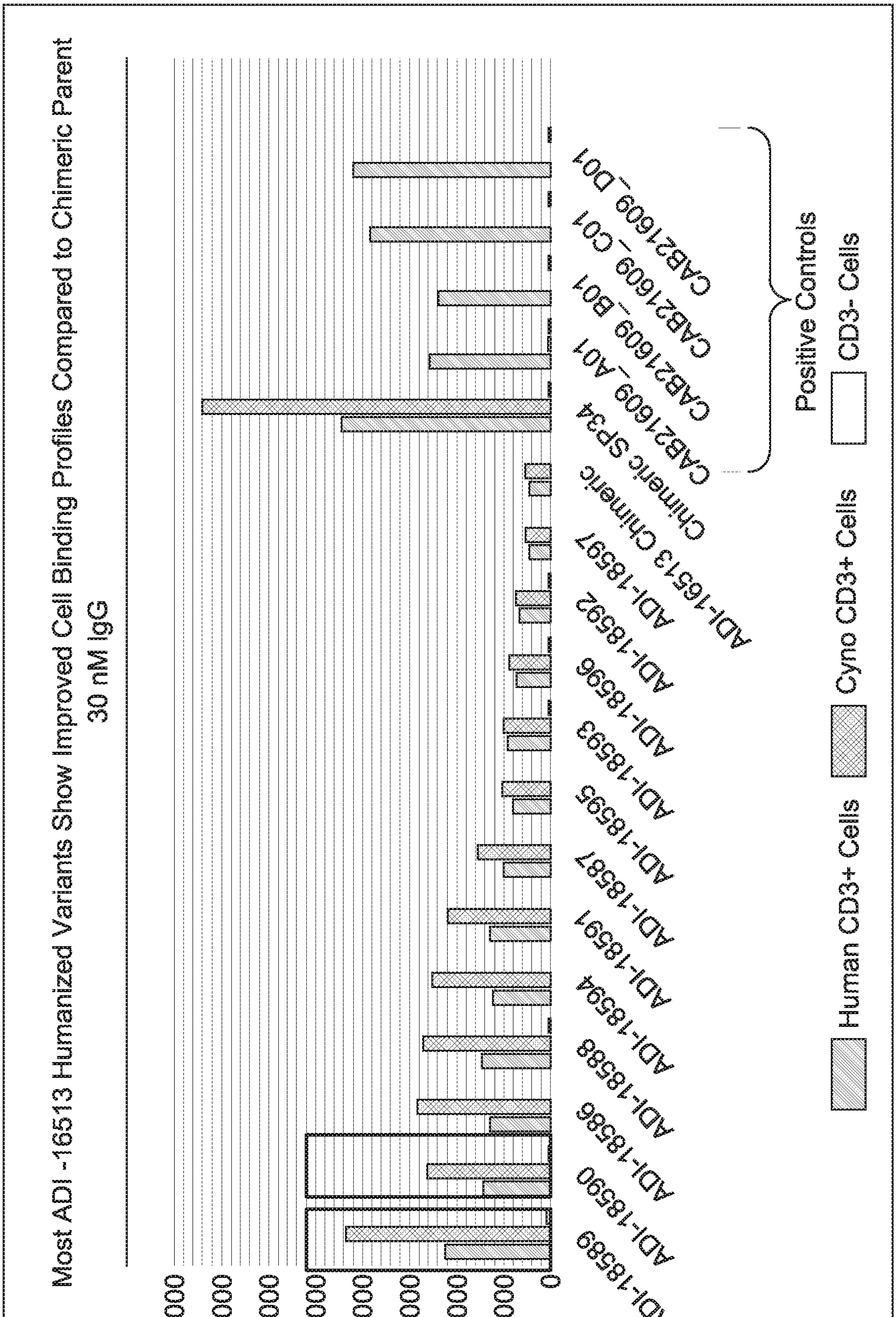

Most ADI -16513 Humanized Variants Show Improved Cell Binding Profiles Compared to Chimeric Parent
30 nM IgG
Median MFI
16000
14000
12000
10000
8000
6000
4000
2000
0
ADI-18589
ADI-18590
ADI-18586
ADI-18588
ADI-18594
ADI-18591
ADI-18587
ADI-18595
ADI-18593
ADI-18596
ADI-18592
ADI-18597
ADI-16513 Chimeric
Chimeric SP34
CAB21609_A01
CAB21609_B01
CAB21609_C01
CAB21609_D01
Positive Controls
Human CD3+ Cells
Cyno CD3+ Cells
CD3- Cells

Figure 10C

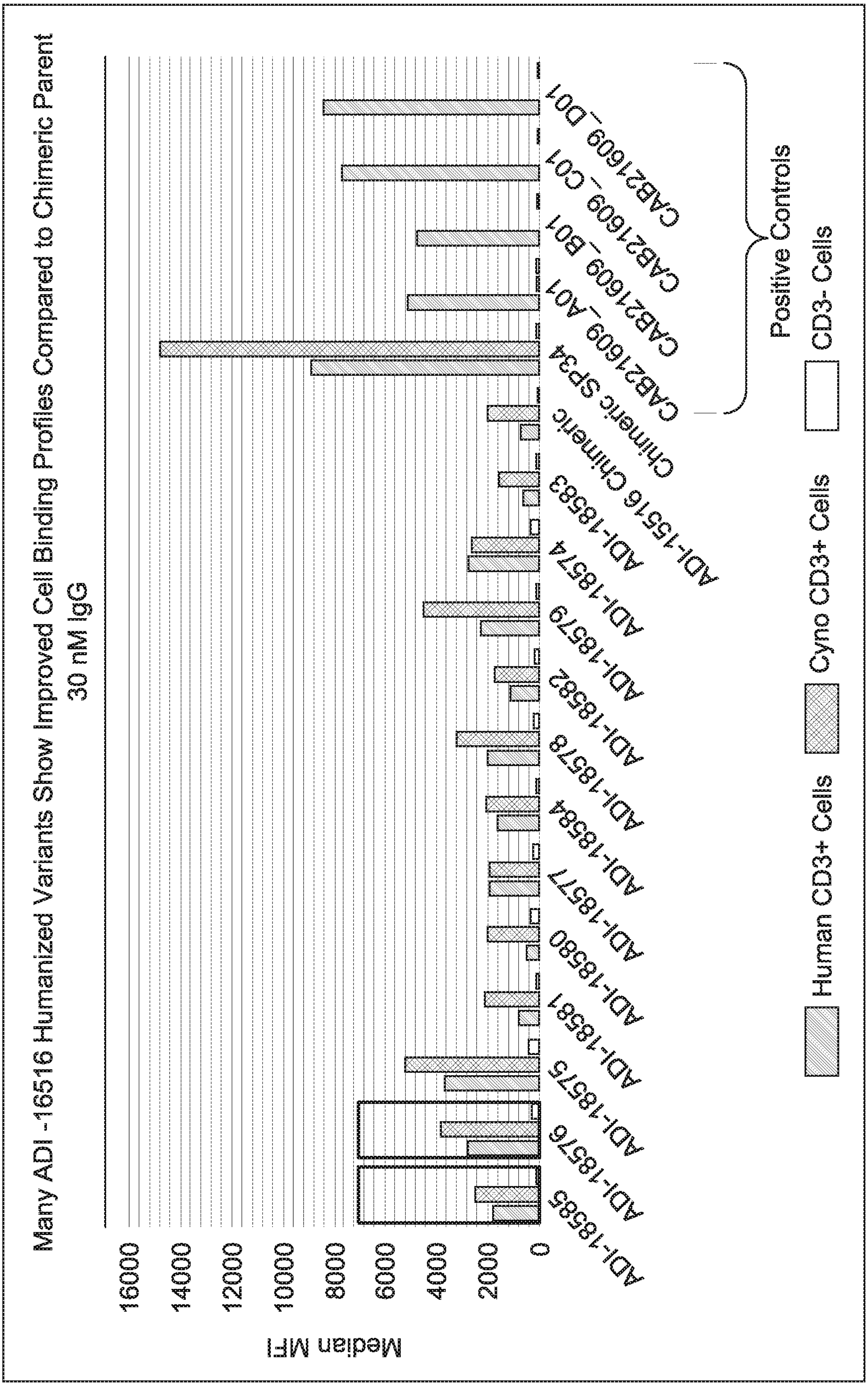

Many ADI -16516 Humanized Variants Show Improved Cell Binding Profiles Compared to Chimeric Parent
30 nM IgG

Figure 10D

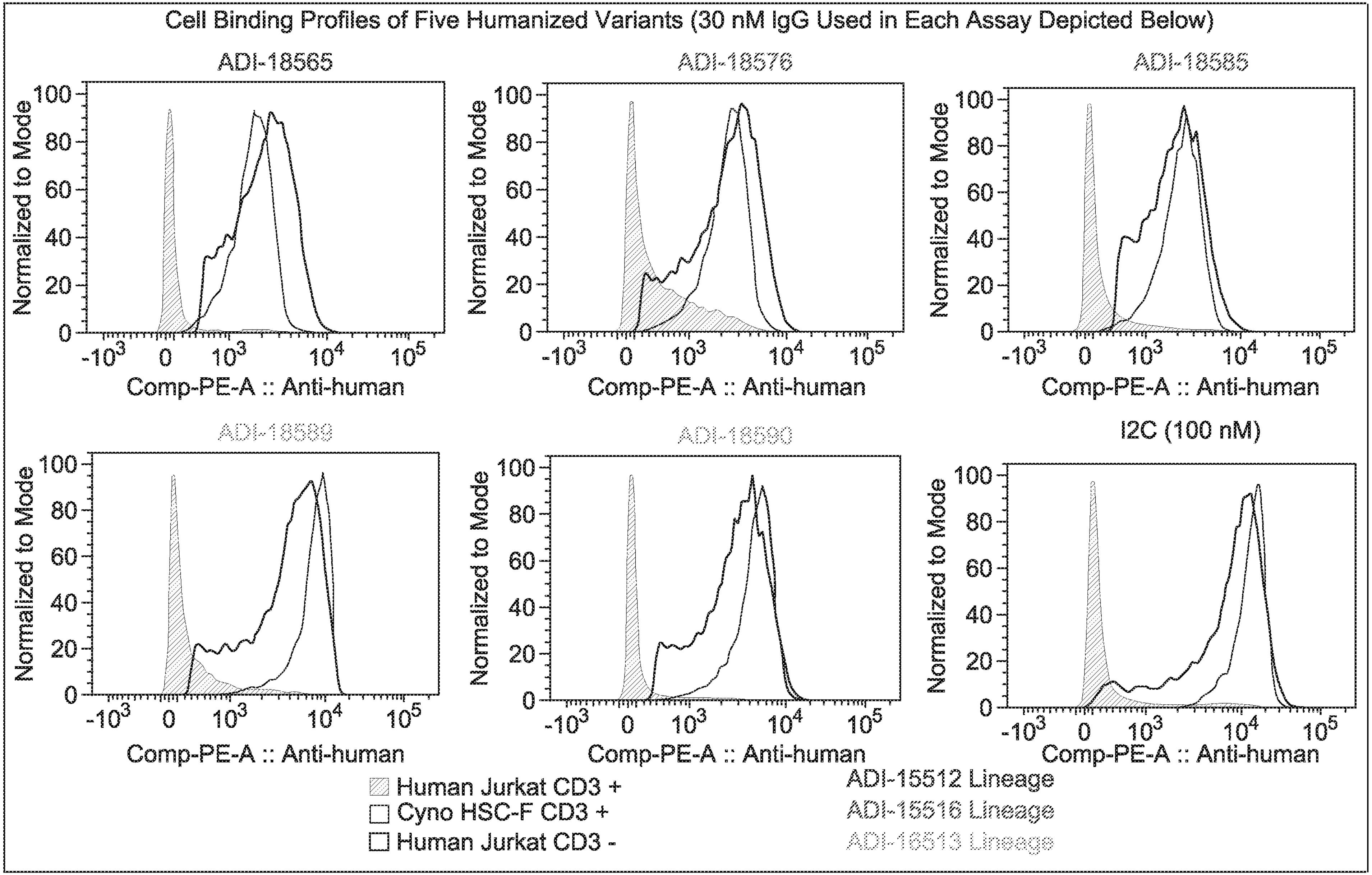

Cell Binding Profiles of Five Humanized Variants (30 nM IgG Used in Each Assay Depicted Below)
ADI-18565
ADI-18576
ADI-18585
ADI-18589
ADI-18590
I2C (100 nM)
Normalized to Mode
0
20
40
60
80
100
-10^3
0
10^3
10^4
10^5
Comp-PE-A :: Anti-human
▨ Human Jurkat CD3 +
☐ Cyno HSC-F CD3 +
☐ Human Jurkat CD3 -
ADI-15512 Lineage
ADI-15516 Lineage
ADI-16513 Lineage

Figure 11A

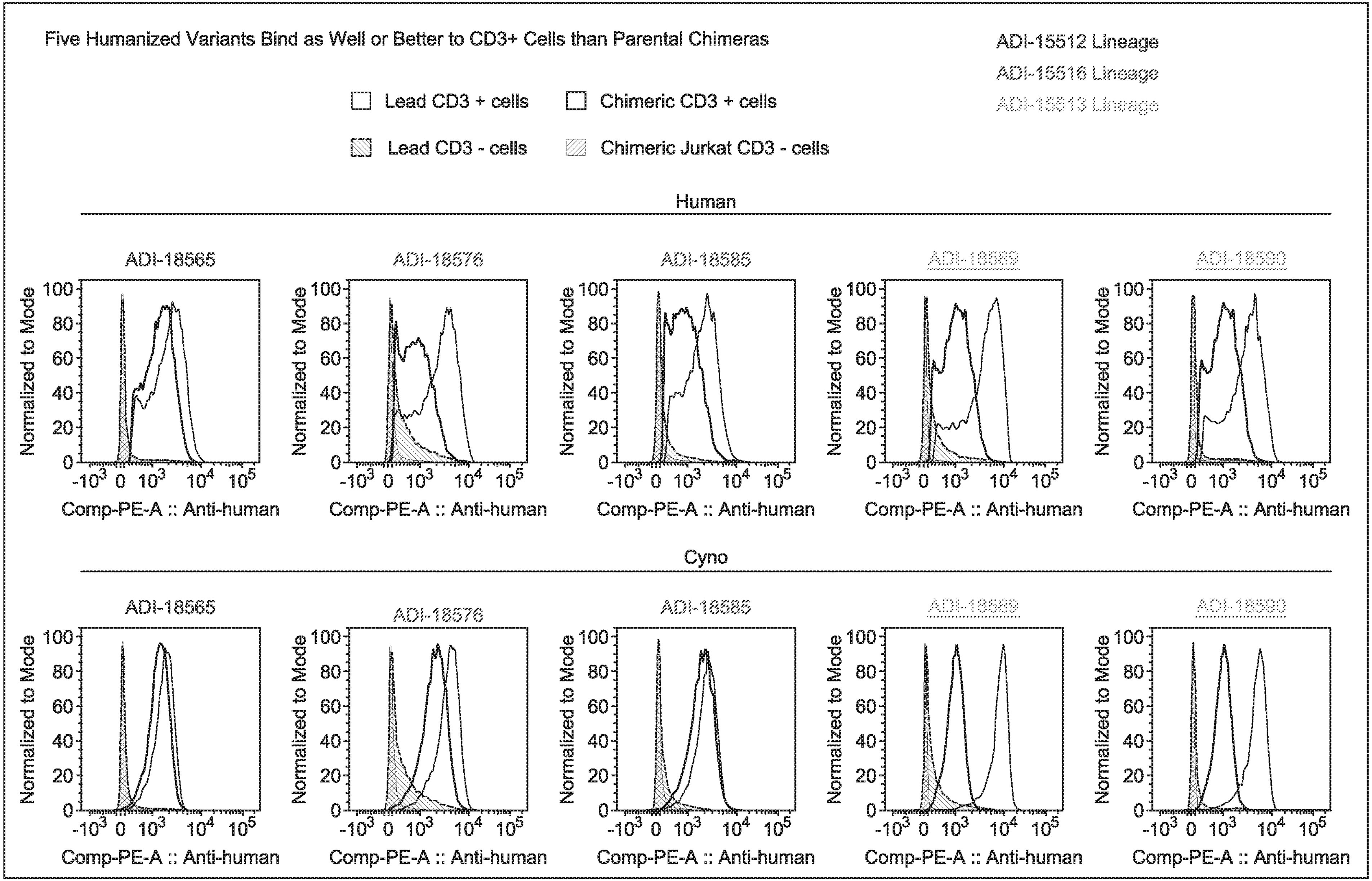

Five Humanized Variants Bind as Well or Better to CD3+ Cells than Parental Chimeras
ADI-15512 Lineage
ADI-15516 Lineage
ADI-15513 Lineage
☐ Lead CD3 + cells
☐ Chimeric CD3 + cells
▨ Lead CD3 - cells
▨ Chimeric Jurkat CD3 - cells
Human
ADI-18565
ADI-18576
ADI-18585
ADI-18589
ADI-18590
Cyno
ADI-18565
ADI-18576
ADI-18585
ADI-18589
ADI-18590
Normalized to Mode
0
20
40
60
80
100
Comp-PE-A :: Anti-human
-10^3
0
10^3
10^4
10^5

Figure 11B

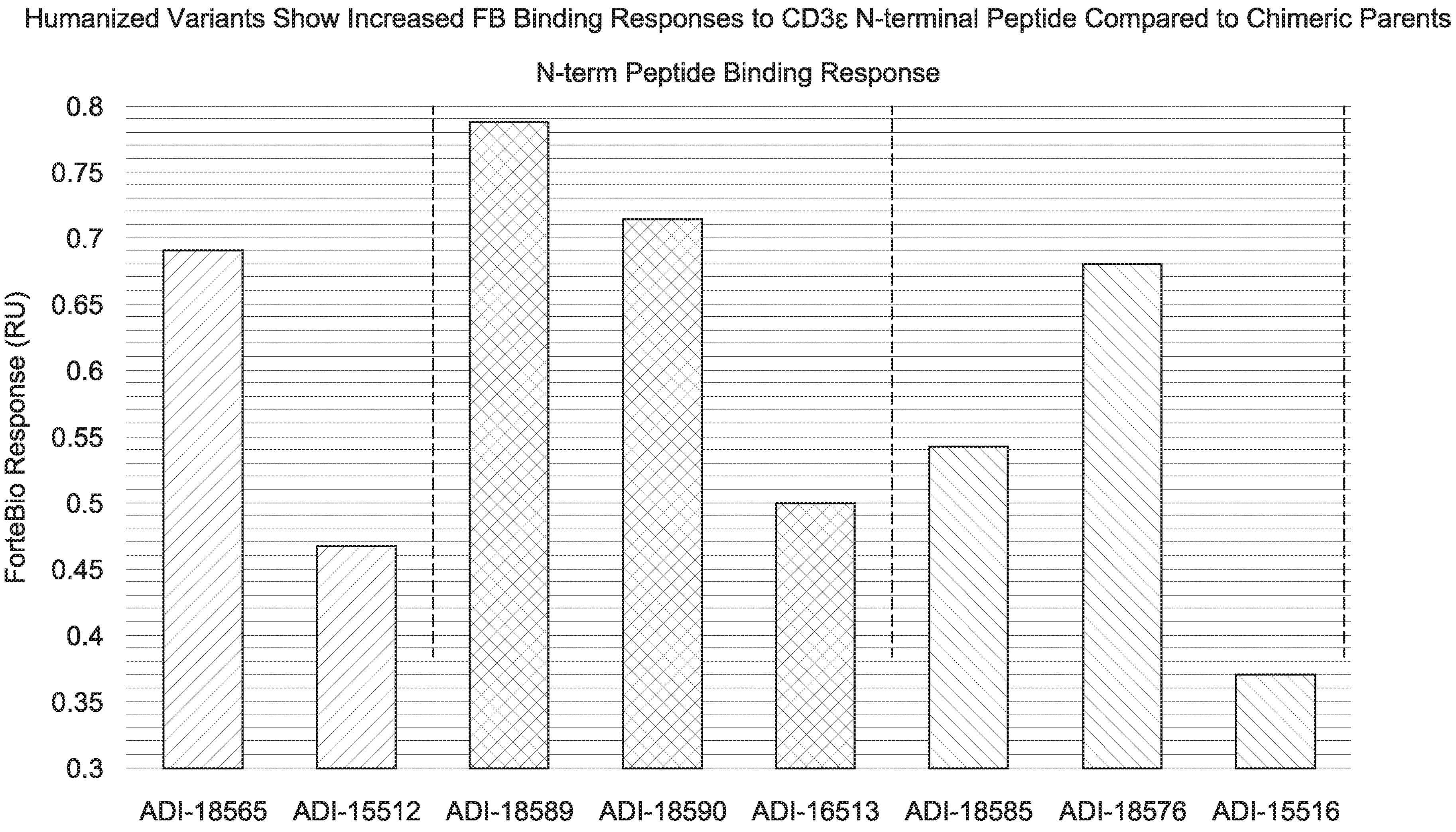

Humanized Variants Show Increased FB Binding Responses to CD3ε N-terminal Peptide Compared to Chimeric Parents
N-term Peptide Binding Response
ForteBio Response (RU)
0.8
0.75
0.7
0.65
0.6
0.55
0.5
0.45
0.4
0.35
0.3
ADI-18565
ADI-15512
ADI-18589
ADI-18590
ADI-16513
ADI-18585
ADI-18576
ADI-15516

Figure 11C

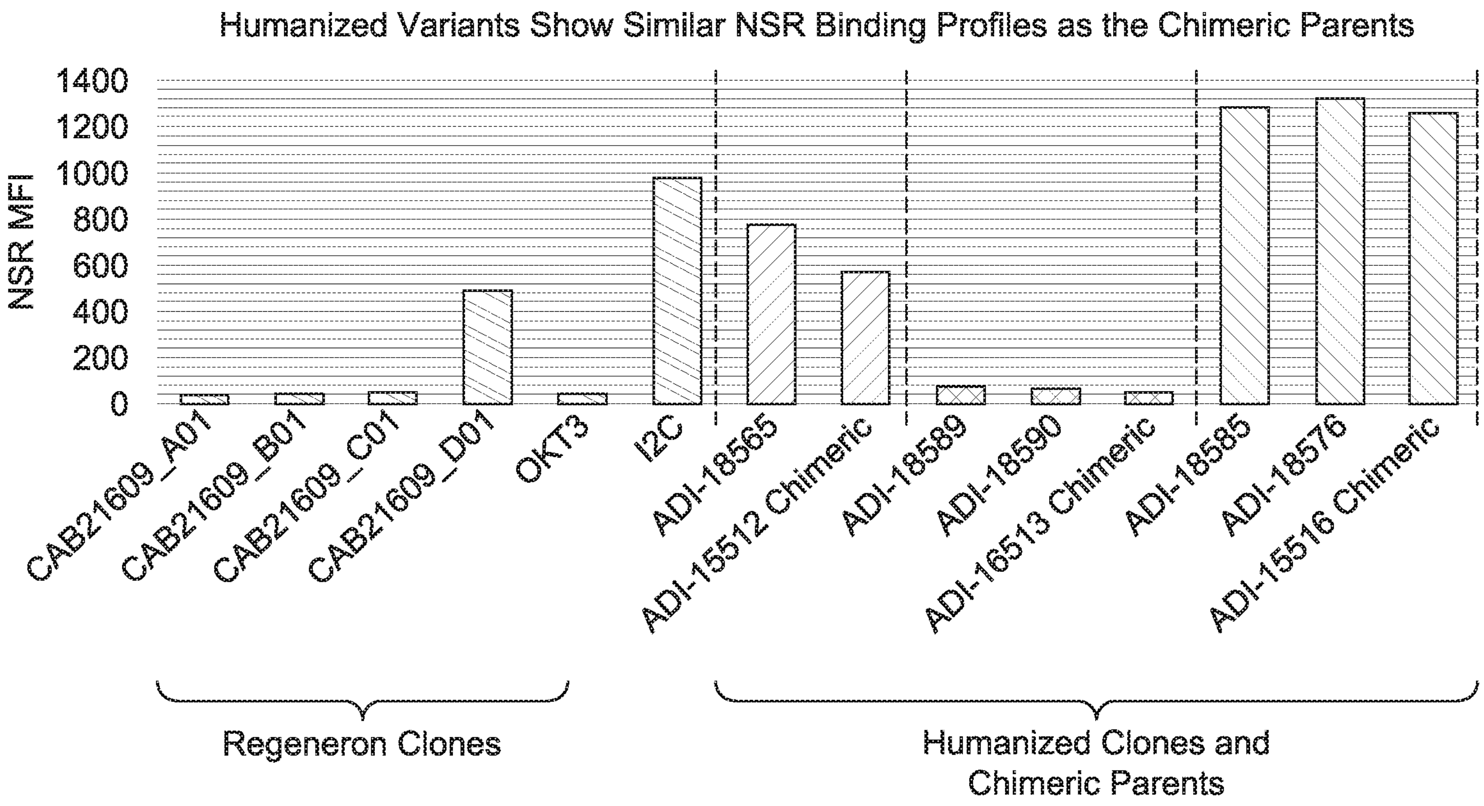

Humanized Variants Show Similar NSR Binding Profiles as the Chimeric Parents
NSR MFI
1400
1200
1000
800
600
400
200
0
CAB21609_A01
CAB21609_B01
CAB21609_C01
CAB21609_D01
OKT3
I2C
ADI-18565
ADI-15512 Chimeric
ADI-18589
ADI-18590
ADI-16513 Chimeric
ADI-18585
ADI-18576
ADI-15516 Chimeric
Regeneron Clones
Humanized Clones and Chimeric Parents

Figure 12A

Developability Profile: Three of the Five Lineages Show Similar or Better PSR and AC-SINS Profiles Compared to I2C

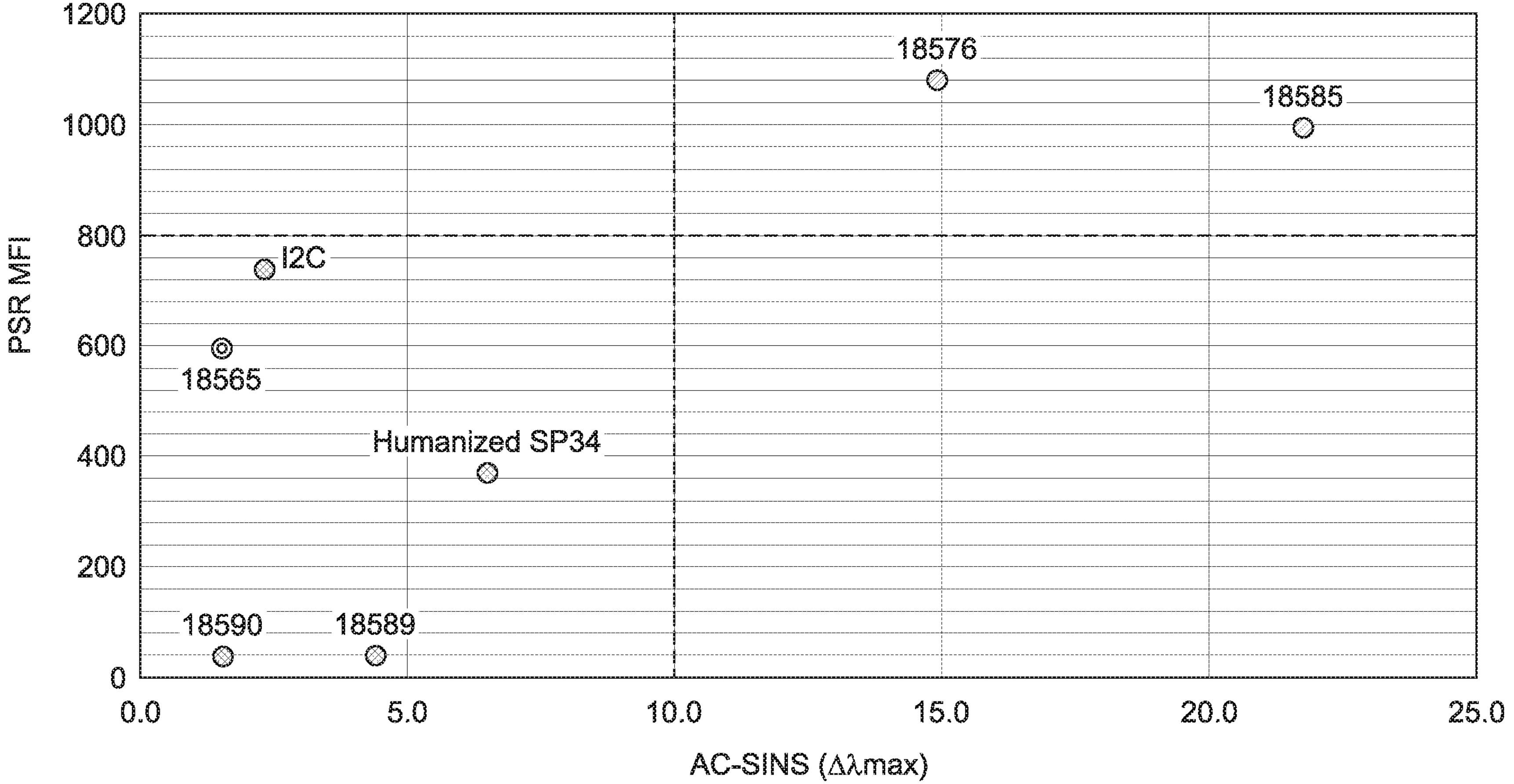


Figure 12B

Sequences of Humanized Clones Selected for Optimization and their Respective Parents

	Clone ID	VH Germ line	VH FR1	VH CDR1	VH FR2
Lead	ADI-18565	VH1-46	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSYYIH	WVRQAPGQGLEWMG
Parent	ADI-15512	V1-125E	EVQLEQSGPELVKPGASVKMSCKASG	YTFTSYYIH	WVKQRPGQGLEWIG
Lead	ADI-18589	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWMG
Lead	ADI-18590	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	FNIKDYYMH	WVRQAPGQRLEWIG
Parent	ADI-16513	V1-039A	QVQLEQSGAELVRPGALVKLSCKASG	FNIKDYYMH	WVKQRPEQGLEWIG
Lead	ADI-18576	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQRLEWIG
Lead	ADI-18585	VH1-3	QVQLVQSGAEVKKPGASVKVSCKASG	YTFTSSYIH	WVRQAPGQGLEWIG
Parent	ADI-15516	V1-125B	EVQLEESGPELVRPGASVRISCKASG	YTFTSSYIH	WVKQRPGQGLEWIG

Ⓐ

	Clone ID	VL Germ line	VL FR1	VL CDR1
Lead	ADI-18565	VK4-1	DIVMTQSPDSLAVSLGERATINC	KSSQSLLNSRTRKNYLA
Parent	ADI-15512	VK08-021	DIQLTQSPSSLAVSAGEKVTMSC	KSSQSLLNSRTRKNYLA
Lead	ADI-18589	VK4-1	DIVMTQSPDSLAVSLGERATINC	KSSQSLLNSRTRKNYLA
Lead	ADI-18590	VK4-1	DIVMTQSPDSLAVSLGERATINC	KSSQSLLNSRTRKNYLA
Parent	ADI-16513	VK08-021	DIQLTQSPSSLAVSAGEKVTMSC	KSSQSLLNSRTRKNYLA
Lead	ADI-18576	VK4-1	DIVMTQSPDSLAVSLGERATINC	KSSQSLLNSRTRKNYLA
Lead	ADI-18585	VK4-1	DIVMTQSPDSLAVSLGERATINC	KSSQSLLNSRTRKNYLA
Parent	ADI-15516	VK08-021	DIVLTQSPSSLAVSAGEKVTMSC	KSSQSLLNSRTRKNYLA

Figure 13

Sequences of Humanized Clones Selected for Optimization and their Respective Parents

VH CDR2	VH FR3	VH CDR3
WIYPGDGSTKYNEKFKG	RVTMTADKSTSTAYMELSSLRSEDTAVYYC	ARDGSYYFDY
WIYPGDGSTKYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSAIYFC	ARDGSYYFDY
WIDPENGNTIYDPKFQG	RVTITRDTSASTAYMELSSLRSEDTAVYYC	ARDGYARYYFDY
WIDPENGNTIYDPKFQG	RVTITADTSASTAYMELSSLRSEDTAVYYC	ARDGYARYYFDY
WIDPENGNTIYDPKFQG	KASITADTSSNTAYLQLSSLTSEDTAVYYC	ARDGYARYYFDY
WIYPGNVNTKYNEKFKG	RVTITADKSASTAYMELSSLRSEDTAVYYC	ARDYGYYFDY
WIYPGNVNTKYNEKFKG	RATLTADKSTSTAYMHLSSLRSEDTAVYYC	ARDYGYYFDY
WIYPGNVNTKYNEKFKG	KATLTADKSSSTAYMHLSSLTSEDSAVYFC	ARDYGYYFDY

Ⓐ

VL FR2	VL CDR2	VL FR3	VL CDR3
WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEOVAVYYC	KQSYSLRT
WYQQKPGQSPKLLIY	WASTRES	GVPDRFTGSGSGTDFTLTISSVQAEOLAVYYC	KQSYSLRT
WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	KQSYSLRT
WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	KQSYSLRT
WYQQKPGQSPKLLIY	WASTRES	GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC	KQSYNLRT
WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	KQSYSLRT
WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	KQSYNLRT
WYQQKAGQSPKLLIY	WASTRES	GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC	KQSYNLRT

Figure 13 (Continued)

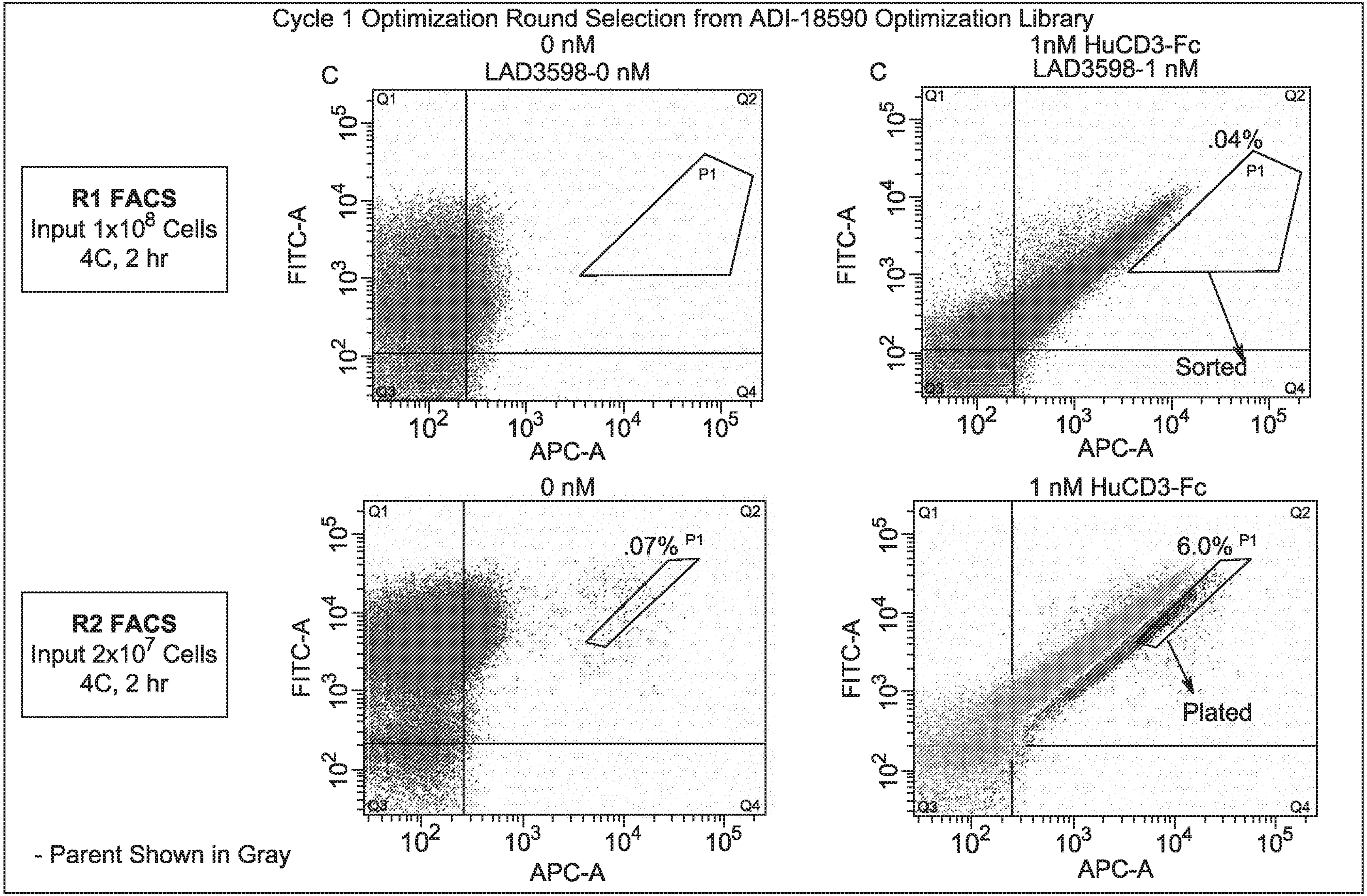

Cycle 1 Optimization Round Selection from ADI-18590 Optimization Library
R1 FACS
Input 1x10^8 Cells
4C, 2 hr
0 nM
LAD3598-0 nM
C
Q1
Q2
Q3
Q4
P1
FITC-A
APC-A
10^2
10^3
10^4
10^5
1nM HuCD3-Fc
LAD3598-1 nM
C
.04%
Sorted
R2 FACS
Input 2x10^7 Cells
4C, 2 hr
0 nM
.07%
1 nM HuCD3-Fc
6.0%
Plated
- Parent Shown in Gray

Figure 14

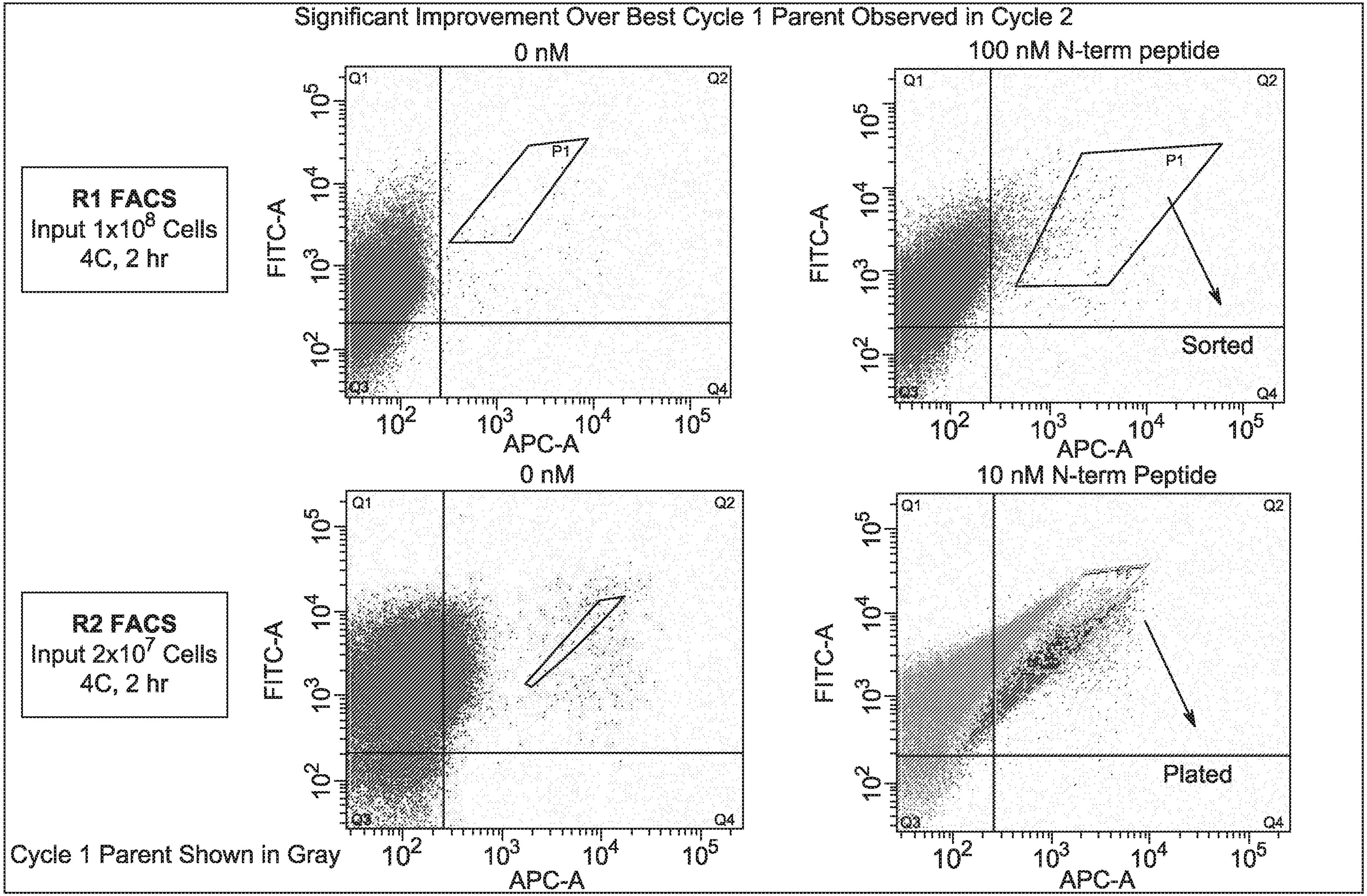
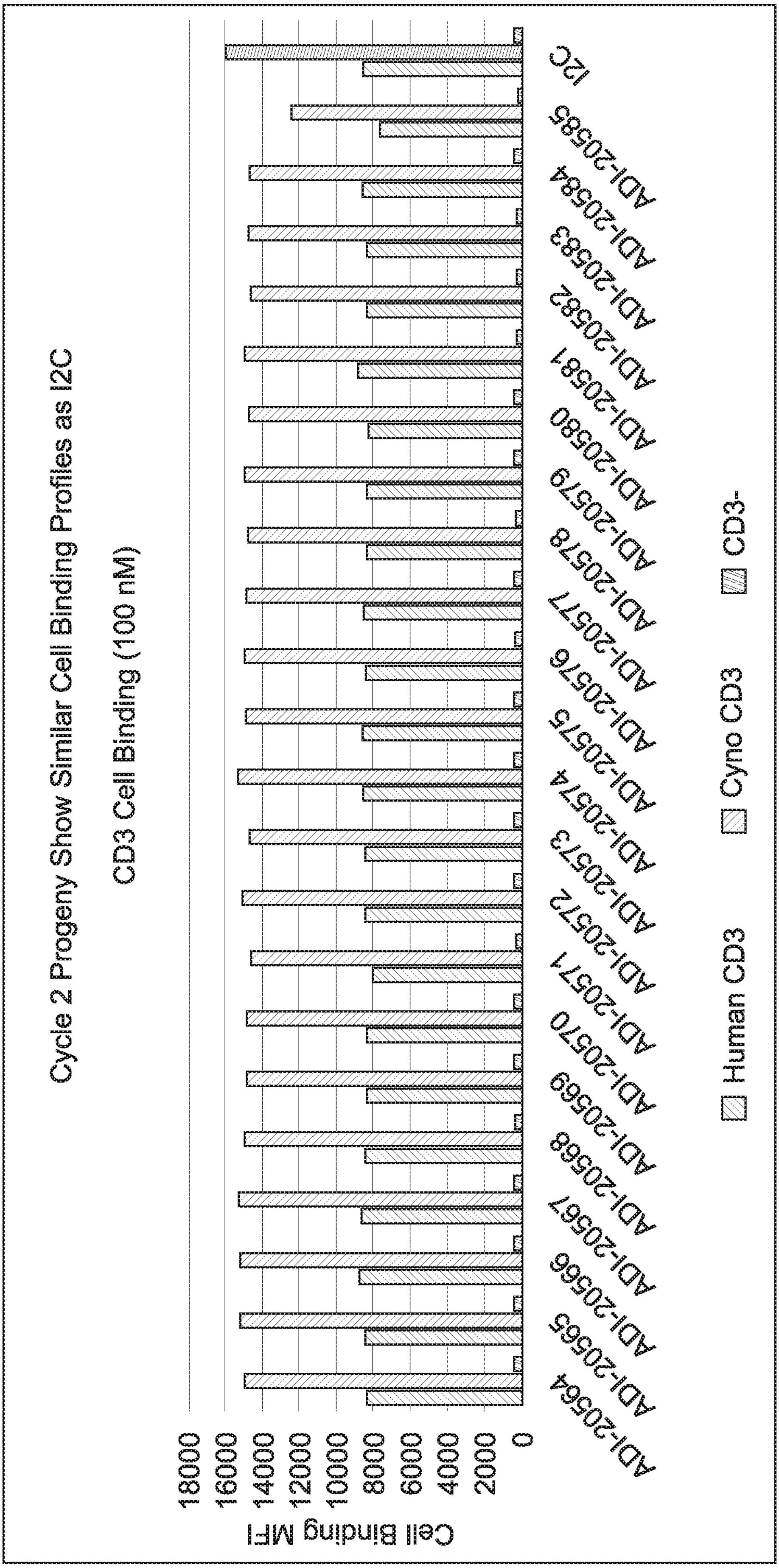

Significant Improvement Over Best Cycle 1 Parent Observed in Cycle 2
R1 FACS
Input 1x10^8 Cells
4C, 2 hr
0 nM
100 nM N-term peptide
P1
Sorted
R2 FACS
Input 2x10^7 Cells
4C, 2 hr
0 nM
10 nM N-term Peptide
Plated
Q1
Q2
Q3
Q4
FITC-A
APC-A
10^2
10^3
10^4
10^5
Cycle 1 Parent Shown in Gray

Figure 15



Cycle 2 Progeny Show Similar Cell Binding Profiles as I2C

CD3 Cell Binding (100 nM)

Figure 16

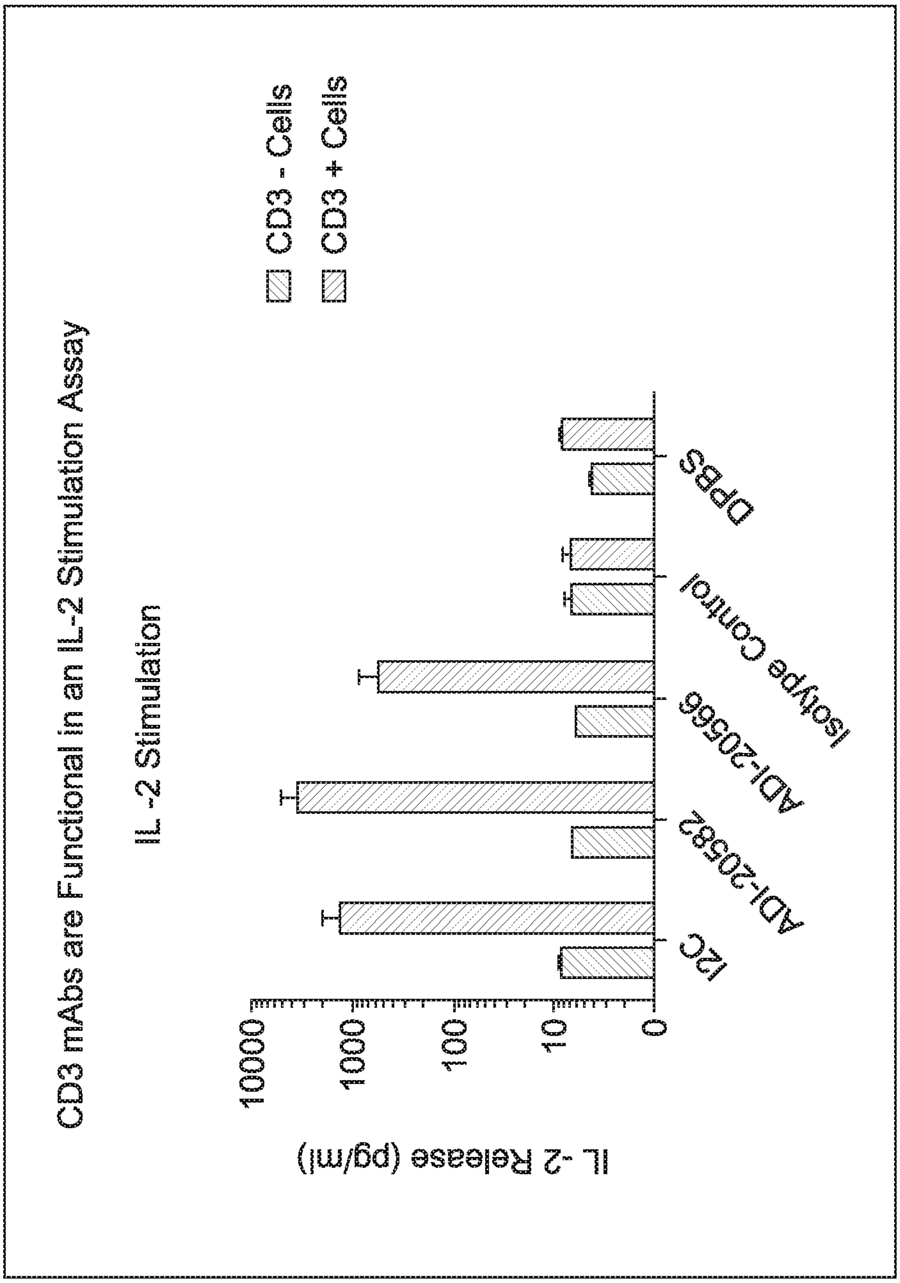
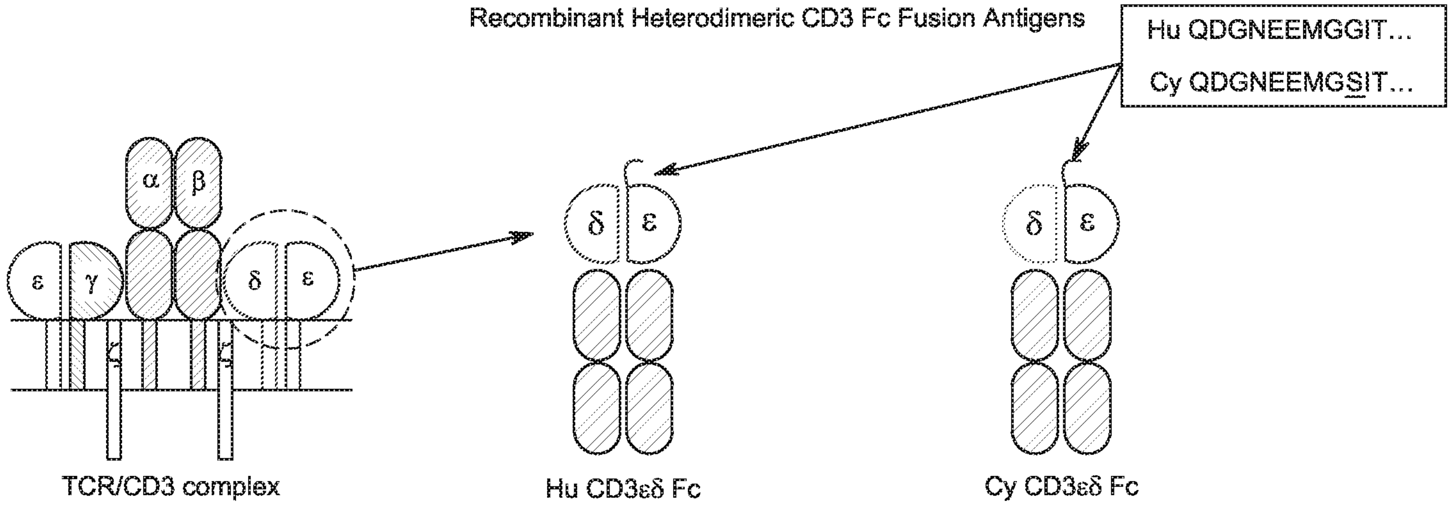

CD3 mAbs are Functional in an IL-2 Stimulation Assay
IL -2 Stimulation
IL -2 Release (pg/ml)
10000
1000
100
10
0
I2C
ADI-20582
ADI-20566
Isotype Control
DPBS
▨ CD3 - Cells
▨ CD3 + Cells

Figure 17



Hu CD3ε Fc

QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMD
GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

Hu CD3δ Fc-HIS

FKIPIEELEDRVFVNCNTSITWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRMCQSCVELDGGSDKTHTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKHHHHHH

Cy CD3ε Fc

QDGNEEMGSITQTPYQVSISGTTVILTCSQHLGSEAQWQHNGKNKEDSGDRLFLPEFSEMEQSGYYVCYPRGSNPEDASHHLYLKARVCENCMEMD
GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK

Cy CD3δ Fc-HIS

FKIPVEELEDRVFVKCNTSVTWVEGTVGTLLTNNTRLDLGKRILDPRGIYRCNGTDIYKDKESAVQVHYRMCQNCVELDPGSDKTHTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKHHHHHH

Figure 18

Parent	Lineage	Selection Type	Theoretical Diversity	Transformation Efficiency
ADI-20580	ADI-18589	H3 Oligo Mutagenesis	>10^4	$2x10^6$

H3 NNK Diversification Scheme

DTAVYYCXXDGYARYYFDYWGQGTLVTVSS
DTAVYYCXRXGYARYYFDYWGQGTLVTVSS
DTAVYYCXRDXYARYYFDYWGQGTLVTVSS
DTAVYYCXRDGXARYYFDYWGQGTLVTVSS
DTAVYYCXRDGYXRYYFDYWGQGTLVTVSS
DTAVYYCXRDGYAXYYFDYWGQGTLVTVSS
DTAVYYCXRDGYARXYFDYWGQGTLVTVSS
DTAVYYCXRDGYARYXFDYWGQGTLVTVSS
DTAVYYCXRDGYARYYXDYWGQGTLVTVSS
DTAVYYCXRDGYARYYFXYWGQGTLVTVSS
DTAVYYCXRDGYARYYFDXWGQGTLVTVSS
DTAVYYCAXXGYARYYFDYWGQGTLVTVSS
DTAVYYCAXDXYARYYFDYWGQGTLVTVSS
DTAVYYCAXDGXARYYFDYWGQGTLVTVSS
DTAVYYCAXDGYXRYYFDYWGQGTLVTVSS
DTAVYYCAXDGYAXYYFDYWGQGTLVTVSS
DTAVYYCAXDGYARXYFDYWGQGTLVTVSS
DTAVYYCAXDGYARYXFDYWGQGTLVTVSS
DTAVYYCAXDGYARYYXDYWGQGTLVTVSS
DTAVYYCAXDGYARYYFXYWGQGTLVTVSS
DTAVYYCAXDGYARYYFDXWGQGTLVTVSS
DTAVYYCARXXYARYYFDYWGQGTLVTVSS
DTAVYYCARXGXARYYFDYWGQGTLVTVSS
DTAVYYCARXGYXRYYFDYWGQGTLVTVSS
DTAVYYCARXGYAXYYFDYWGQGTLVTVSS
DTAVYYCARXGYARXYFDYWGQGTLVTVSS
DTAVYYCARXGYARYXFDYWGQGTLVTVSS
DTAVYYCARXGYARYYXDYWGQGTLVTVSS
DTAVYYCARXGYARYYFXYWGQGTLVTVSS
DTAVYYCARXGYARYYFDXWGQGTLVTVSS
DTAVYYCARDXXARYYFDYWGQGTLVTVSS
DTAVYYCARDXYXRYYFDYWGQGTLVTVSS
DTAVYYCARDXYAXYYFDYWGQGTLVTVSS
DTAVYYCARDXYARXYFDYWGQGTLVTVSS
DTAVYYCARDXYARYXFDYWGQGTLVTVSS
DTAVYYCARDXYARYYXDYWGQGTLVTVSS
DTAVYYCARDXYARYYFXYWGQGTLVTVSS
DTAVYYCARDXYARYYFDXWGQGTLVTVSS
DTAVYYCARDGXXRYYFDYWGQGTLVTVSS
DTAVYYCARDGXAXYYFDYWGQGTLVTVSS
DTAVYYCARDGXARXYFDYWGQGTLVTVSS
DTAVYYCARDGXARYXFDYWGQGTLVTVSS
DTAVYYCARDGXARYYXDYWGQGTLVTVSS
DTAVYYCARDGXARYYFXYWGQGTLVTVSS
DTAVYYCARDGXARYYFDXWGQGTLVTVSS
DTAVYYCARDGYXXYYFDYWGQGTLVTVSS
DTAVYYCARDGYXRXYFDYWGQGTLVTVSS
DTAVYYCARDGYXRYXFDYWGQGTLVTVSS
DTAVYYCARDGYXRYYXDYWGQGTLVTVSS
DTAVYYCARDGYXRYYFXYWGQGTLVTVSS
DTAVYYCARDGYXRYYFDXWGQGTLVTVSS
DTAVYYCARDGYAXXYFDYWGQGTLVTVSS
DTAVYYCARDGYAXYXFDYWGQGTLVTVSS
DTAVYYCARDGYAXYYXDYWGQGTLVTVSS
DTAVYYCARDGYAXYYFXYWGQGTLVTVSS
DTAVYYCARDGYAXYYFDXWGQGTLVTVSS
DTAVYYCARDGYARXXFDYWGQGTLVTVSS
DTAVYYCARDGYARXYXDYWGQGTLVTVSS
DTAVYYCARDGYARXYFXYWGQGTLVTVSS
DTAVYYCARDGYARXYFDXWGQGTLVTVSS
DTAVYYCARDGYARYXXDYWGQGTLVTVSS
DTAVYYCARDGYARYXFXYWGQGTLVTVSS
DTAVYYCARDGYARYXFDXWGQGTLVTVSS
DTAVYYCARDGYARYYXXYWGQGTLVTVSS
DTAVYYCARDGYARYYXDXWGQGTLVTVSS
DTAVYYCARDGYARYYFXXWGQGTLVTVSS

Figure 19

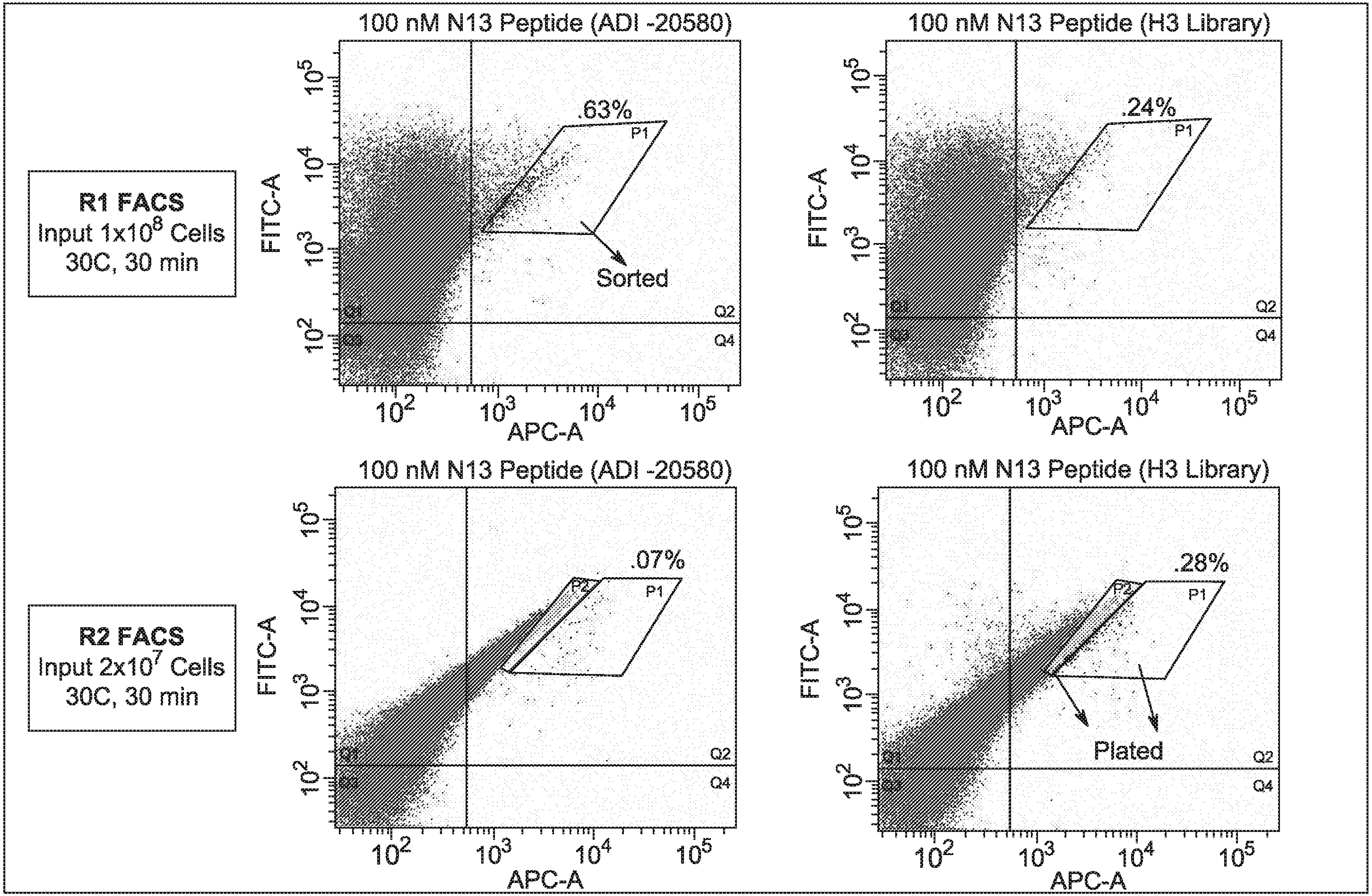

R1 FACS
Input 1x10^8 Cells
30C, 30 min
R2 FACS
Input 2x10^7 Cells
30C, 30 min
100 nM N13 Peptide (ADI -20580)
100 nM N13 Peptide (H3 Library)
FITC-A
APC-A
10^2
10^3
10^4
10^5
.63%
.24%
.07%
.28%
P1
P2
Q1
Q2
Q3
Q4
Sorted
Plated

Figure 20

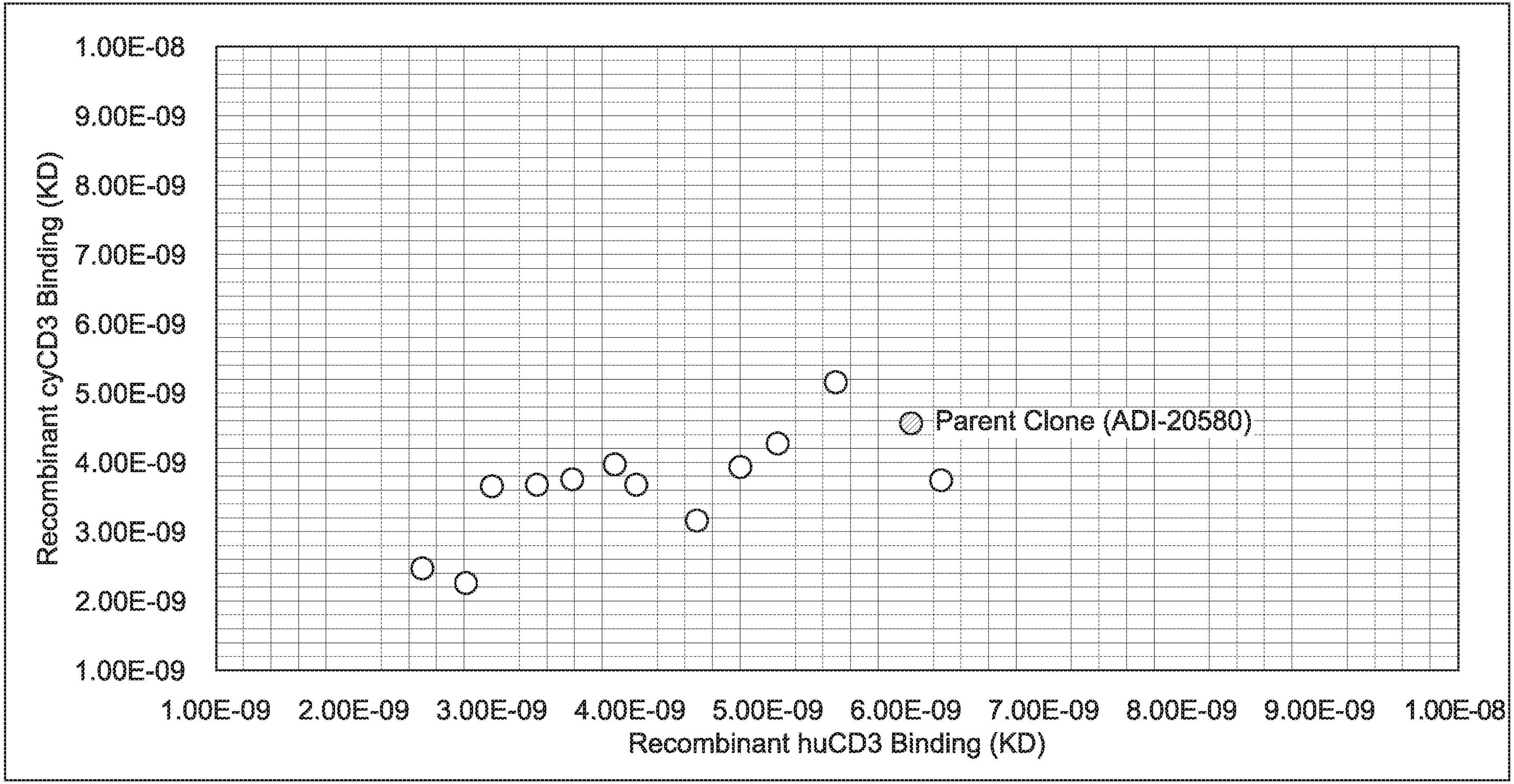

1.00E-08
9.00E-09
8.00E-09
7.00E-09
6.00E-09
5.00E-09
4.00E-09
3.00E-09
2.00E-09
1.00E-09
Recombinant cyCD3 Binding (KD)
Parent Clone (ADI-20580)
1.00E-09
2.00E-09
3.00E-09
4.00E-09
5.00E-09
6.00E-09
7.00E-09
8.00E-09
9.00E-09
1.00E-08
Recombinant huCD3 Binding (KD)

Figure 21

ADI ID	Type	H3	Repeats	K_D Cy CD3εδ Fc (M)	Jurkat CD3+ (Median MFI)	Jurkat CD3- (Median MFI)	Cy HSC-F (Median MFI)	PSR Score	Fab Tm (°C)
ADI-20580	Parent	ARDGYARYYFDY	50	3.0E-09	5829	220	11651	0.45	N.D.
ADI-21959	Progeny	ARDGYGRYYFDY	64	7.8E-09	7735	159	11765	0.28	81.5
ADI-21961	Progeny	ARDGYARYYYDY	32	4.0E-09	7123	162	11681	0.23	80.0
ADI-21967	Progeny	ARDGYARYFFDY	2	7.9E-09	7227	147	11808	0.19	79.5
ADI-21969	Progeny	GSDGYARYYFDY	1	1.3E-08	1175	70	1977	0.16	69.0
ADI-21970	Progeny	ARDGYGRYFFDY	1	2.9E-09	7059	170	12091	0.29	81.0
ADI-21960	Progeny	ARDGYARYYFDV	3	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
ADI-21962	Progeny	SRDGYARYYFDY	2	1.2E-08	7072	137	11697	0.14	76.0
ADI-21963	Progeny	ARDGYARYYFDI	1	6.0E-09	6844	141	11676	0.17	81.5
ADI-21964	Progeny	NRDGYARYYYDY	1	8.6E-09	7354	148	12083	0.22	72.0
ADI-21965	Progeny	ARDGYGRYYFDA	1	1.0E-09	7110	146	12038	0.28	82.0
ADI-21966	Progeny	ARDGYARYFFDN	1	1.6E-09	6952	157	11501	0.20	77.0
ADI-21968	Progeny	ARDGYGRYYFDR	1	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
ADI-21973	Rational	ARDGYGRYFYDY	N.A.	3.4E-09	7466	190	12573	0.30	81.5
ADI-21978	Rational	ARDGYGRYFYDV	N.A.	2.2E-09	7432	187	12230	0.29	81.5
ADI-21974	Rational	ARDGYGRYFFDV	N.A.	2.7E-09	7268	170	11486	0.29	82.5
ADI-21971	Rational	ARDGYGRYYYDY	N.A.	1.7E-09	7297	180	12398	0.27	81.5
ADI-21972	Rational	ARDGYGRYYYDV	N.A.	3.8E-09	7569	183	12670	0.30	83.0

Figure 22

ADI-21978 Potential Degradation Motifs

ADI ID	CDR H2	CDR H3	CDR L1	Fab KD Cy CD3εδ Fc (nM)
ADI-21978 (ADI-22523)	WIDLENGNTIYDPKFQG	ARDGYGRYFYDV	KSSQSLLNSRTGKNYLA	2.1
ADI-23667	WIDLENANTIYDPKFQG	ARDGYGRYFYDV	KSSQSLLNSRTGKNYLA	2.3
ADI-23668	WIDLENGNTIYDAKFQG	ARDGYGRYFYDV	KSSQSLLNSRTGKNYLA	1.5
ADI-23669	WIDLENGNTIYDPKFQG	ARDAYGRYFYDV	KSSQSLLNSRTGKNYLA	4.1
ADI-23660	WIDLENGNTIYDAKFQG	ARDGYGRYFYDV	KSSQSLLNARTGKNYLA	1.7

ADI ID	CDR H2	CDR H3	CDR L1	Fab KD Cy CD3εδ Fc (nM)
ADI-21978 (ADI-22523)	WIDLENGNTIYDPKFQG	ARDGYGRYFYDV	KSSQSLLNSRTGKNYLA	3.4
ADI-25133	WIDLENANTIYDAKFQG	ARDAYGRYFYDV	KSSQSLLNARTGKNYLA	4.2

Figure 23A

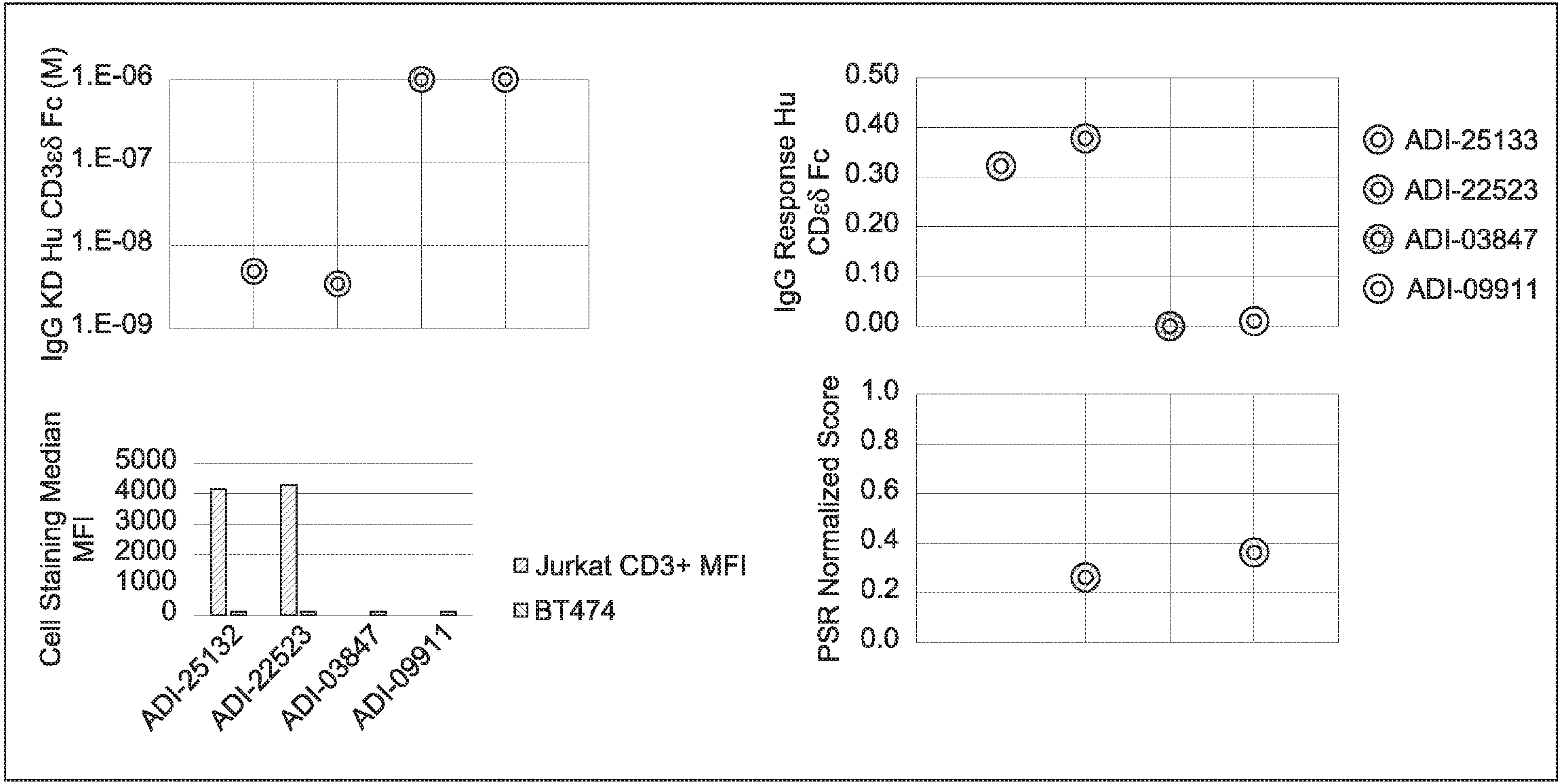

IgG KD Hu CD3εδ Fc (M)
1.E-06
1.E-07
1.E-08
1.E-09
IgG Response Hu CDεδ Fc
0.50
0.40
0.30
0.20
0.10
0.00
ADI-25133
ADI-22523
ADI-03847
ADI-09911
Cell Staining Median MFI
5000
4000
3000
2000
1000
0
ADI-25132
ADI-22523
ADI-03847
ADI-09911
▨ Jurkat CD3+ MFI
▨ BT474
PSR Normalized Score
1.0
0.8
0.6
0.4
0.2
0.0

Figure 23B

Parent	Lineage	Selection Type	Theoretical Diversity
ADI-21978 (ADI-22523)	ADI-18589	H3 Oligo Mutagenesus	$<10^4$

ADI-21978(ADI-22523) FR3-CDR H3-FR4

EDTAVYYCARDGYGRYFYDVWGQGTLVTVS

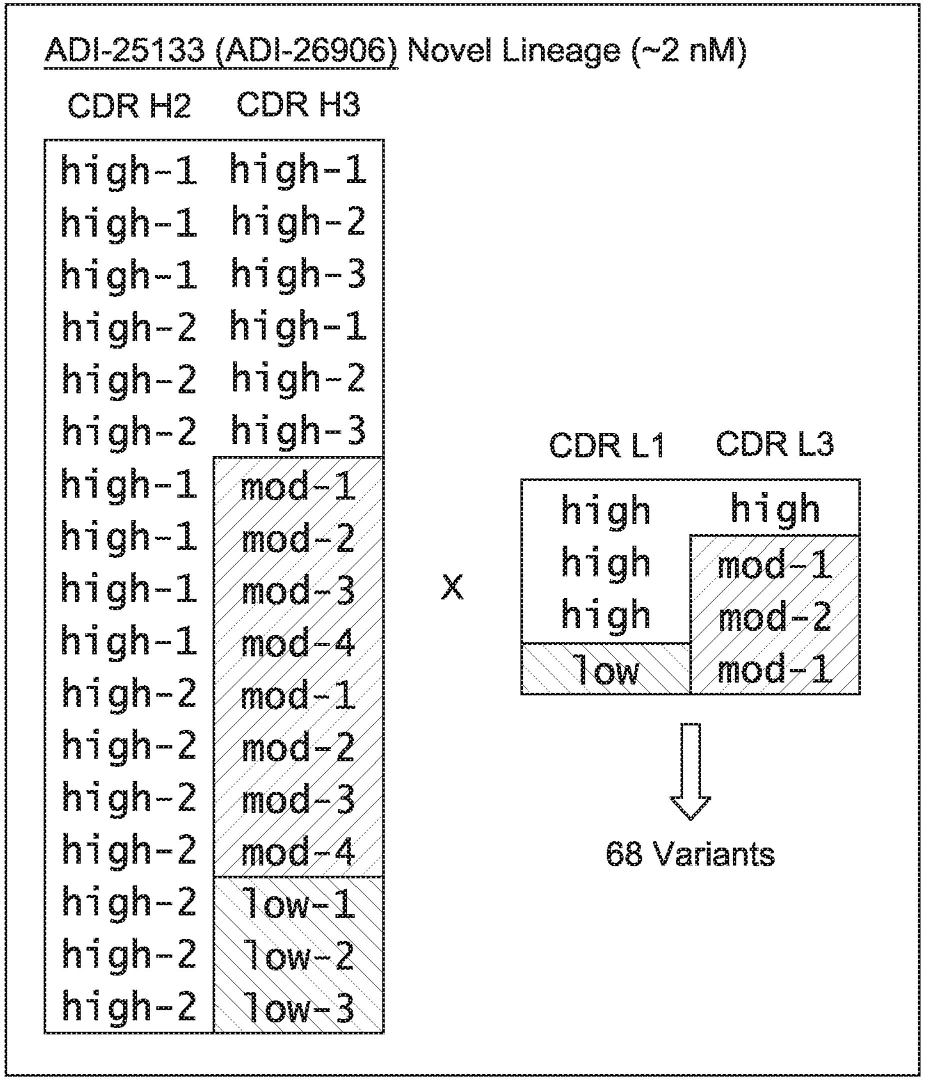
EDTAVYYCXRXGYGRYFYDVWGQGTLVTVS
EDTAVYYCXRDXYGRYFYDVWGQGTLVTVS
EDTAVYYCAXXGYGRYFYDVWGQGTLVTVS
EDTAVYYCAXDXYGRYFYDVWGQGTLVTVS
EDTAVYYCARXXYGRYFYDVWGQGTLVTVS
EDTAVYYCARXGXGRYFYDVWGQGTLVTVS
EDTAVYYCARXGYXRYFYDVWGQGTLVTVS
EDTAVYYCARXGYGXYFYDVWGQGTLVTVS
EDTAVYYCARXGYGRXFYDVWGQGTLVTVS
EDTAVYYCARXGYGRYXYDVWGQGTLVTVS
EDTAVYYCARXGYGRYFXDVWGQGTLVTVS
EDTAVYYCARXGYGRYFYXVWGQGTLVTVS
EDTAVYYCARXGYGRYFYDXWGQGTLVTVS
EDTAVYYCARDXXGRYFYDVWGQGTLVTVS
EDTAVYYCARDXYXRYFYDVWGQGTLVTVS
EDTAVYYCARDXYGXYFYDVWGQGTLVTVS
EDTAVYYCARDXYGRXFYDVWGQGTLVTVS
EDTAVYYCARDXYGRYXYDVWGQGTLVTVS
EDTAVYYCARDXYGRYFXDVWGQGTLVTVS
EDTAVYYCARDXYGRYFYXVWGQGTLVTVS
EDTAVYYCARDXYGRYFYDXWGQGTLVTVS

Selection →

Novel CD3 Binder ADI -21978 (ADI-22523) H3 Mutagenesis Progeny

Clone ID	CDR H3	KD Hu CD3εδ Fc (M)	Response Hu CD3εδ Fc
ADI-21978	ARDGYGRYFYDV	3.3E-09	0.25
ADI-26907	GRDAYGRYFYDV	3.8E-09	0.18
ADI-29607	ARDAYGRYFYRV	4.1E-09	0.15
ADI-29608	PRDAYGRYFYDV	4.3E-09	0.20
ADI-29609	ARDAYGRYFYDG	6.4E-09	0.27
ADI-29610	ARDRYGAYFYDV	6.7E-09	0.26
ADI-29611	ARDRYGRYFYDV	7.3E-09	0.27
ADI-29613	ARDSYGRYFYDV	7.8E-09	0.28
ADI-29614	ARDVYGRYLYDV	9.9E-09	0.14
ADI-26912	ARDVLGRYFYDV	1.1E-08	0.18
ADI-26913	ARDQYGRYFYDV	1.2E-08	0.27
ADI-29617	ARDVYRRYFYDV	1.2E-08	0.15
ADI-29618	VRDLRGRYFYDV	1.3E-08	0.15
ADI-26916	ARDVYGRYFYDL	1.3E-08	0.22
ADI-26917	ARDAYGGYFYDV	2.1E-08	0.22
ADI-26918	ARDNYGGYFYDV	2.5E-08	0.17

Figure 24



ADI-25133 (ADI-26906) Novel Lineage (~2 nM)

CDR H2	CDR H3
high-1	high-1
high-1	high-2
high-1	high-3
high-2	high-1
high-2	high-2
high-2	high-3
high-1	mod-1
high-1	mod-2
high-1	mod-3
high-1	mod-4
high-2	mod-1
high-2	mod-2
high-2	mod-3
high-2	mod-4
high-2	low-1
high-2	low-2
high-2	low-3

×

CDR L1	CDR L3
high	high
high	mod-1
high	mod-2
low	mod-1

68 Variants

Figure 25A

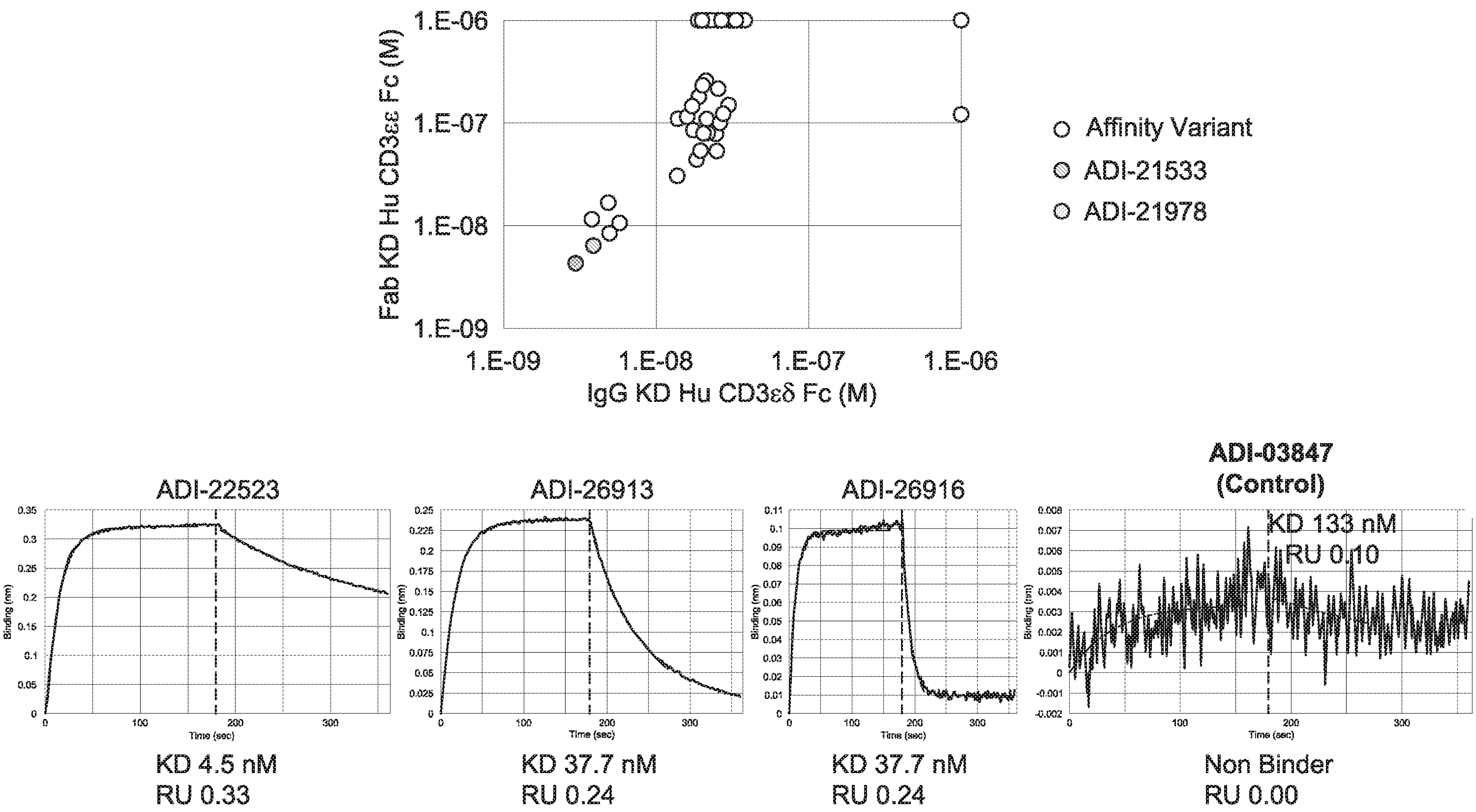

1.E-06
1.E-07
1.E-08
1.E-09
Fab KD Hu CD3εε Fc (M)
1.E-09
1.E-08
1.E-07
1.E-06
IgG KD Hu CD3εδ Fc (M)
○ Affinity Variant
◍ ADI-21533
◍ ADI-21978
ADI-22523
ADI-26913
ADI-26916
ADI-03847
(Control)
Binding (nm)
Time (sec)
0
100
200
300
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0.225
0.175
0.125
0.075
0.025
0.11
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.008
0.007
0.006
0.005
0.004
0.003
0.002
0.001
-0.001
-0.002
KD 4.5 nM
RU 0.33
KD 37.7 nM
RU 0.24
KD 37.7 nM
RU 0.24
KD 133 nM
RU 0.10
Non Binder
RU 0.00

Figure 25B

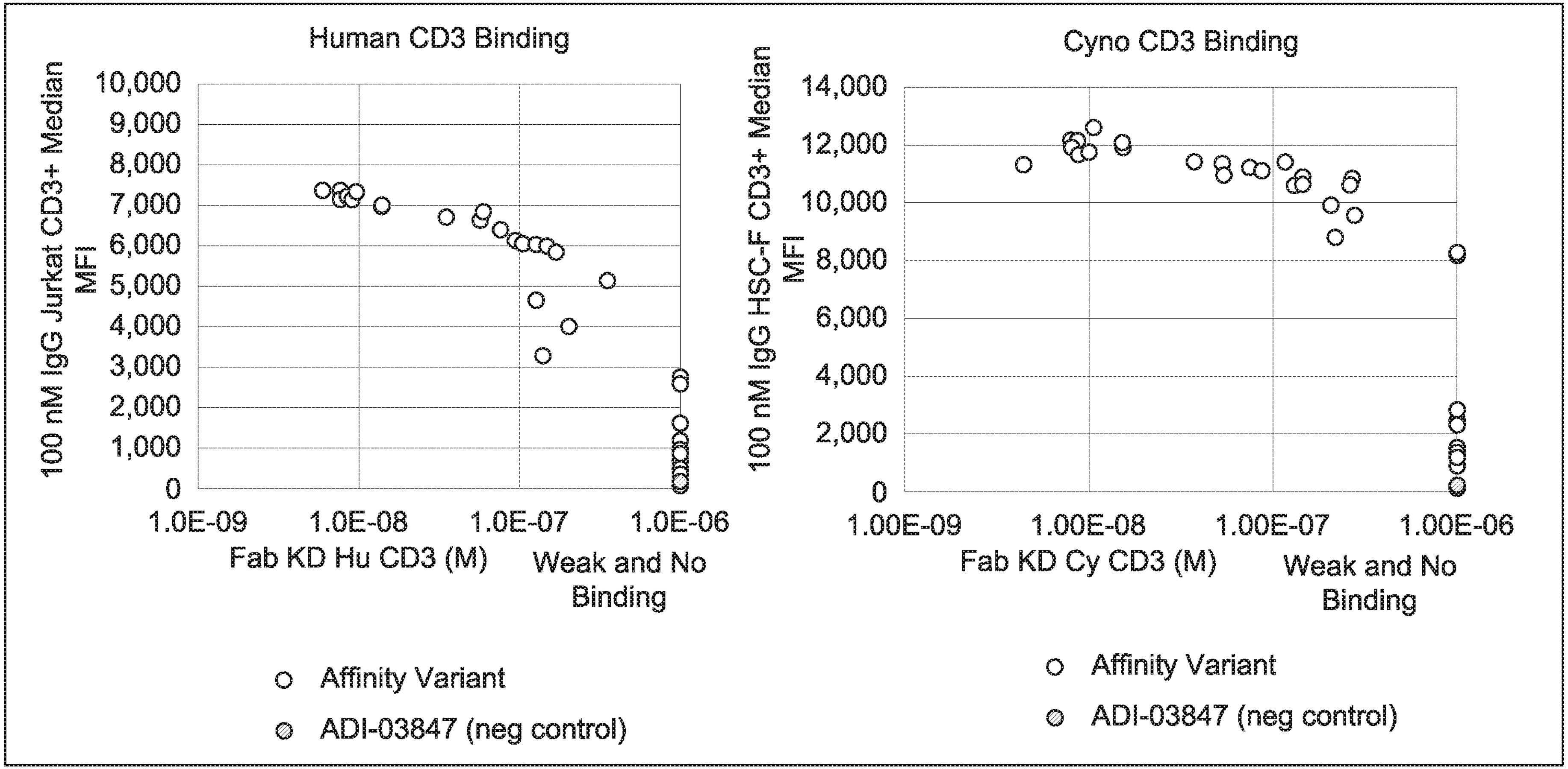
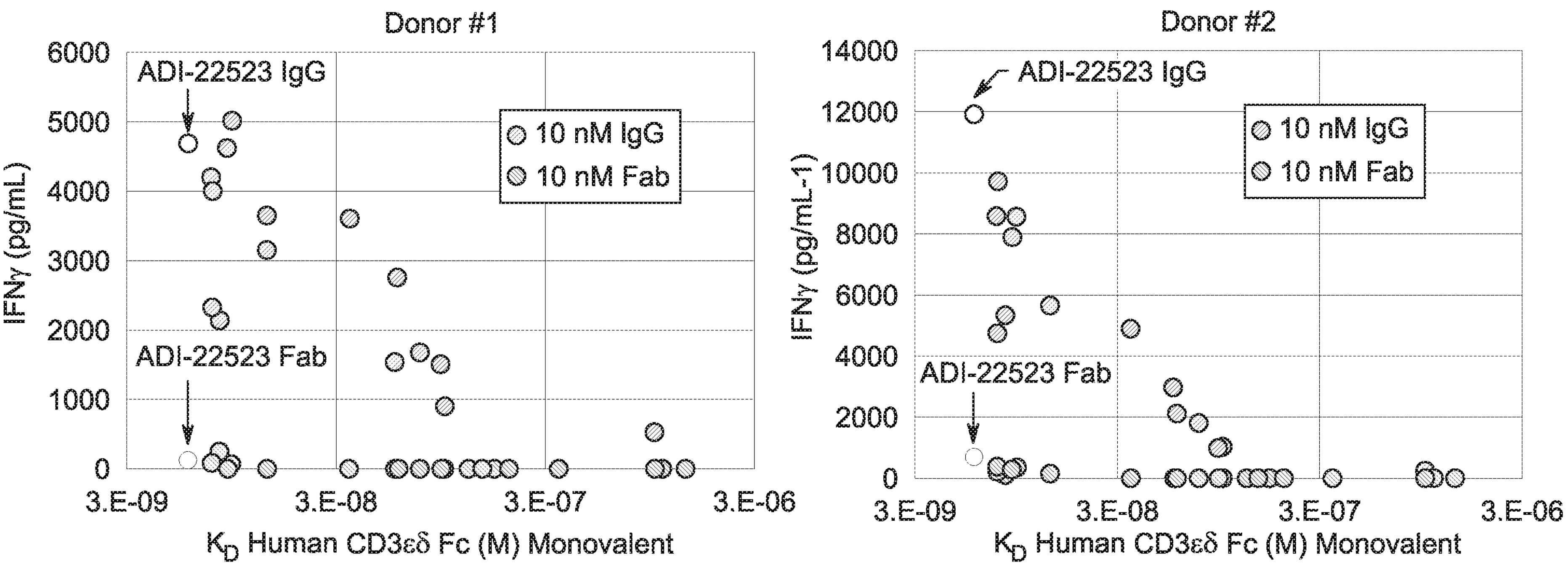
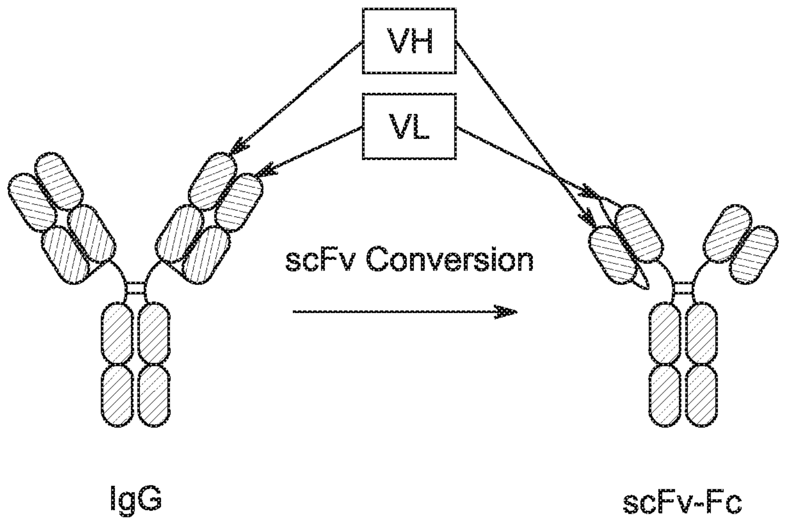

Human CD3 Binding
100 nM IgG Jurkat CD3+ Median MFI
10,000
9,000
8,000
7,000
6,000
5,000
4,000
3,000
2,000
1,000
0
1.0E-09
1.0E-08
1.0E-07
1.0E-06
Fab KD Hu CD3 (M)
Weak and No Binding
○ Affinity Variant
▨ ADI-03847 (neg control)
Cyno CD3 Binding
100 nM IgG HSC-F CD3+ Median MFI
14,000
12,000
10,000
8,000
6,000
4,000
2,000
0
1.00E-09
1.00E-08
1.00E-07
1.00E-06
Fab KD Cy CD3 (M)
Weak and No Binding
○ Affinity Variant
▨ ADI-03847 (neg control)

Figure 25C



Anti-CD3 Clones with Strong Soluble IgG1 Activity Show Low IFNγ Production by PBMC as Fab at 10 nM

Figure 25D



scFv Matrix

- H/L or L/H Orientation
- +/- H44-L100 Disulfide
- **Linker** Length 15, 20, 25, 30 Using Repeats of $(Gly_4Ser)_n$
- **Tether** Length Direct Fusion to Hinge or Tether Length 10

ADI ID	DS	VH FR2	VL FR4
ADI-21978	No DS	WVRQAPGQRLEWMG	FGGGTKVEIK
	DS1	WVRQAPGQ**C**LEWMG	FG**C**GTKVEIK
	DS2	WVRQAPG**GC**LEWMG	FG**C**GTKVEIK

Figure 26A

Parent	Type	#	KD Hu CD3εδ Fc (M)	Fold Reduction	KD Cy CD3εδ Fc (M)	Fold Reduction
ADI-21978	IgG	1	2.7E-09	N/A	1.9E-09	N/A
	scFv-Fc	15	5.9E-09	2.2	4.8E-09	2.5
	scFv-Fc (DS1)	13	6.0E-09	2.6	6.9E-08	3.6
	scFv-Fc (DS2)	1	7.2E-09	2.7	6.4E-09	3.4

Figure 26B

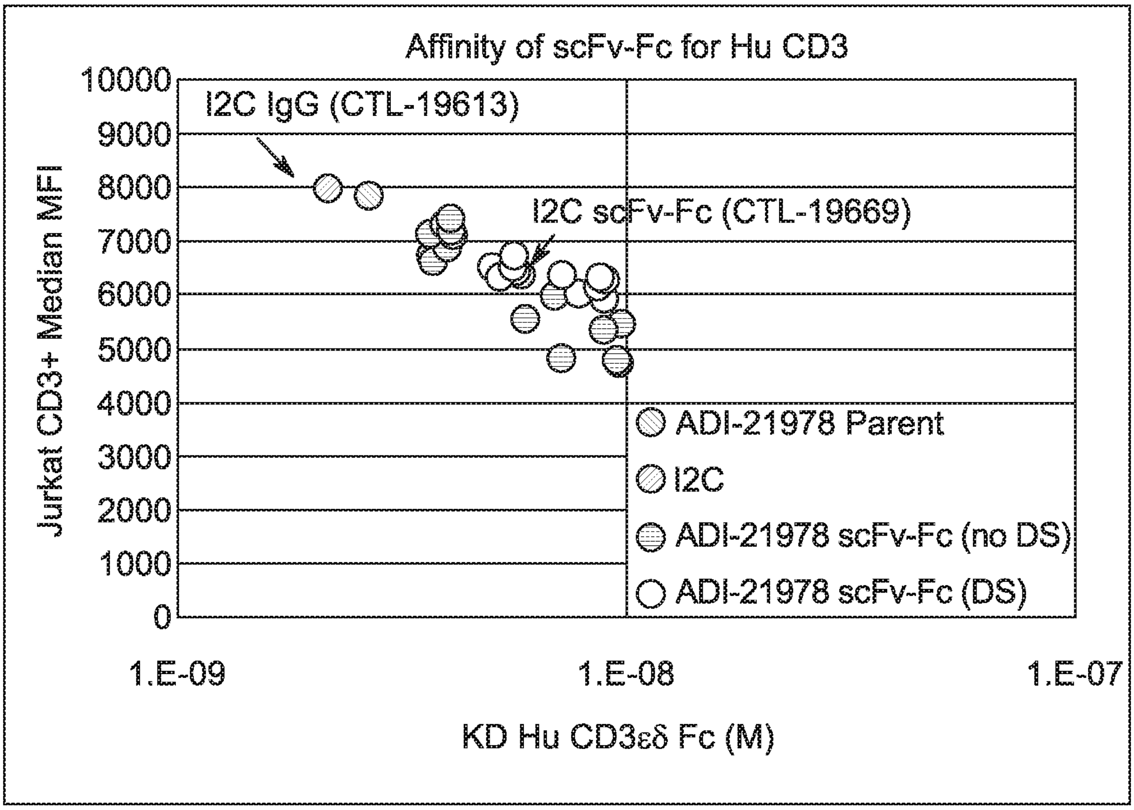
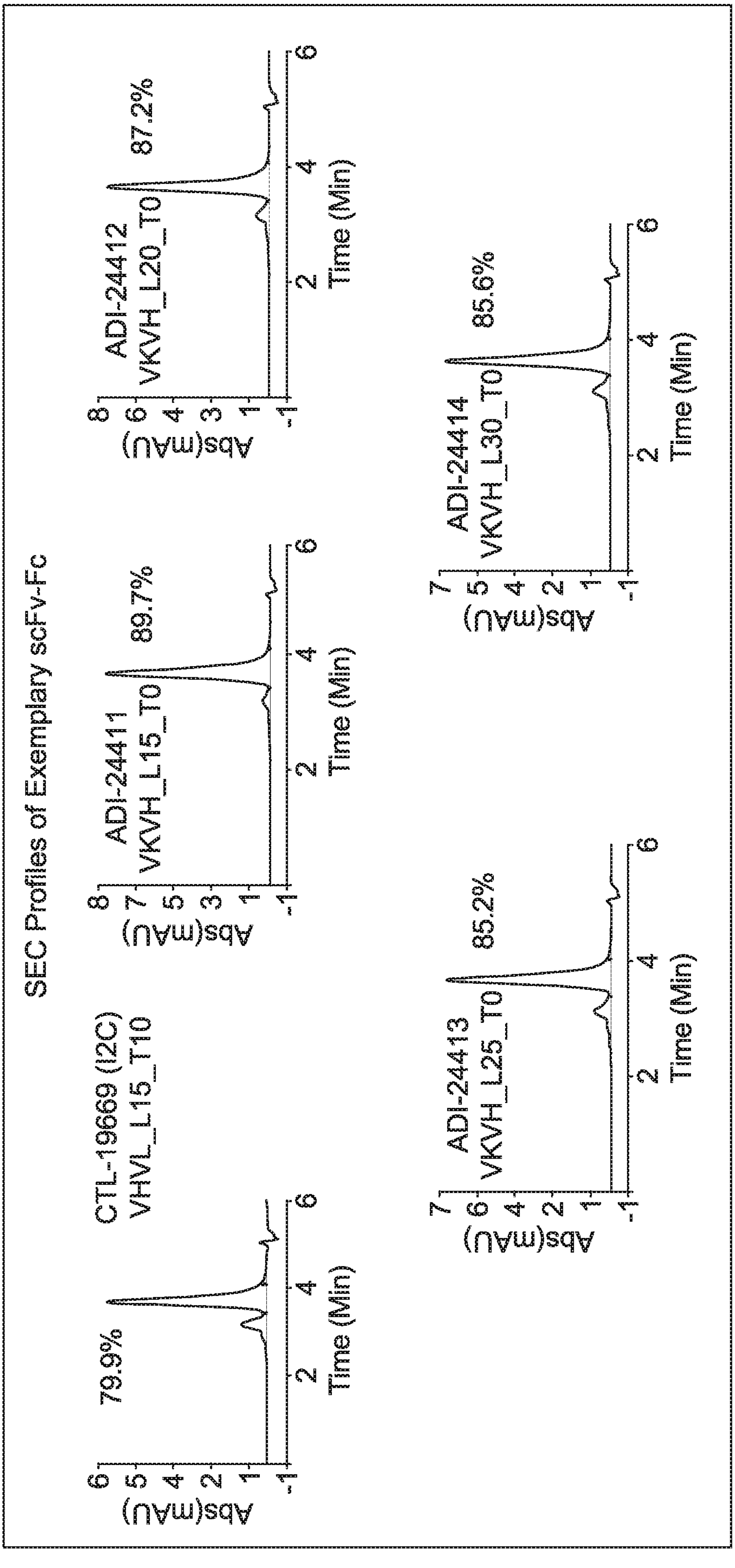


Figure 26C



SEC Profiles of Exemplary scFv-Fc

Figure 26D

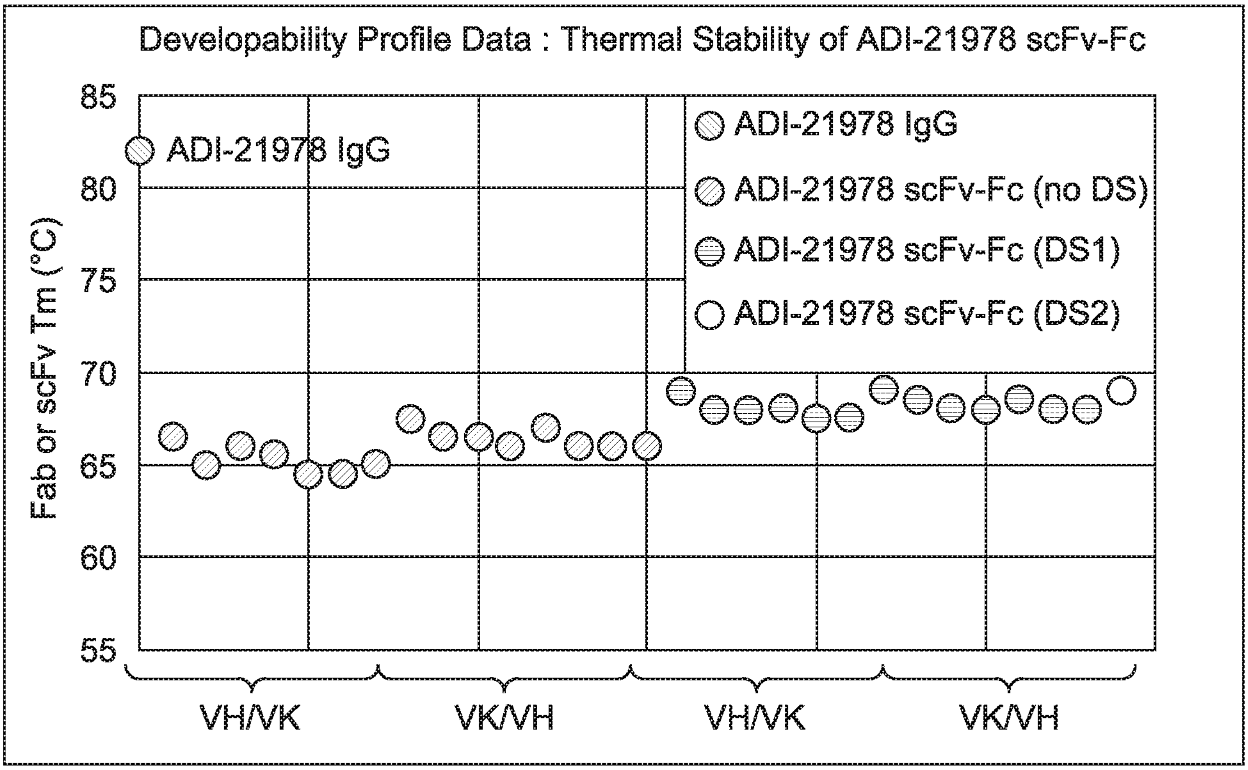


Figure 26E

Developability Profile Data

Parent	Type	#	DSF Tm (°C)	ΔTM Fab/scFv	ΔTM +/-DS
ADI-21978	IgG	1	82.0	N/A	N/A
	scFv-Fc	15	65.9	-16.1	N/A
	scFv-Fc (DS1)	13	68.2	-13.8	+2.3
	scFv-Fc (DS2)	1	69.0	-13.0	+3.1

Figure 26F

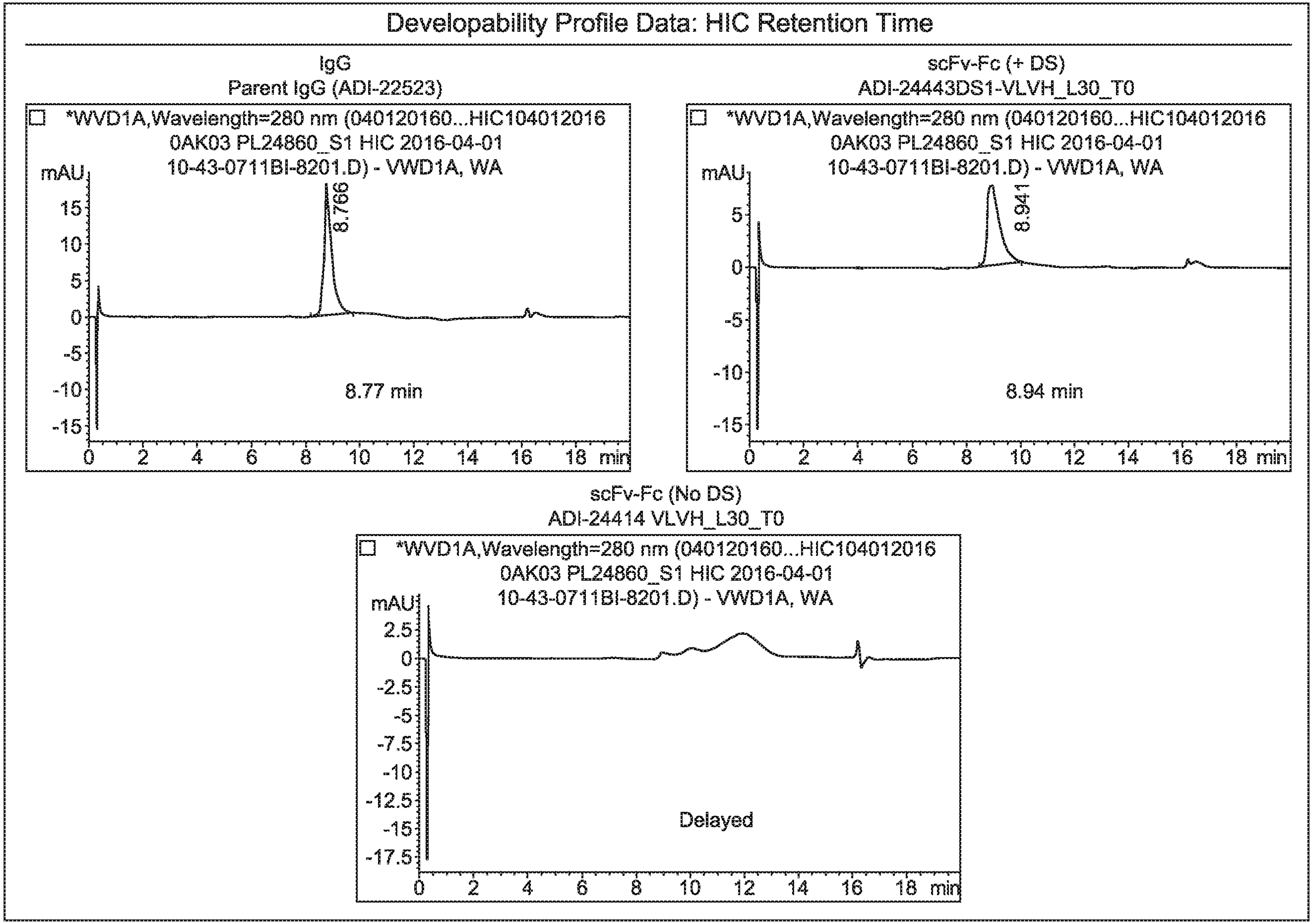

Developability Profile Data: HIC Retention Time
IgG
Parent IgG (ADI-22523)
☐ *WVD1A,Wavelength=280 nm (040120160...HIC104012016
0AK03 PL24860_S1 HIC 2016-04-01
10-43-0711BI-8201.D) - VWD1A, WA
mAU
15
10
5
0
-5
-10
-15
8.766
8.77 min
0
2
4
6
8
10
12
14
16
18
min
scFv-Fc (+ DS)
ADI-24443DS1-VLVH_L30_T0
☐ *WVD1A,Wavelength=280 nm (040120160...HIC104012016
0AK03 PL24860_S1 HIC 2016-04-01
10-43-0711BI-8201.D) - VWD1A, WA
mAU
5
0
-5
-10
-15
8.941
8.94 min
0
2
4
6
8
10
12
14
16
18
min
scFv-Fc (No DS)
ADI-24414 VLVH_L30_T0
☐ *WVD1A,Wavelength=280 nm (040120160...HIC104012016
0AK03 PL24860_S1 HIC 2016-04-01
10-43-0711BI-8201.D) - VWD1A, WA
mAU
2.5
0
-2.5
-5
-7.5
-10
-12.5
-15
-17.5
Delayed
0
2
4
6
8
10
12
14
16
18
min

Figure 26G

HC Design	Germline	FR Mutations	Proteing Sequence
HuSP34-HC1	VH3-23	0	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVSRIRSKYNNYATYY ADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS
HuSP34-HC2	VH3-23	3	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKSTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS
HuSP34-HC3	VH3-72	0	EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYY ADSVKDRFTISRDDSKNSLYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS
HuSP34-HC4	VH3-72	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNSLYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

LC Design	Germline	FR Mutations	Proteing Sequence
HuSP34-LC1	VL8-61	0	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWYQQTPGQAPRTLIYGTNKRAPGVPDR FSGSILGNKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL
HuSP34-LC2	VL8-61	1	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWYQQTPGQAPRTLIGGTNKRAPGVPDR FSGSILGNKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL
HuSP34-LC3	VL8-61	5	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDR FSGSLLGDKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL
HuSP34-LC4	VL7-46	0	QAVVTQEPSLTVSPGGTVTLTCRSSTGAVTTSNYANWFQQKPGQAPRTLIYGTNKRAPWTPAR FSGSLLGGKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL
HuSP34-LC5	VL7-46	6	QAVVTQEPSLTVSPGGTVTLTCRSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPAR FSGSLLGDKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL
HuSP34-LC6	VH3-15	0	EIVMTQSPATLSVSPGERATLSCRSSTGAVTTSNYANWYQQKPGQAPRLLIYGTNKRAPGIPAR FSGSGSGTEFTLTISSLQSEDFAVYYCALWYSNLWVFGGGTKVEIK
HuSP34-LC7	VH3-15	6	EIVVTQSPATLSVSPGERATLSCRSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPAR FSGSGSGDEATLTISSLQSEDFAVYYCALWYSNLWVFGGGTKVEIK

Mutations Occurring with Respect to Human Germline Highlighted in **RED**

Figure 27

Type	HC	LC	ADI ID	Fab K_D Hu CDεδ Fc (M)	Fab K_D Cy CDεδ Fc (M)	Jurkat CD3+ 100nM Fab (MFI)	Jurkat CD3- 100nM Fab (MFI)	HSC-F 100 nM Fab (MFI)	Fab Tm (°C)	AC-SINS Δλmax (nm)	PSR Norm. MFI
ChSP34				5.8E-09	8.7E-09	1404.9	77.7	11806.1	60.5	9.9	1125.3
HuSP34	HuSP34-HC3	HuSP34-LC5		3.6E-09	4.9E-09	1992.6	79.1	11843.6	N.D.	26.5	885.8
	HuSP34-HC4	HuSP34-LC7		1.8E-08	2.1E-08	982.1	103.6	10735.0	N.D.	18.3	N.D.
	HuSP34-HC2	HuSP34-LC3	ADI-16606	5.8E-09	8.0E-09	1628.9	80.5	11885.9	60.5	5.1	400.2
	HuSP34-HC2	HuSP34-LC5		5.3E-09	7.5E-09	1918.0	102.2	12048.5	N.D.	12.3	N.D.
	HuSP34-HC4	HuSP34-LC5		5.9E-09	7.1E-09	1713.6	84.0	11435.5	N.D.	20.0	720.1

Figure 27 (Continued)

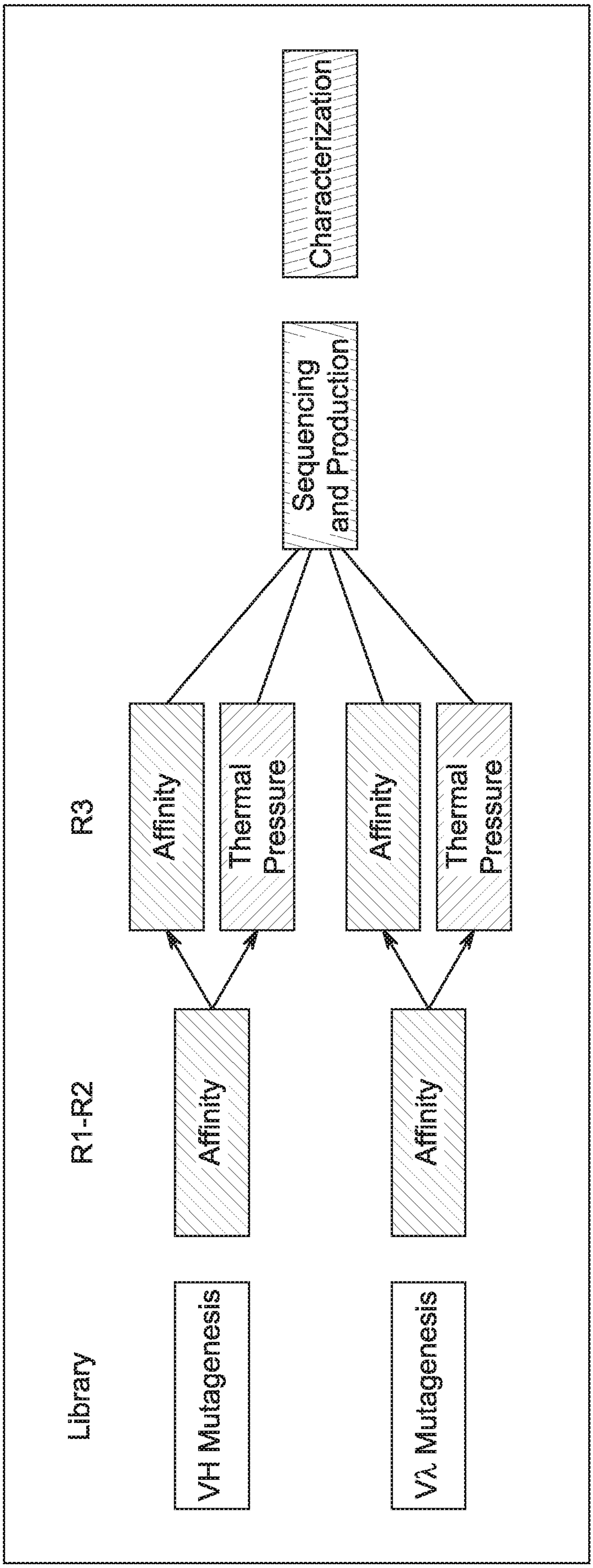

Library
R1-R2
R3
VH Mutagenesis
Affinity
Affinity
Thermal Pressure
Vλ Mutagenesis
Affinity
Affinity
Thermal Pressure
Sequencing and Production
Characterization

Figure 28A

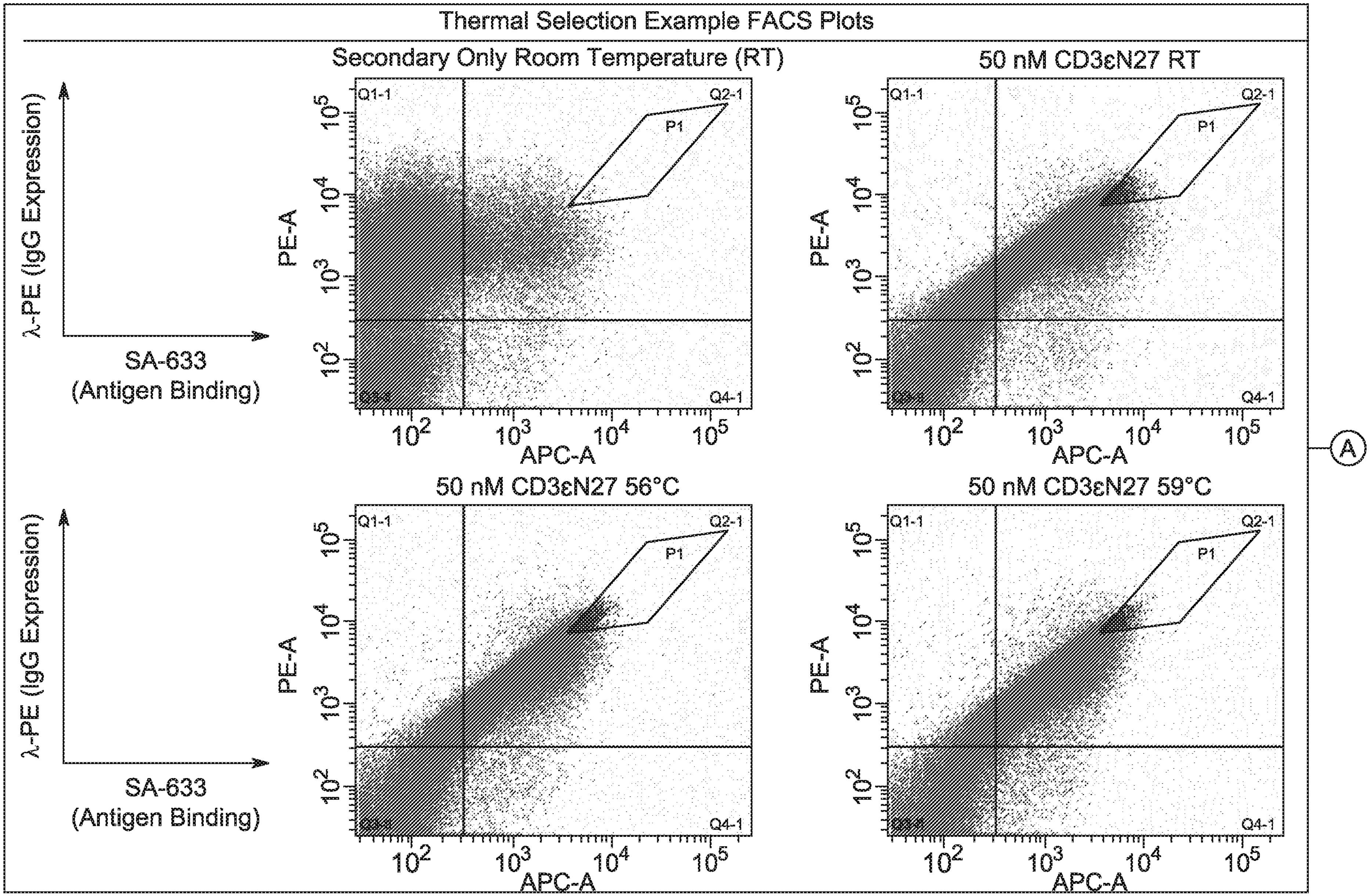

Thermal Selection Example FACS Plots
λ-PE (IgG Expression)
SA-633
(Antigen Binding)
Secondary Only Room Temperature (RT)
50 nM CD3εN27 RT
50 nM CD3εN27 56°C
50 nM CD3εN27 59°C
PE-A
APC-A
10^2
10^3
10^4
10^5
Q1-1
Q2-1
Q3-1
Q4-1
P1
A

Figure 28B

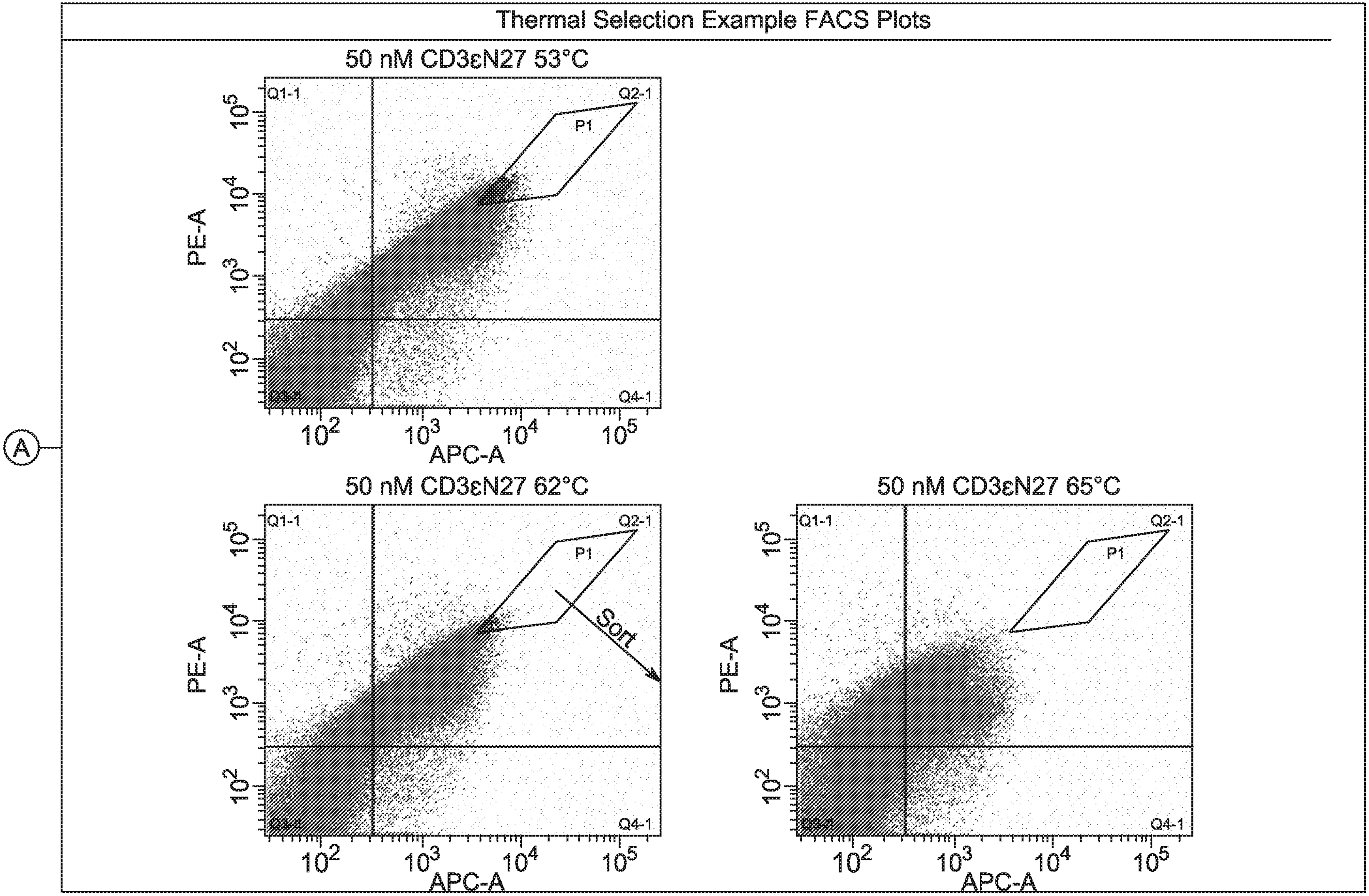


Figure 28B (Continued)

Vλ Mutagenesis Affinity-pressured Output Sequencing

Parent	Vλmut	Repeats	VL-FR1	VL-CDR L1	VL-FR2	VL-CDR L2	VL-FR3	VL-CDR L3	VL-FR4
ADI-16606	Parent	2	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	L95R	45	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	R24G, L95R	9	QTVVTQEPSFSVSPGGTVTLTC	GSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	T27A, L95R	7	QTVVTQEPSFSVSPGGTVTLTC	RSSAGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	F11L, L95R	6	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	K70R, L95R	4	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDRAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	T2A, L95R	4	QAVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	T2A, T27I, L95R	4	QAVVTQEPSFSVSPGGTVTLTC	RSSIGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	S30cG, L95R	2	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTGNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	T39A, A43T, L95R	2	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQAPGQTPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	N52S, L95R	2	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTSKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	R24G, K53R	1	QTVVTQEPSFSVSPGGTVTLTC	GSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNRRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	Q37R, L95R	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVRQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	T74I, L95R	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALIITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	K53R, S93N	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNRRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYNNLWV	FGGGTKLTVL
	R24K, L95R	1	QTVVTQEPSFSVSPGGTVTLTC	KSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	L95H	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNHWV	FGGGTKLTVL
	K53R, L95R	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNRRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL

VH Mutagenesis Affinity-pressured Output Sequencing

Parent	VHmut	Repeats	VH-FR1	VH-CDR H1	VH-FR2	VH-CDR H2	VH-FR3	VH-CDR H3	VH-FR4
ADI-16606	Parent	80	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	G96D, G99R	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHDNFRNSYVSWFAY	WGQGTLVTVSS
	N30D, Y102H	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFDTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAH	WGQGTLVTVSS
	Y100bH	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSHVSWFAY	WGQGTLVTVSS
	L5V, N54D, Y100bH	1	EVQLVESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNDYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSHVSWFAY	WGQGTLVTVSS
	Y102H	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAH	WGQGTLVTVSS
	N30D	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFDTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	L5S	1	EVQLSESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	T31A	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNAYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS

Figure 28C

Vλ Mutagenesis Thermal-pressured Output Sequencing

Parent	VλMut	Repeats	VL-FR1	VL-CDR L1	VL-FR2	VL-CDR L2	VL-FR3	VL-CDR L3	VL-FR4
ADI-16606	Parent	2	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	L95R	20	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	T27A, L95R	10	QTVVTQEPSFSVSPGGTVTLTC	RSSAGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	F11L, L95R	9	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	R24G, L95R	6	QTVVTQEPSFSVSPGGTVTLTC	GSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	F11L, S93N	6	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYNNLWV	FGGGTKLTVL
	T2A, T27I, L95R	6	QAVVTQEPSFSVSPGGTVTLTC	RSSIGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	F11L	4	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	F11L, R24G	2	QTVVTQEPSLSVSPGGTVTLTC	GSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	F11L, T74I, S84A	2	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALIITGAQADDEADYYC	ALWYSNLWV	FGGGTKLTVL
	Q1R, F11L, S93N	2	RTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYNNLWV	FGGGTKLTVL
	S93N	2	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYNNLWV	FGGGTKLTVL
	R24G, N52D, D69G	2	QTVVTQEPSFSVSPGGTVTLTC	GSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTDKRAP	GVPDRFSGSLLGGKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	T2P	2	QPVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	T2A, L95R	2	QAVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	R24G	2	QTVVTQEPSFSVSPGGTVTLTC	GSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	Q1R, R24G, T74I	1	RTVVTQEPSFSVSPGGTVTLTC	GSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALIITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	F11L, S12A, N52D, K53Q, A72T	1	QTVVTQEPSLAVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTDQRAP	GVPDRFSGSLLGDKATLTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	T2A, P8Q, T27I, L95R	1	QAVVTQEQSFSVSPGGTVTLTC	RSSIGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	F11L, R24G, S25P	1	QTVVTQEPSLSVSPGGTVTLTC	GPSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	T39A, K53Q, S84A	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQAPGQAPRGLIG	GTNQRAP	GVPDRFSGSLLGDKAALTITGAQADDEADYYC	ALWYSNLWV	FGGGTKLTVL
	A78V, L95R	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGVQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	N52D, A78V	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTDKRAP	GVPDRFSGSLLGDKAALTITGVQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	A72V	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAVLTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	S84A	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDEADYYC	ALWYSNLWV	FGGGTKLTVL
	P8T, F11L, N52D, D81E	1	QTVVTQETSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTDKRAP	GVPDRFSGSLLGDKAALTITGAQAEDESDYYC	ALWYSNLWV	FGGGTKLTVL
	T74I, L95R	1	QTVVTQEPSFSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALIITGAQADDESDYYC	ALWYSNRWV	FGGGTKLTVL
	R24G, T27A	1	QTVVTQEPSFSVSPGGTVTLTC	GSSAGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYSNLWV	FGGGTKLTVL
	F11L, S84A	1	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDEADYYC	ALWYSNLWV	FGGGTKLTVL
	T2P, T30bA, T39A, K53Q, S93N	1	QPVVTQEPSFSVSPGGTVTLTC	RSSTGAVTASNYAN	WVQQAPGQAPRGLIG	GTNQRAP	GVPDRFSGSLLGDKAALTITGAQADDESDYYC	ALWYNNLWV	FGGGTKLTVL
	F11L, N52D, D81E	1	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTDKRAP	GVPDRFSGSLLGDKAALTITGAQAEDESDYYC	ALWYSNLWV	FGGGTKLTVL
	F11L, S84A, S93N	1	QTVVTQEPSLSVSPGGTVTLTC	RSSTGAVTTSNYAN	WVQQTPGQAPRGLIG	GTNKRAP	GVPDRFSGSLLGDKAALTITGAQADDEADYYC	ALWYNNLWV	FGGGTKLTVL

Figure 28D

VH Mutagenesis Thermal-pressured Output Sequencing

Parent	VHMut	Repeats	VH-FR1	VH-CDR H1	VH-FR2	VH-CDR H2	VH-FR3	VH-CDR H3	VH-FR4
ADI-16606	Parent	78	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	N30D	4	EVQLLESGGGLVQPGGSLRLSCAASG	FTFDTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	V100cI	3	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYISWFAY	WGQGTLVTVSS
	L5S, N30S	3	EVQLSESGGGLVQPGGSLRLSCAASG	FTFSTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	G96S	2	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHSNFGNSYVSWFAY	WGQGTLVTVSS
	V48I	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWIA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	N82aD	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMDSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	N54D	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNDYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	N30D, D72N	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFDTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRNDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSYVSWFAY	WGQGTLVTVSS
	V100cS	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSSVSWFAY	WGQGTLVTVSS
	V100cH	1	EVQLLESGGGLVQPGGSLRLSCAASG	FTFNTYAMN	WVRQAPGKGLEWVA	RIRSKYNNYATYYADSVKD	RFTISRDDSKSTLYLQMNSLRAEDTAVYYC	VRHGNFGNSHVSWFAY	WGQGTLVTVSS

Figure 28D (Continued)

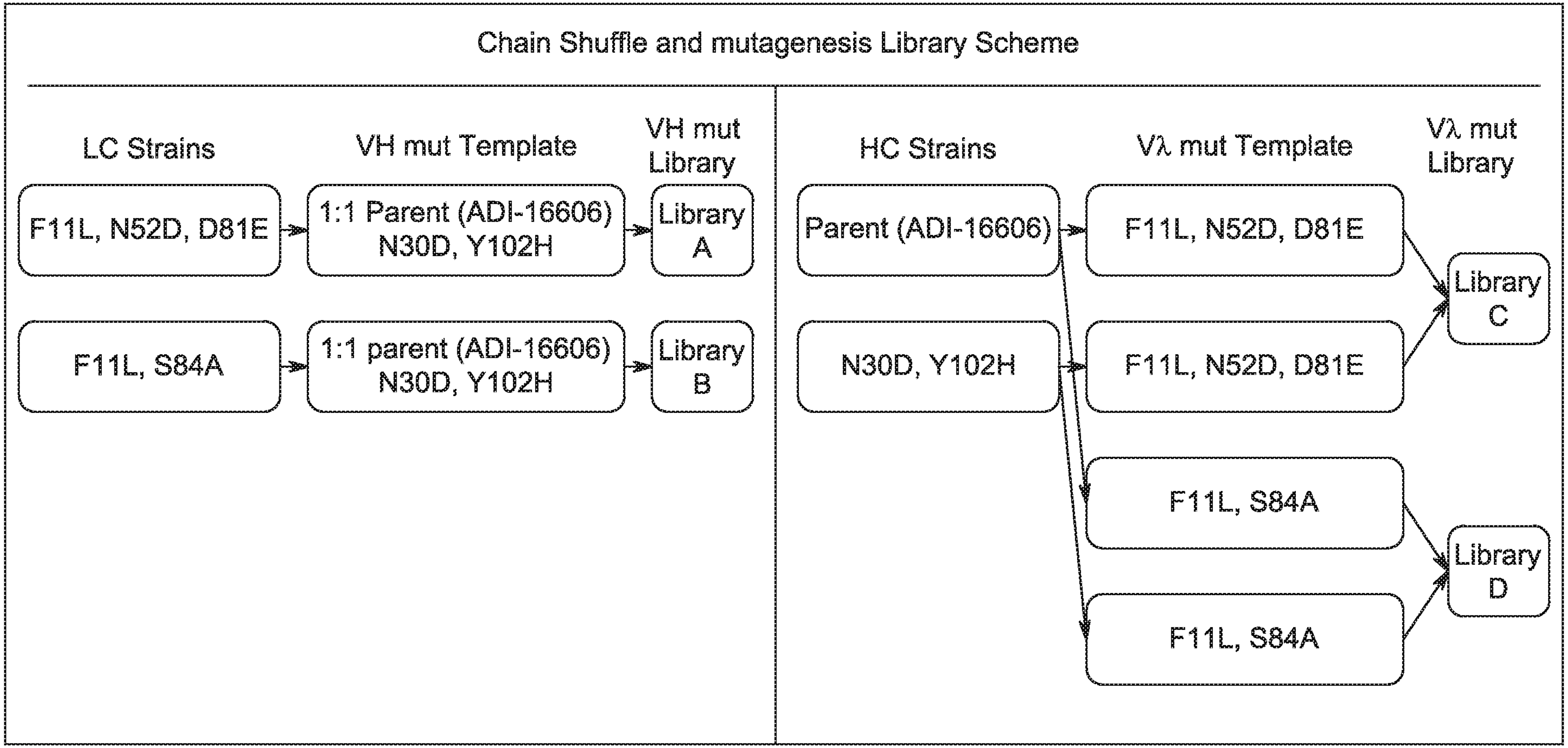

Chain Shuffle and mutagenesis Library Scheme
LC Strains
VH mut Template
VH mut Library
F11L, N52D, D81E
1:1 Parent (ADI-16606) N30D, Y102H
Library A
F11L, S84A
1:1 parent (ADI-16606) N30D, Y102H
Library B
HC Strains
Vλ mut Template
Vλ mut Library
Parent (ADI-16606)
F11L, N52D, D81E
Library C
N30D, Y102H
F11L, N52D, D81E
F11L, S84A
Library D
F11L, S84A

Figure 29A

Parents for Cycle 2 Optimization -Binding and Developability Profile Data

Name	VH mut	Vλ mut	Fab Tm (°C)	IgG Hu CD3εδ Fc-HIS KD (M)	IgG Cy CD3εγ Fc-HIS RU (M)	Jurkat CD3+ MFI	Jurkat CD3- MFI	Jurkat FOB	Cyno HSC-F MFI
CTL-19613			67.5	2.1E-09	2.7E-09	5101	150	34	11654
ADI-16606			61.5	3.5E-09	4.9E-09				
ADI-29601	Parent	F11L, N52D, D81E	66.0	4.5E-09	6.1E-09	5369	92	59	12368
ADI-29602	Parent	F11L, S84A	66.5	4.0E-09	5.3E-09	5737	113	51	12230
ADI-29603	N30D, Y102H	Parent	61.5	3.0E-09	3.5E-09				

Figure 29B

ADI-20587
K_D4.1 nM, Tm 66.5°C

ADI-20607
K_D1.1 nM, Tm 66.0°C

ADI-20590
K_D4.3 nM, Tm 65.5°C

28X Vλ Rational Combinations X 3X HC

▨ Stability
○ Expression
▨ PSR
▥ Affinity

Variant	VL Chain	Muts Versus ADI-16606
ADI-16606	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL	
LC1	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T74I
LC2	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T74I, A78V
LC3	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T74I, T27A
LC4	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T74I, D81E
LC5	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T74I, S93N
LC6	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T74I, A89V
LC7	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T74I, L95H
LC8	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A78V
LC9	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A78V, T27A
LC10	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQAEDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A78V, D81E
LC11	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYNNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A78V, S93N
LC12	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCVLWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A78V, A89V
LC13	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGVQADDEADYYCALWYSNHWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A78V, L95H
LC14	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T27A
LC15	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T27A, D81E
LC16	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T27A, S93N
LC17	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T27A, A89V
LC18	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	F11L, R24G, N52D, S84A, T27A, L95H
LC19	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, D81E
LC20	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYNNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, D81E, S93N
LC21	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCVLWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, D81E, A89V
LC22	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYSNHWVFGGGTKLTVL	F11L, R24G, N52D, S84A, D81E, L95H
LC23	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, S93N
LC24	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYNNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, S93N, A89V
LC25	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYNNHWVFGGGTKLTVL	F11L, R24G, N52D, S84A, S93N, L95H
LC26	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNLWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A89V
LC27	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCVLWYSNHWVFGGGTKLTVL	F11L, R24G, N52D, S84A, A89V, L95H
LC28	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQADDEADYYCALWYSNHWVFGGGTKLTVL	F11L, R24G, N52D, S84A, L95H

Figure 30

HuSP34 ADI-21952 Potential Degradation Motifs

ADI-ID	VH FR3	VH CDR H13	Fab KD Hu CD3εδ-Fc (nM)	Fab KD Cy CD3εδ-Fc (nM)
ADI-21952	RFTISRDDSKSTLYLQM**NS**LRAEDTAVYYC	VRHGNFG**NG**YVSWFAH	4.5	3.4
ADI-23633	RFTISRDDSKSTLYLQM**ES**LRAEDTAVYYC	VRHGNFG**NG**YVSWFAH	4.2	4.1
ADI-23634	RFTISRDDSKSTLYLQM**NS**LRAEDTAVYYC	VRHGNFG**NE**YVSWFAH	18.0	12.0
ADI-23636	RFTISRDDSKSTLYLQM**NA**LRAEDTAVYYC	VRHGNFG**NG**YVSWFAH	3.9	4.1
ADI-23637	RFTISRDDSKSTLYLQM**NS**LRAEDTAVYYC	VRHGNFG**NA**YVSWFAH	21.0	13.0

Figure 31

ADI-21952 CDR H3 Designs

DTAVYYCVRHGNFGNGYVSWFAHWGQGTLV

DTAVYYCXRHGNFGXGYVSWFAHWGQGTLV
DTAVYYCXRHGNFGNXYVSWFAHWGQGTLV
DTAVYYCVXHGNFGXGYVSWFAHWGQGTLV
DTAVYYCVXHGNFGNXYVSWFAHWGQGTLV
DTAVYYCVRXGNFGXGYVSWFAHWGQGTLV
DTAVYYCVRXGNFGNXYVSWFAHWGQGTLV
DTAVYYCVRHXNFGXGYVSWFAHWGQGTLV
DTAVYYCVRHXNFGNXYVSWFAHWGQGTLV
DTAVYYCVRHGXFGXGYVSWFAHWGQGTLV
DTAVYYCVRHGXFGNXYVSWFAHWGQGTLV
DTAVYYCVRHGNXGXGYVSWFAHWGQGTLV
DTAVYYCVRHGNXGNXYVSWFAHWGQGTLV
DTAVYYCVRHGNFXXGYVSWFAHWGQGTLV
DTAVYYCVRHGNFXNXYVSWFAHWGQGTLV
DTAVYYCVRHGNFGXXYVSWFAHWGQGTLV
DTAVYYCVRHGNFGXGXVSWFAHWGQGTLV
DTAVYYCVRHGNFGXGYXSWFAHWGQGTLV
DTAVYYCVRHGNFGXGYVXWFAHWGQGTLV
DTAVYYCVRHGNFGXGYVSXFAHWGQGTLV
DTAVYYCVRHGNFGXGYVSWXAHWGQGTLV
DTAVYYCVRHGNFGXGYVSWFXHWGQGTLV
DTAVYYCVRHGNFGXGYVSWFAXWGQGTLV
DTAVYYCVRHGNFGNXXVSWFAHWGQGTLV
DTAVYYCVRHGNFGNXYXSWFAHWGQGTLV
DTAVYYCVRHGNFGNXYVXWFAHWGQGTLV
DTAVYYCVRHGNFGNXYVSXFAHWGQGTLV
DTAVYYCVRHGNFGNXYVSWXAHWGQGTLV
DTAVYYCVRHGNFGNXYVSWFXHWGQGTLV
DTAVYYCVRHGNFGNXYVSWFAXWGQGTLV

Selection →

Parent	Selection Type	Theoretical Diversity
ADI-21952	H3 Oligo Mutagenesis	$<10^4$

HuSP34 ADI -21952 H3 Mutagenesis Progeny

Clone ID	CDR H3	KD Hu CD3εδ Fc (M)	PSR Score
ADI-23633	VRHGNFGNGYVSWFAH	3.1E-09	0.19
ADI-29716	VRHGNFGGGYVSWFAH	1.9E-09	0.21
ADI-29717	VRHGNFGNSYVSWFAH	3.4E-09	0.27
ADI-29718	VRHGNFGGGYVAWFAH	2.0E-09	0.19
ADI-29719	VRHGNFQGGYVSWFAH	2.5E-09	0.09
ADI-29720	VRHGNVGGGYVSWFAH	2.0E-09	0.00
ADI-29721	VRHDNFGAGYVSWFAH	5.9E-09	0.00
ADI-29722	VRHGNFGVGYVSWFAS	6.3E-09	0.00
ADI-29723	VRHGNFGNYAVSWFAH	3.2E-09	0.09
ADI-29724	VRHGSFGNHIVSWFAH	4.9E-08	0.00

Figure 32

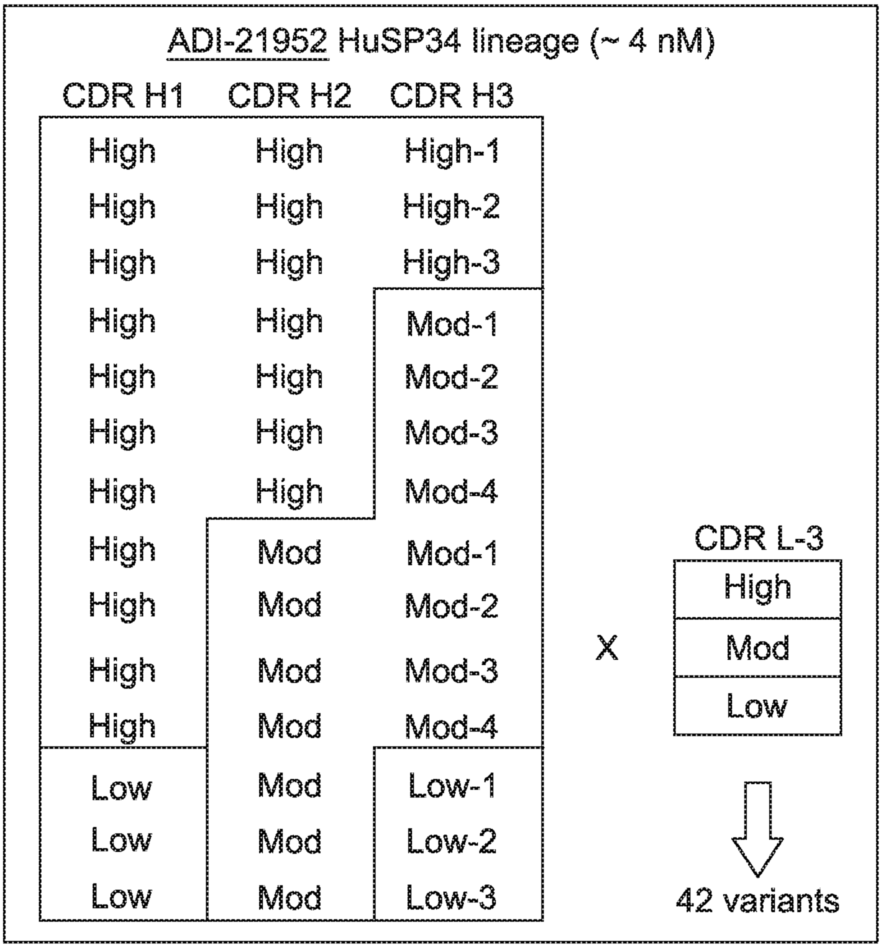


Figure 33A

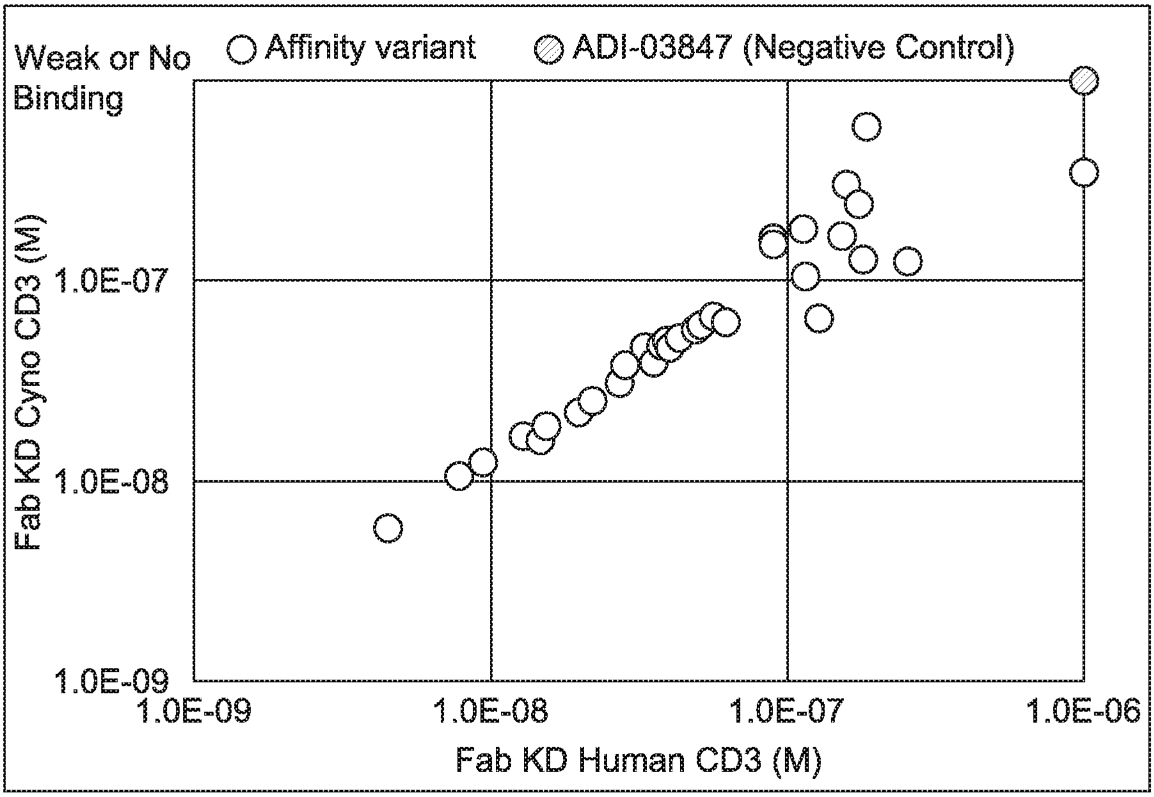


Figure 33B

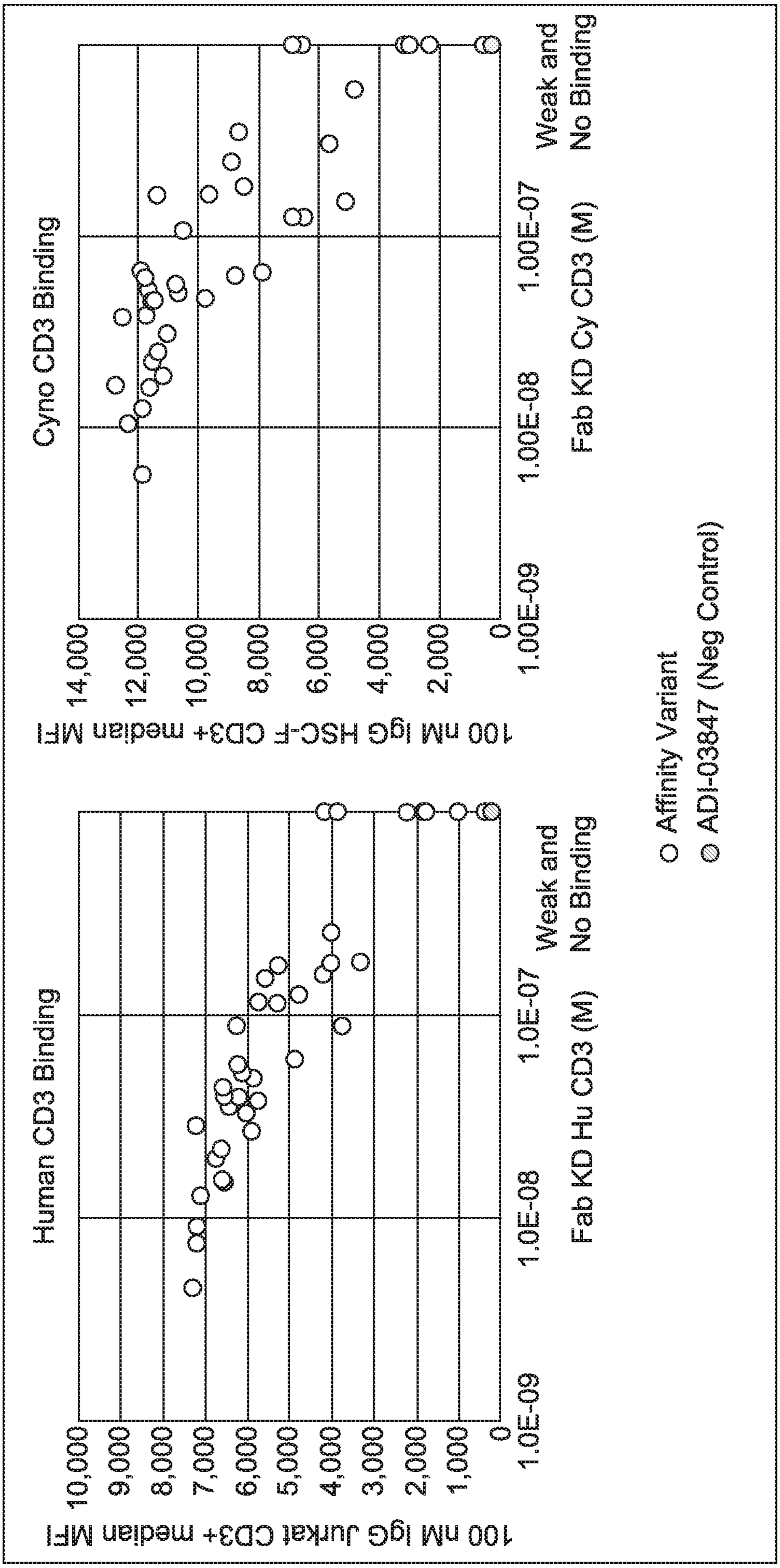

Human CD3 Binding
100 nM IgG Jurkat CD3+ median MFI
10,000
9,000
8,000
7,000
6,000
5,000
4,000
3,000
2,000
1,000
0
1.0E-09
1.0E-08
1.0E-07
Weak and No Binding
Fab KD Hu CD3 (M)
Cyno CD3 Binding
100 nM IgG HSC-F CD3+ median MFI
14,000
12,000
10,000
8,000
6,000
4,000
2,000
0
1.00E-09
1.00E-08
1.00E-07
Weak and No Binding
Fab KD Cy CD3 (M)
○ Affinity Variant
● ADI-03847 (Neg Control)

Figure 33C

Parent	Type	#	KD Hu CD3εδ Fc (M)	Fold Reduction	KD Cy CD3εδ Fc (M)	Fold Reduction
ADI-21952	IgG	1	2.7E-09	N/A	2.5E-09	N/A
	scFv-Fc	15	4.9E-09	1.8	4.3E-09	1.7
	scFv-Fc (DS1)	15	2.0E-08	7.4	2.1E-08	8.4
	scFv-Fc (DS2)	2	2.1E-08	7.8	2.3E-08	9.2

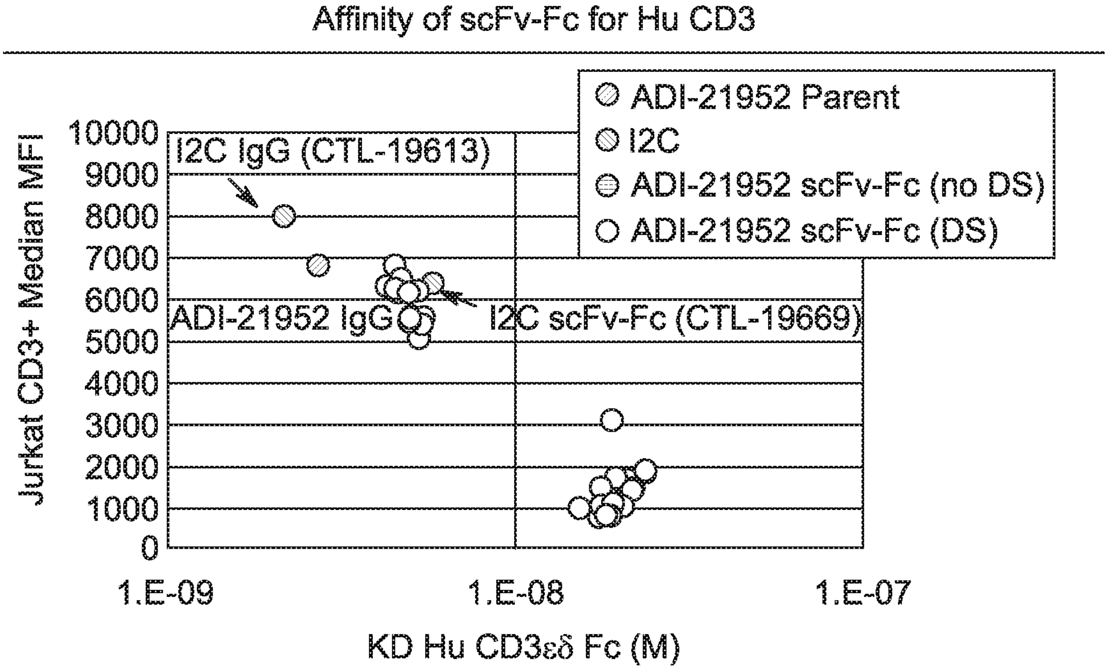


Figure 34A

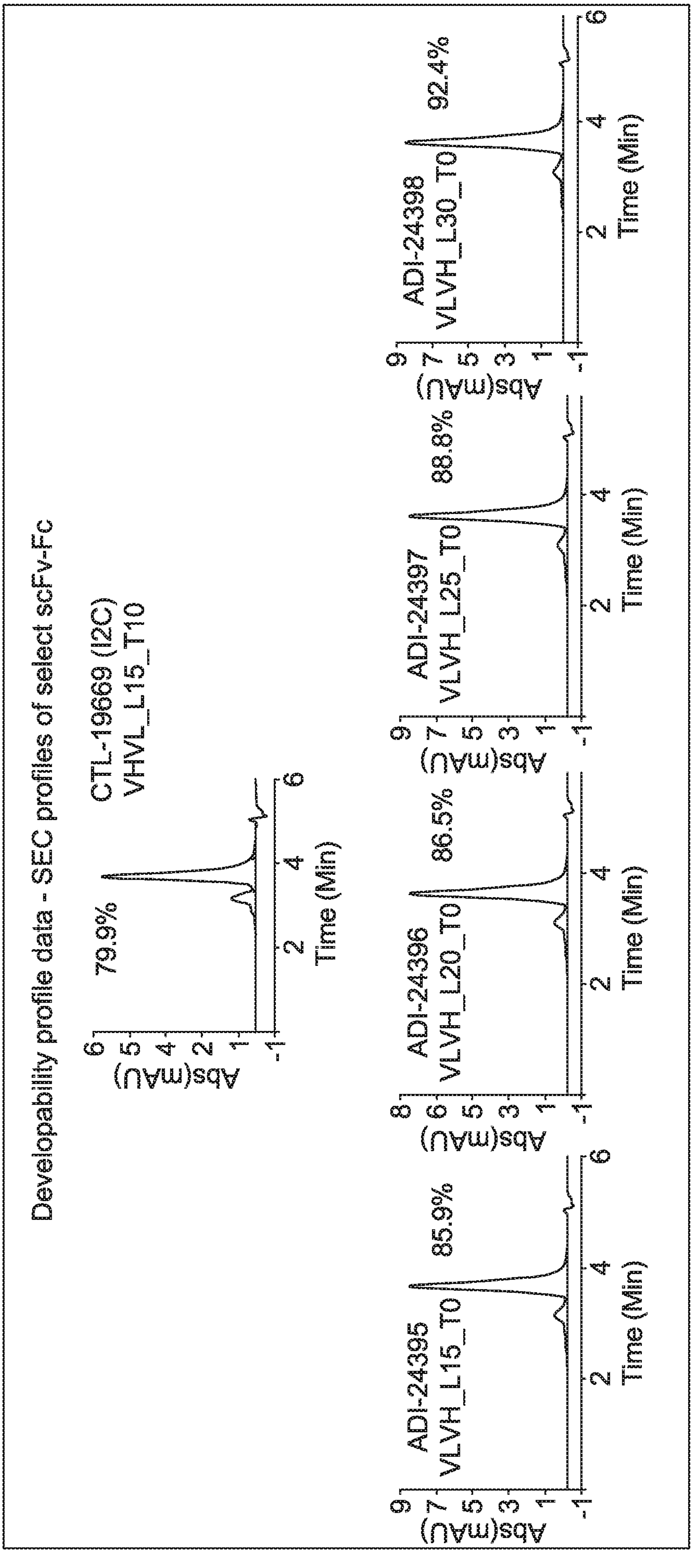

Developability profile data - SEC profiles of select scFv-Fc
CTL-19669 (I2C)
VHVL_L15_T10
79.9%
Abs(mAU)
6
5
4
2
1
-1
2
4
6
Time (Min)
ADI-24395
VLVH_L15_T0
85.9%
Abs(mAU)
9
7
5
3
1
-1
2
4
6
Time (Min)
ADI-24396
VLVH_L20_T0
86.5%
Abs(mAU)
8
6
5
3
1
-1
2
4
Time (Min)
ADI-24397
VLVH_L25_T0
88.8%
Abs(mAU)
9
7
5
3
1
-1
2
4
Time (Min)
ADI-24398
VLVH_L30_T0
92.4%
Abs(mAU)
9
7
5
3
1
-1
2
4
6
Time (Min)

Figure 34B

Developability Profile Data

Parent	Type	#	DSF Tm (°C)	ΔTM Fab/scFv	ΔTM +/-DS
ADI-21952	IgG	1	69.5	N/A	N/A
	scFv-Fc	15	59.7	-9.8	N/A
	scFv-Fc (DS1)	15	63.7	-5.8	+4.0
	scFv-Fc (DS2)	2	65.0	-4.8	+5.3

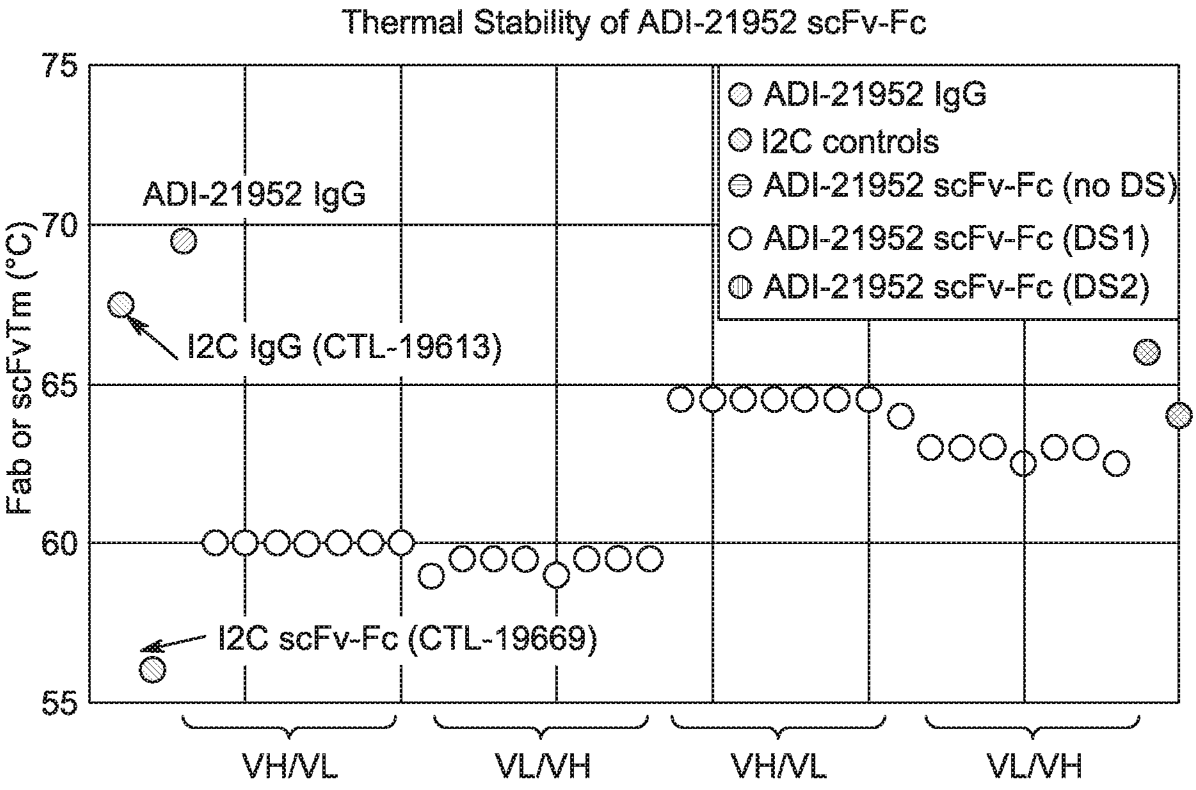


Figure 34C

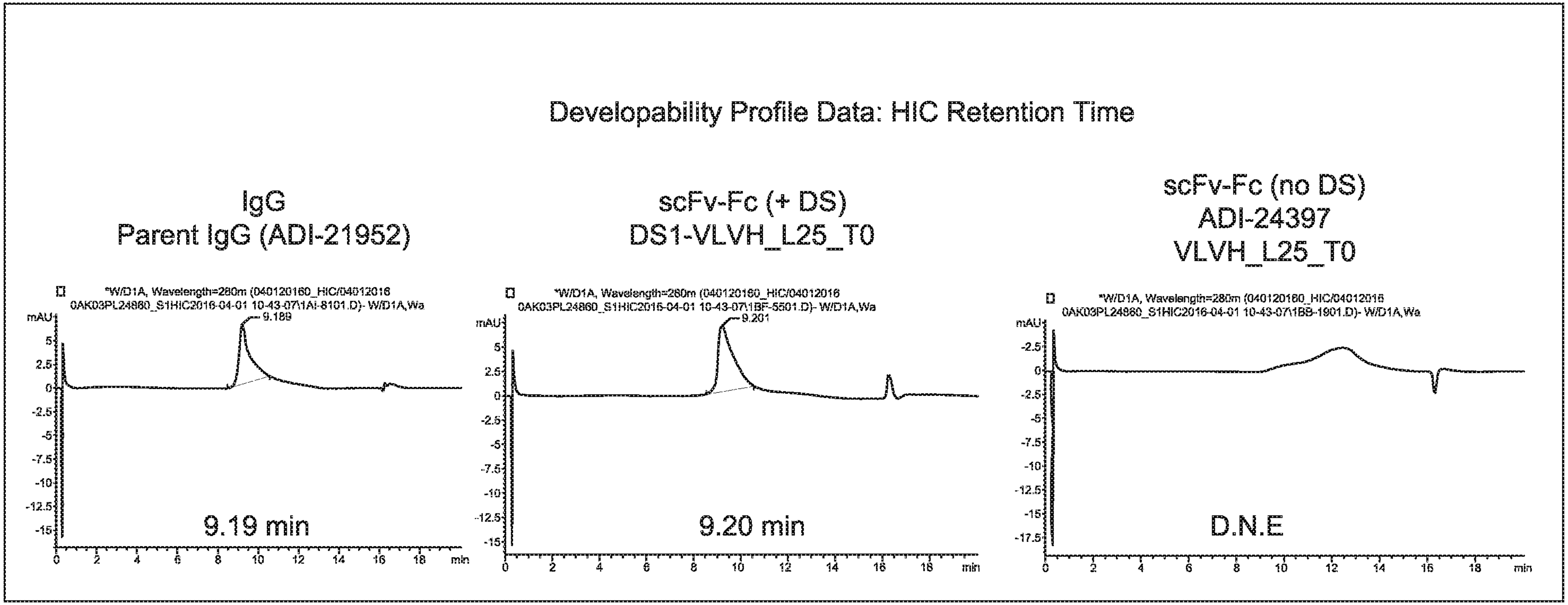

Developability Profile Data: HIC Retention Time
IgG
Parent IgG (ADI-21952)
*W/D1A, Wavelength=280m (040120160_HIC/04012016
0AK03PL24860_S1HIC2016-04-01 10-43-07\1AI-8101.D)- W/D1A,Wa
9.189
mAU
5
2.5
0
-2.5
-5
-7.5
-10
-12.5
-15
0
2
4
6
8
10
12
14
16
18
min
9.19 min
scFv-Fc (+ DS)
DS1-VLVH_L25_T0
*W/D1A, Wavelength=280m (040120160_HIC/04012016
0AK03PL24860_S1HIC2016-04-01 10-43-07\1BF-5501.D)- W/D1A,Wa
9.201
mAU
5
2.5
0
-2.5
-5
-7.5
-10
-12.5
-15
0
2
4
6
8
10
12
14
16
18
min
9.20 min
scFv-Fc (no DS)
ADI-24397
VLVH_L25_T0
*W/D1A, Wavelength=280m (040120160_HIC/04012016
0AK03PL24860_S1HIC2016-04-01 10-43-07\1BB-1901.D)- W/D1A,Wa
mAU
-2.5
0
-2.5
-5
-7.5
-10
-12.5
-15
-17.5
0
2
4
6
8
10
12
14
16
18
min
D.N.E

Figure 34D

Binding and Developability Profile Data

ADI ID	VH CDR H3 sequence	BiaCore Fab K_D Hu CD3ed-Fc (M) Monovalent	BiaCore Fab K_D Cy CD3ed-Fc (M) Monovalent	ForteBio IgG K_D Hu CD3ed-Fc (M) Avid	ForteBio IgG K_D Cy CD3ed-Fc (M) Avid	ForteBio IgG K_D Hu CD28-Fc (M) Avid	Jurkat CD3+ median MFI
CTL-19672	ARDGYSRYYFDY	9.69E-10	1.05E-09	1.46E-10	1.39E-10	N.B.	5626
ADI-22523	ARDGYGRYFYDV	1.64E-09	1.39E-09	1.83E-10	1.66E-10	N.B.	6058
ADI-26906	ARDAYGRYFYDV	3.52E-09	3.34E-09	2.36E-10	1.98E-10	N.B.	5825
ADI-26907	GRDAYGRYFYDV	4.46E-09	3.87E-09	2.57E-10	2.32E-10	N.B.	5937
ADI-26908	ARDAYGRYFYDV	5.18E-09	4.49E-09	2.74E-10	2.32E-10	N.B.	5612
ADI-26910	ARDRYGAYFYDV	7.62E-09	6.98E-09	3.07E-10	2.68E-10	N.B.	5467
ADI-26913	ARDQYGRYFYDV	2.92E-08	2.72E-08	5.03E-10	4.28E-10	N.B.	5275
ADI-26915	ARDVLGRYFYDV	W.B.	W.B.	1.94E-09	3.06E-09	N.B.	1310
ADI-26919	ARDAYGRYFYDV	5.56E-08	4.05E-08	5.07E-10	4.40E-10	N.B.	4448
ADI-26920	GRDAYGRYFYDV	5.15E-08	5.11E-08	5.86E-10	5.76E-10	N.B.	4987
ADI-26921	ARDAYGRYFYDV	4.61E-08	3.84E-08	6.16E-10	5.35E-10	N.B.	5202
ADI-26943	ARDAYGGYFYDV	W.B.	W.B.	4.09E-09	2.50E-09	N.B.	1083
ADI-26954	ARDNYGGYFYDV	N.B.	N.B.	N.B.	N.B.	N.B.	31
CTL-19613	VRHGNFGNSYISYWAY	1.43E-09	1.62E-09	1.67E-10	1.59E-10	N.B.	6137
ADI-21952	VRHGNFGNGYVSWFAH	4.13E-09	5.04E-09	7.41E-10	7.42E-10	N.B.	5724
ADI-26955	VRHGNFQGGYVSWFAH	3.28E-09	3.81E-09	2.97E-10	3.05E-10	N.B.	5200
ADI-26956	VRHGNFGGGYVSWFAW	3.77E-09	4.31E-09	2.33E-10	2.34E-10	N.B.	5222
ADI-26962	VRHGNFGEGYVSWFAH	2.39E-08	2.67E-08	3.94E-10	3.87E-10	N.B.	4014
ADI-26978	VRHGNFGGAYVSWFAH	2.92E-08	2.93E-08	5.41E-10	5.30E-10	N.B.	2956
ADI-26983	VRHGNFGGGYVSWFAW	2.03E-08	2.25E-08	N.D.	N.D.	N.B.	4513
ADI-26994	VRHGNVGGGYVSWFAH	W.B.	W.B.	3.26E-09	2.23E-09	N.B.	750
ADI-18965	GRDWDGAIRVLDY	N.B.	N.B.	N.B.	N.B.	N.B.	20

CTL-19672 is 38E4	Highlighted Mutations to ADI-22523 H3 in **RED**	W.B. = Weak-binder
CTL-19613 is I2C	Highlighted Mutations to SP34 H3 in **BLUE**: VRHGNFGNSYVSWFAY	N.B. = Non-binder
VH1-3/VK4-1 Negative Control		Multiple Concentration Global Fitting

100 nM IgG

N.D. = Not Determined

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Figure 35A

Cy HSC-F Median MFI	Poly-Specificity Reagent (PSR) Score (0-1)	BVP ELISA Fold Over Background (FOB)	HIC Retention Time (min)	AC-SINS Δλmax (nm)	SEC (% mono)	Fab Tm (°C)	HEK titer (mg/L)
12831	0.71	22.8	8.1	25.2	98.0	74.5	38.2
12276	0.40	13.6	8.3	19.3	94.8	74.5	147.4
12000	0.29	9.4	8.3	11.2	98.1	81.5	163.6
11751	0.23	7.4	8.4	10.4	98.0	73.5	204.3
11831	0.23	10.1	8.3	9.0	97.8	81.5	172.8
11887	0.30	5.1	8.3	8.2	97.9	81.5	173.4
11471	0.10	3	8.2	2.6	98.1	81.0	190.4
6165	0.00	1.3	8.2	0.8	98.1	79.0	180.3
9742	0.05	3.7	8.5	6.8	94.7	82.0	123.5
11962	0.02	2.9	8.5	7.0	97.2	75.5	93.2
11723	0.06	3.3	8.5	5.5	93.8	82.0	175.7
7180	0.00	1.3	8.8	0.9	96.7	75.5	127.6
23	0.00	1.2	8.6	0.3	97.6	79.0	176.6
13240	0.71	26	9.6	20.0	93.1	60.0	104.8
13125	0.43	14.8	9.8	7.0	94.9	72.5	34.1
12893	0.26	2.8	9.1	0.4	97.2	71.5	207.6
11775	0.24	5.8	9.9	0.3	97.5	69.5	136.0
12297	0.10	3.3	9.2	0.1	93.4	67.5	96.6
11524	0.10	5.6	9.2	0.4	96.2	69.5	156.4
12504	0.11	N.D.	N.D.	0.7	96.3	69.0	154.2
3555	0.10	1.6	9.1	0.7	96.3	70.5	198.5
25	0.14	N.D.	9.5	N.D.	97.4	73.0	69.7
100 nM IgG	Clean PSR: 0.00 -0.10	N.D. = Not Determined	Clean to Low HIC: < 10.5 min	ΔλMax < 5 nM Implies Low Self-interaction			
	Low PSR: 0.10-0.33	Clean BVP: FOB < 2.1 Implies Clean	Medium HIC: ≥ 10.5 and < 11.5 min	ΔλMax ≥ 5 nm and < 20 nM Implies Medium Self-interaction			Titer < 50 mg/L
	Medium PSR: 0.33 -0.66	Medium BVP: FOB ≥ 2.1 and < 6.5					
	High PSR: 0.66 -1.00	High BVP: FOB ≥ 6.5 Implies High BVP Reactivity	High HIC: ≥ 11.5 Min	ΔλMax ≥ 20 nM Implies high Self-interaction			

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Figure 35A (Continued)

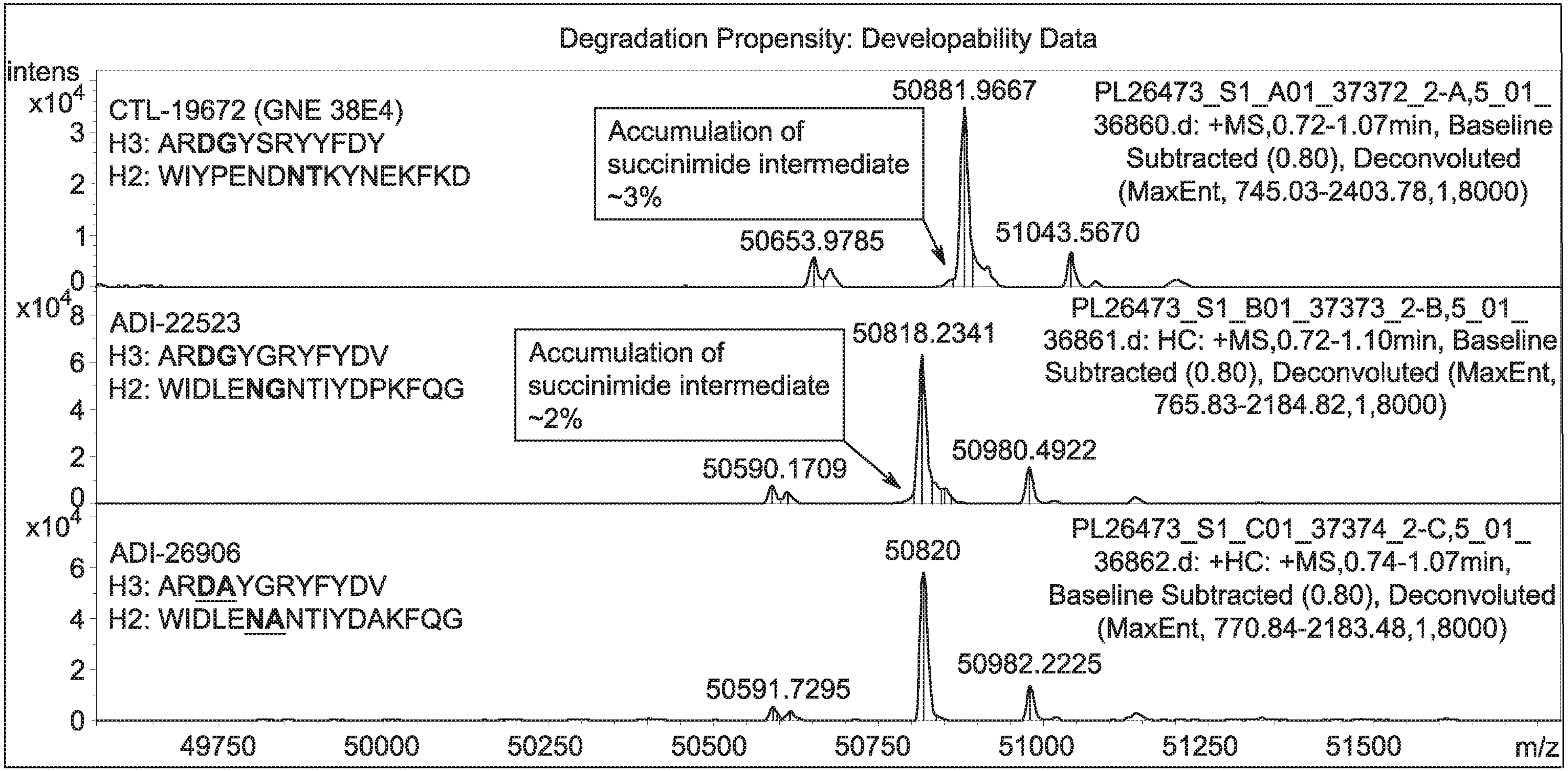
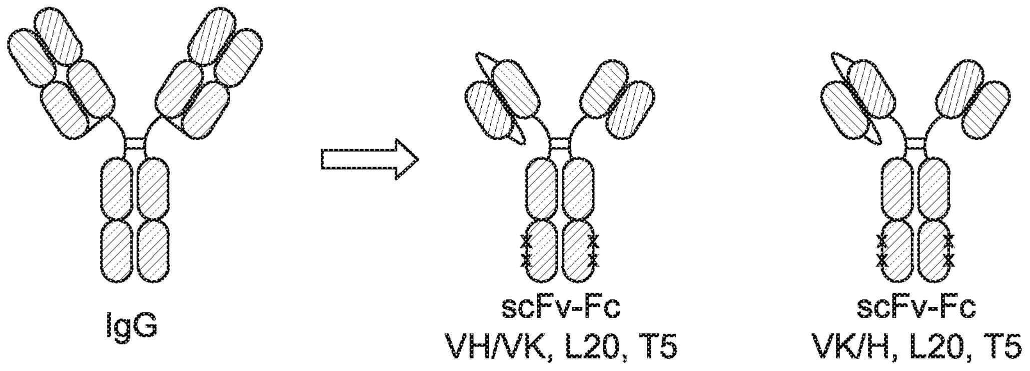

Degradation Propensity: Developability Data
intens
x10^4
3
2
1
0
CTL-19672 (GNE 38E4)
H3: ARDGYSRYYFDY
H2: WIYPENDNTKYNEKFKD
Accumulation of succinimide intermediate ~3%
50881.9667
50653.9785
51043.5670
PL26473_S1_A01_37372_2-A,5_01_36860.d: +MS,0.72-1.07min, Baseline Subtracted (0.80), Deconvoluted (MaxEnt, 745.03-2403.78,1,8000)
x10^4
8
6
4
2
0
ADI-22523
H3: ARDGYGRYFYDV
H2: WIDLENGNTIYDPKFQG
Accumulation of succinimide intermediate ~2%
50818.2341
50590.1709
50980.4922
PL26473_S1_B01_37373_2-B,5_01_36861.d: HC: +MS,0.72-1.10min, Baseline Subtracted (0.80), Deconvoluted (MaxEnt, 765.83-2184.82,1,8000)
x10^4
6
4
2
0
ADI-26906
H3: ARDAYGRYFYDV
H2: WIDLENANTIYDAKFQG
50820
50591.7295
50982.2225
PL26473_S1_C01_37374_2-C,5_01_36862.d: +HC: +MS,0.74-1.07min, Baseline Subtracted (0.80), Deconvoluted (MaxEnt, 770.84-2183.48,1,8000)
49750
50000
50250
50500
50750
51000
51250
51500
m/z

Figure 35B

Anti-TAA



Properties of Monospecific TAA scFv-Fc: Binding and Developability profile data

Name	Target	Format	Design	Titer (mg/L)	Tm (°C)	AC-SINS	HIC Retention Time (min)	SEC
Trastuzumab	HER2	scFv-Fc	IgG4 scFv-Fc H/L, L20, T5	227.9	N.D.	N.D.	N.D.	97.0
Trastuzumab	HER2	scFv-Fc	IgG4 scFv-Fc L/H, L20, T5	208.0	61.5	5.1	10.9	97.8
Lintuzumab	CD33	scFv-Fc	IgG4 scFv-Fc H/L, L20, T5	117.2	N.D.	N.D.	N.D.	98.2
Lintuzumab	CD33	scFv-Fc	IgG4 scFv-Fc L/H, L20, T5	169.2	60.0	4.0	11.8	97.1
ADI-03847	HEL	scFv-Fc	IgG4 scFv-Fc H/L, L20, T5	16.0	N.D.	N.D.	N.D.	98.8
ADI-03847	HEL	scFv-Fc	IgG4 scFv-Fc L/H, L20, T5	76.3	55.5	2.4	D.N.E.	95.1

▨ Selected for Bispecific Assembly

D.N.E. = Does not Elute

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Figure 36A

Jurkat CD3+ 10nM IgG	Jurkat CD3- 10nM IgG	Jurkat FOB 10nM	Hu HER2 mono K_D (M)	Hu HER2 mono RU	Hu HER2 Fc K_D (M)	Hu HER2 Fc RU	Hu HER2 mono K_D (M)	Hu HER2 mono RU
26.8	34.9	0.8	9.0E-09	0.20	2.2E-09	0.36	N.B.	-0.03
26.2	33.0	0.8	6.6E-09	0.17	9.3E-10	0.32	N.B.	-0.02
25.4	31.0	0.8	N.B.	0.00	N.B.	0.03	8.9E-09	0.22
23.8	30.3	0.8	N.B.	0.00	N.B.	0.01	7.3E-09	0.27
23.5	29.9	0.8	N.B.	0.02	N.B.	0.02	N.B.	-0.03
24.5	31.7	0.8	N.B.	0.01	N.B.	0.01	N.B.	-0.03

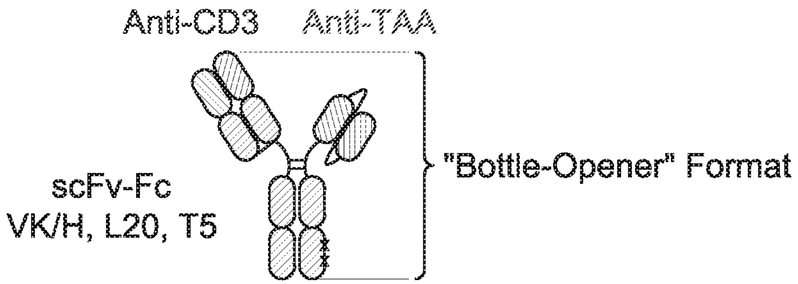
Figure 36A (Continued)

Hu HER2 Fc K_D (M)	Hu HER2 Fc Ru	Hu HER2 mono k_D (M)	Hu HER2 mono RU	Hu HER2 Fc k_D (M)	Hu HER2 Fc Ru
N.B.	0.00	N.B.	0.00	N.B.	0.00
N.B.	0.01	N.B.	0.01	N.B.	0.01
5.6E-09	0.40	N.B.	0.01	N.B.	0.01
2.7E-09	0.39	N.B.	0.00	N.B.	0.01
N.B.	0.02	6.7E-10	0.22	N.B.	0.02
N.B.	0.02	7.4E-10	0.24	N.B.	0.01

Figure 36A (Continued)

Bispecific Characteristics

- IgG4 Ser228Phe
- His435->Arg, Tyr436->Phe Mutations (**X**)



Purification of Fab/scFv-Fc Heterodimer (Aka "Bottle-Opener" Format) Bispecifics

Figure 36B

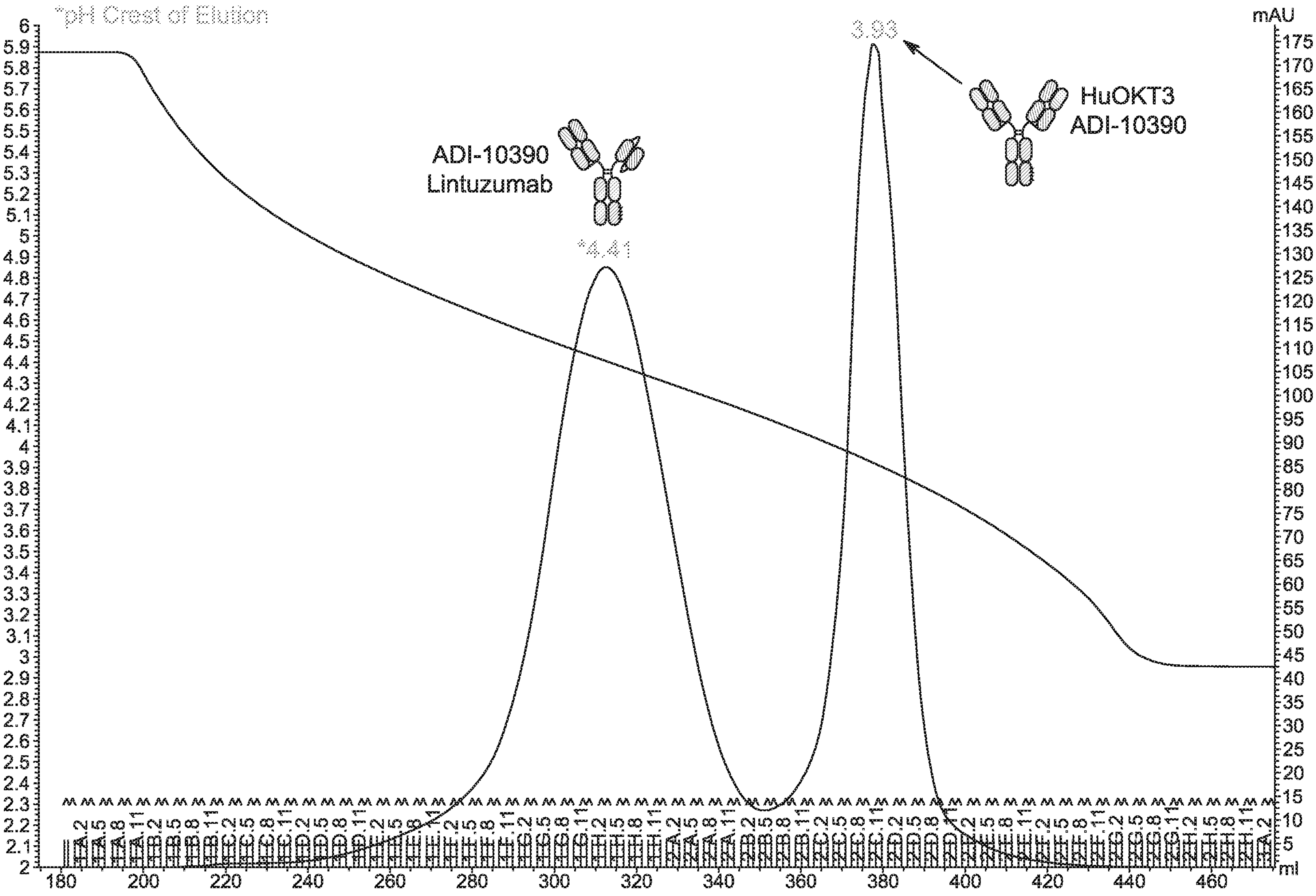


Figure 36B (Continued)

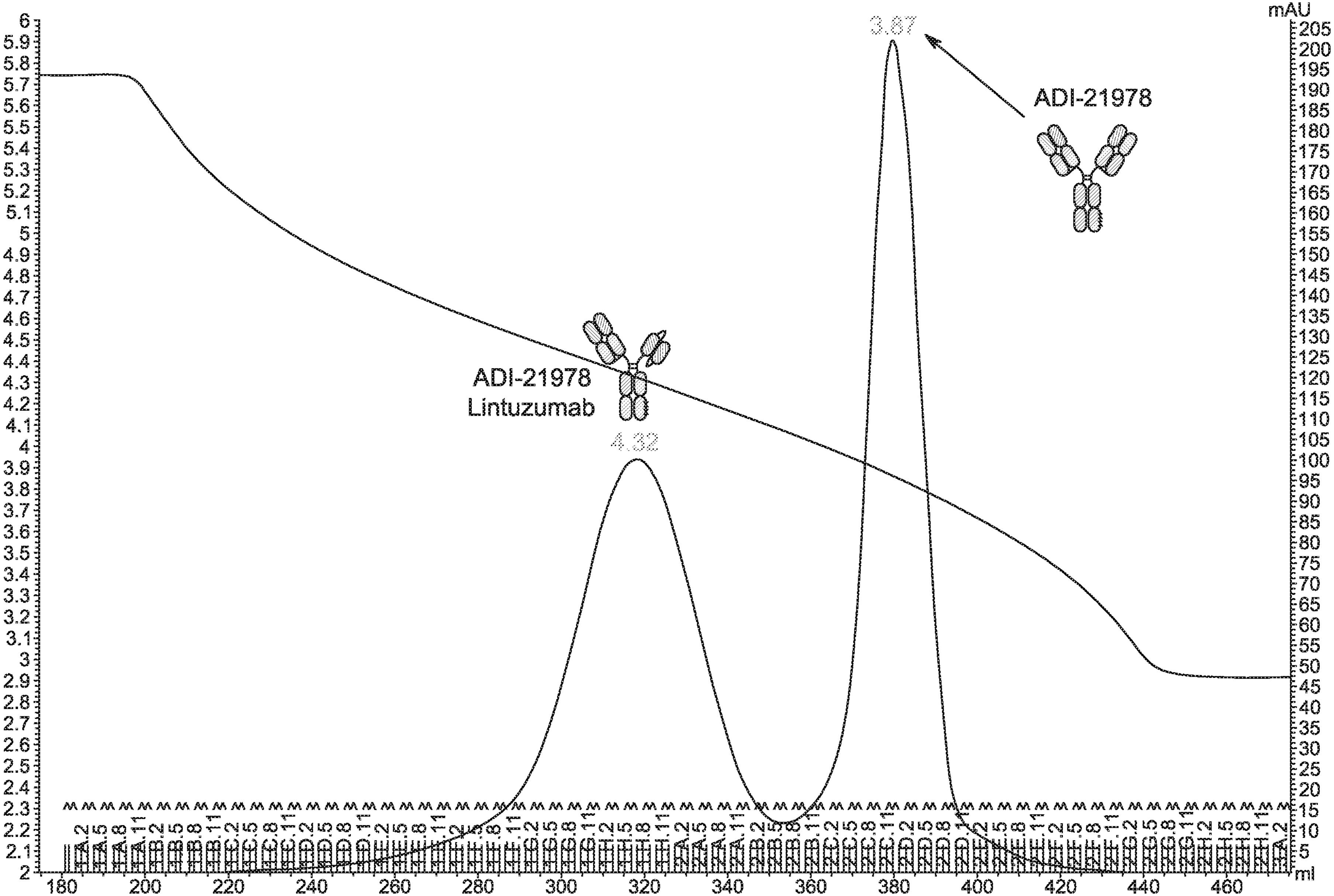
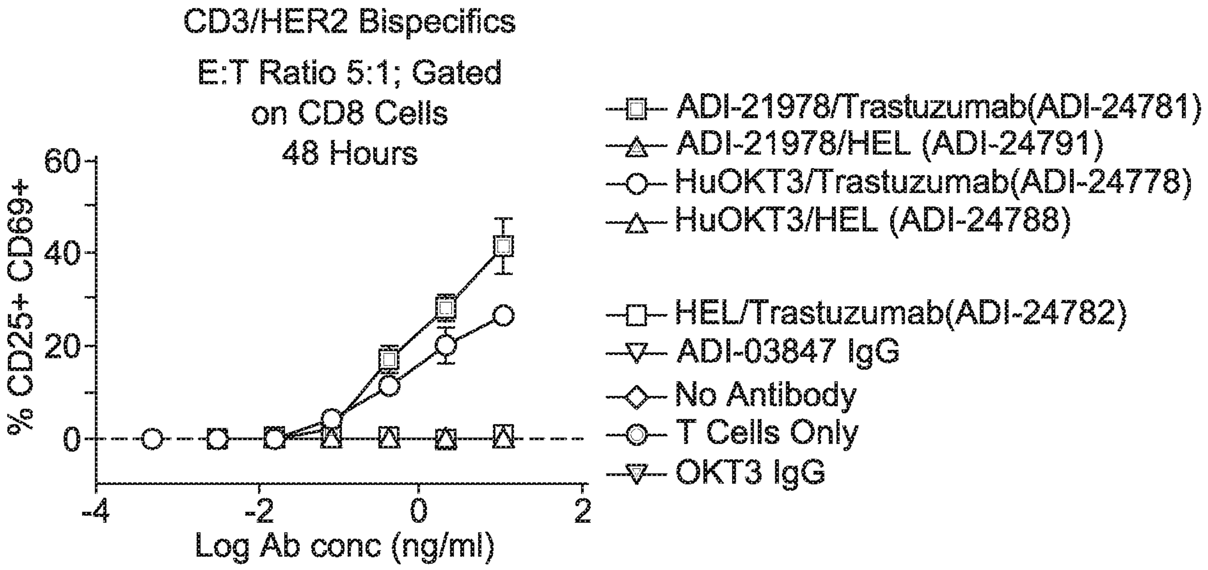


Figure 36B (Continued)

SK-BR-3 + Pan T Cells



Pan T Cells Only

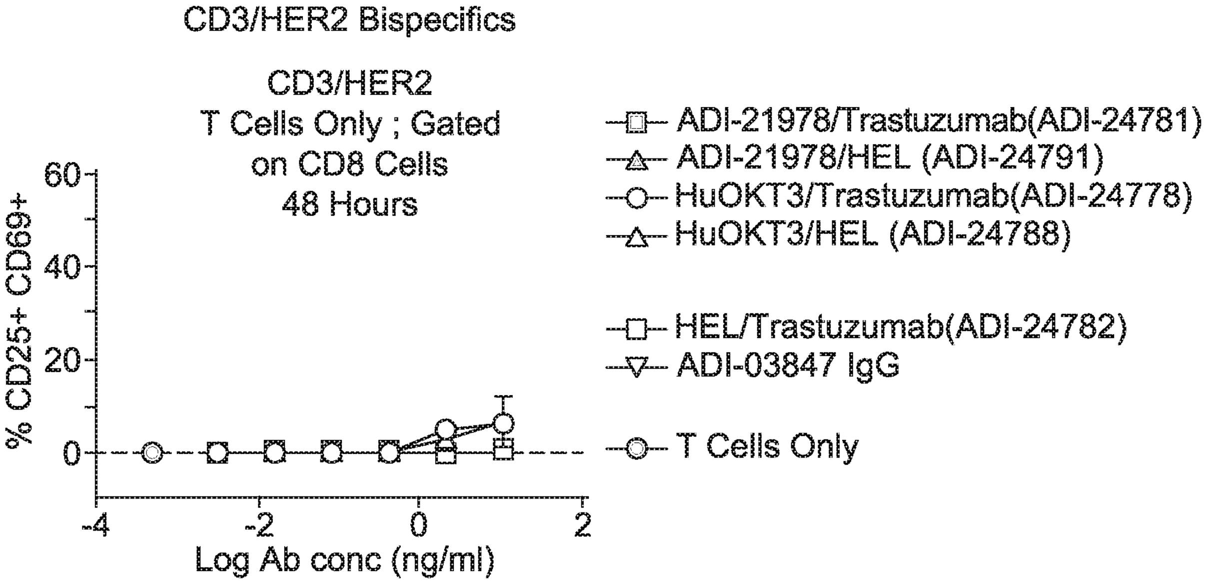
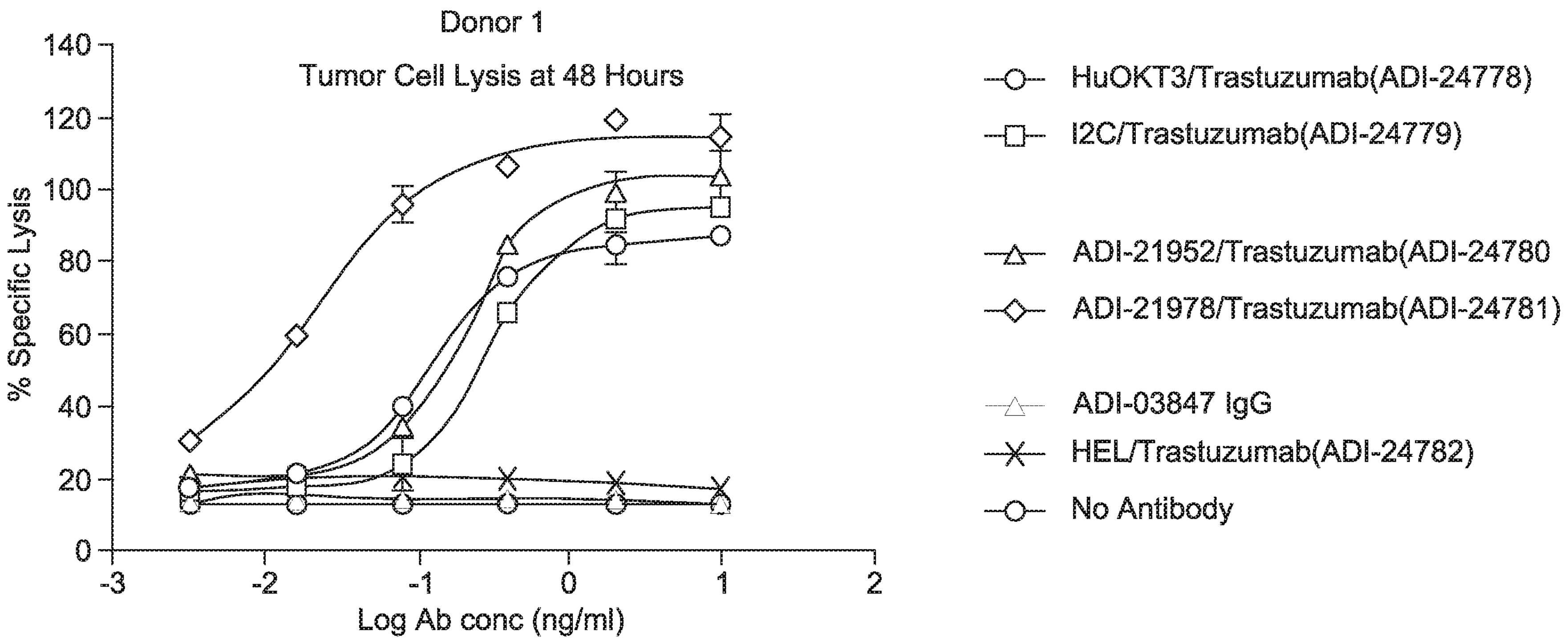


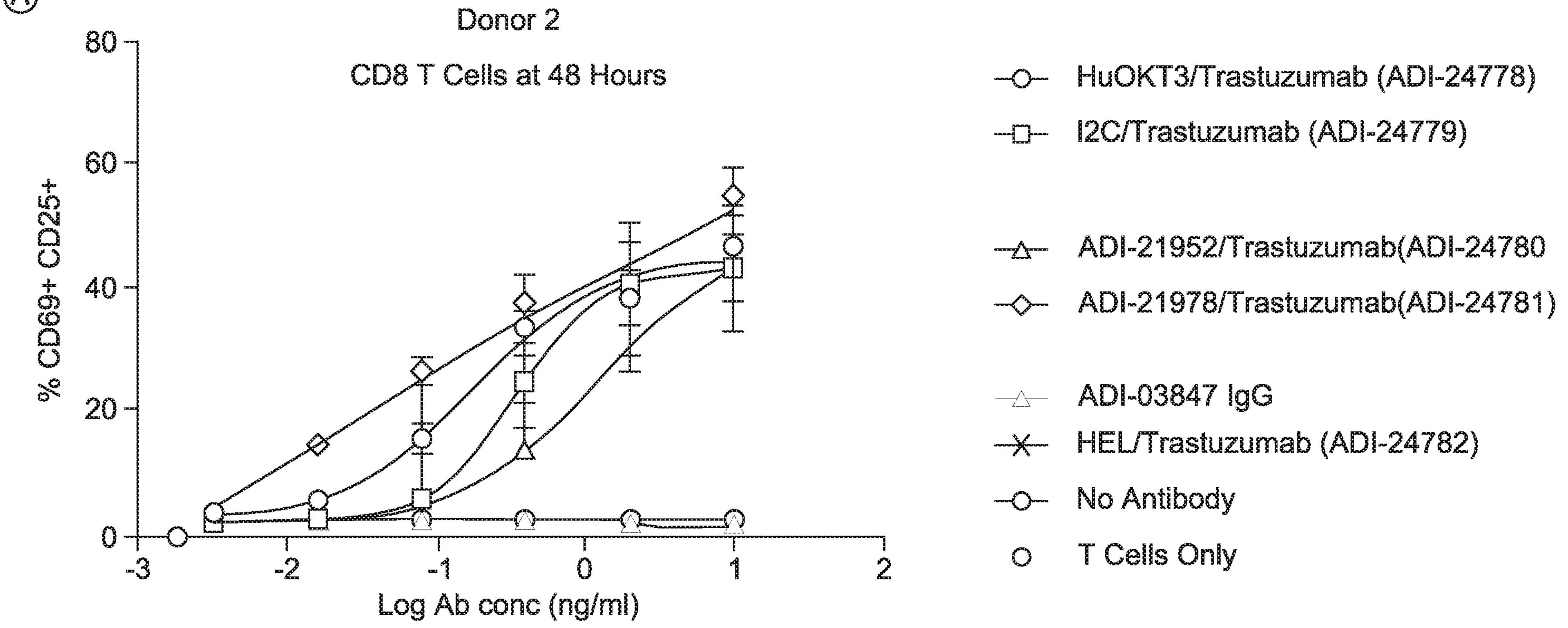
Figure 36C



Format	CD3/HER2	CD3/HER2	CD3/HER2	CD3/HER2	HEL
	HuOKT3/Trastuzumab	I2C/Trastuzumab	ADI-21952 (HuSP34)/HER2	ADI-21978 (novel)/HER2	ADI-03847
ADI ID	ADI-24778	ADI-24779	ADI-24780	ADI-24781	
LogEC50	-0.8948	-0.5235	-0.691	-1.707	~2.301
EC50	0.1274	0.2996	0.2037	0.01963	~199.9

Figure 37

Ⓐ



Format	CD3/HER2	CD3/HER2	CD3/HER2	CD3/HER2	HEL
	HuOKT3/Trastuzumab	I2C/Trastuzumab	ADI-21952 (HuSP34)/HER2	ADI-21978 (novel)/HER2	ADI-03847
ADI ID	ADI-24778	ADI-24779	ADI-24780	ADI-24781	
LogEC50	-0.7737	-0.4608	0.07197	~-30.75	~0.3563
EC50	0.1684	0.3461	1.180	~0.0	~0.0

Ⓐ

Figure 37 (Continued)

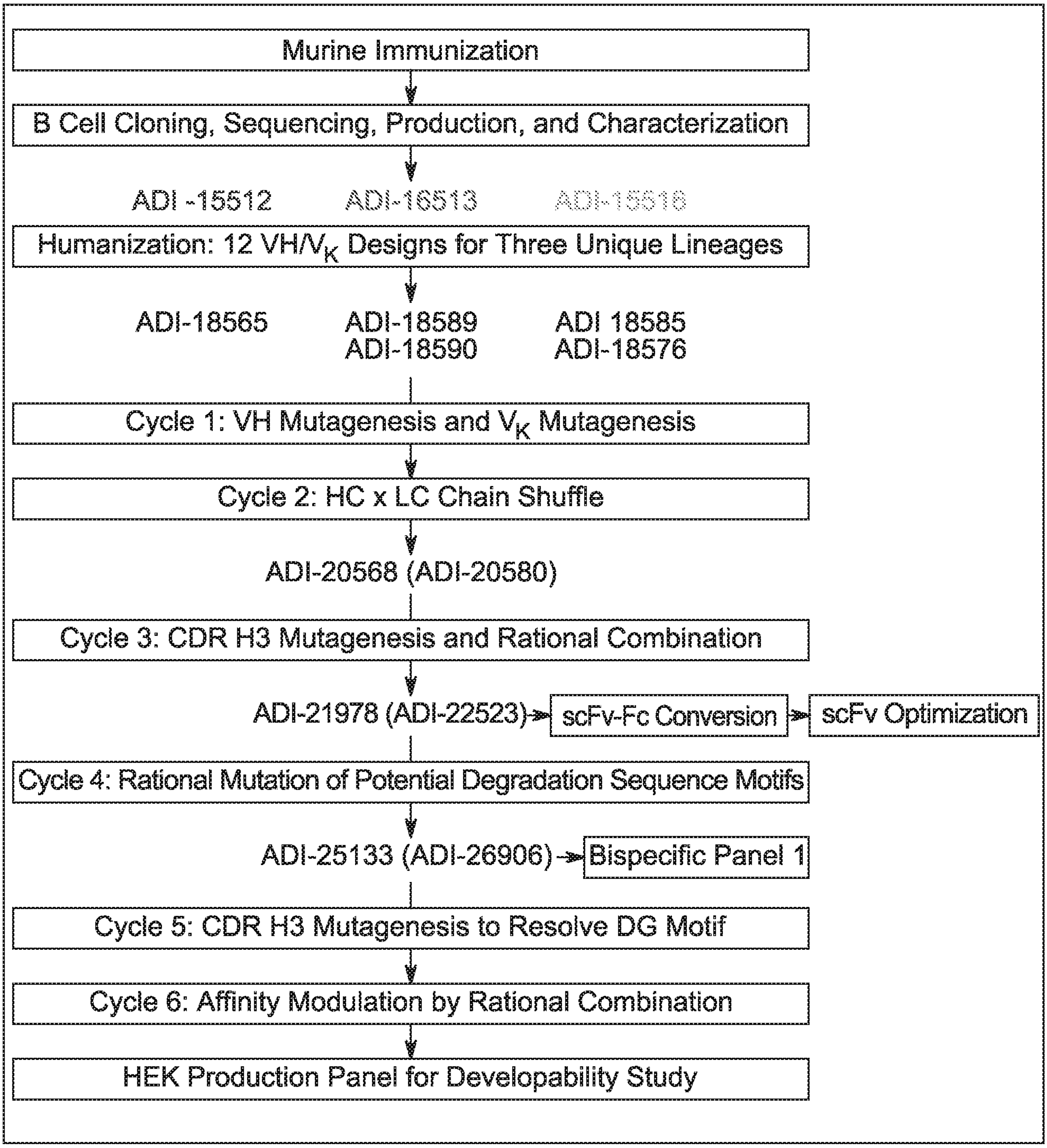

Murine Immunization
B Cell Cloning, Sequencing, Production, and Characterization
ADI -15512
ADI-16513
ADI-15516
Humanization: 12 VH/V$_K$ Designs for Three Unique Lineages
ADI-18565
ADI-18589
ADI-18590
ADI 18585
ADI-18576
Cycle 1: VH Mutagenesis and V$_K$ Mutagenesis
Cycle 2: HC x LC Chain Shuffle
ADI-20568 (ADI-20580)
Cycle 3: CDR H3 Mutagenesis and Rational Combination
ADI-21978 (ADI-22523)
scFv-Fc Conversion
scFv Optimization
Cycle 4: Rational Mutation of Potential Degradation Sequence Motifs
ADI-25133 (ADI-26906)
Bispecific Panel 1
Cycle 5: CDR H3 Mutagenesis to Resolve DG Motif
Cycle 6: Affinity Modulation by Rational Combination
HEK Production Panel for Developability Study

Figure 38A

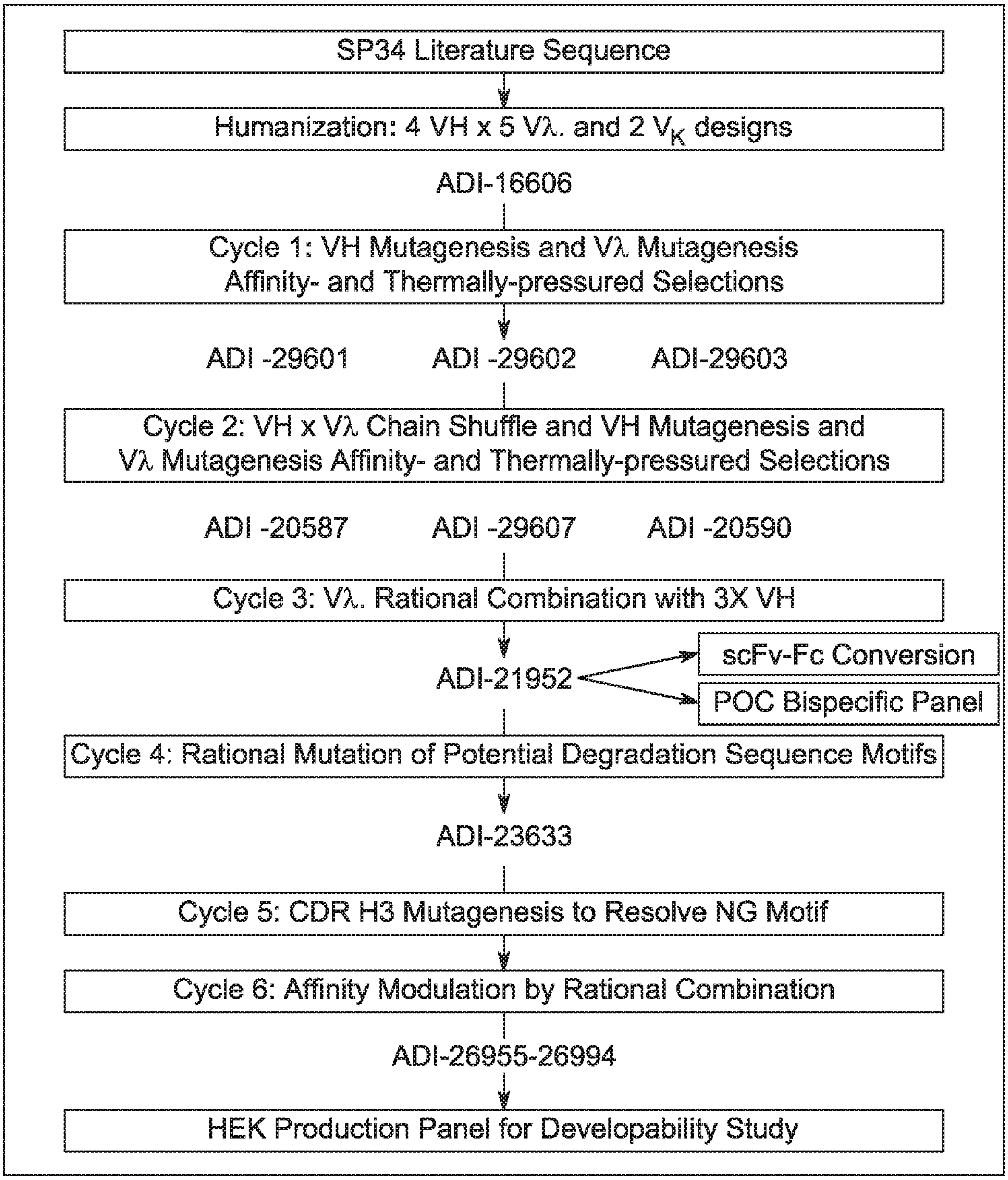

SP34 Literature Sequence
Humanization: 4 VH x 5 Vλ. and 2 V$_K$ designs
ADI-16606
Cycle 1: VH Mutagenesis and Vλ Mutagenesis Affinity- and Thermally-pressured Selections
ADI -29601
ADI -29602
ADI-29603
Cycle 2: VH x Vλ Chain Shuffle and VH Mutagenesis and Vλ Mutagenesis Affinity- and Thermally-pressured Selections
ADI -20587
ADI -29607
ADI -20590
Cycle 3: Vλ. Rational Combination with 3X VH
ADI-21952
scFv-Fc Conversion
POC Bispecific Panel
Cycle 4: Rational Mutation of Potential Degradation Sequence Motifs
ADI-23633
Cycle 5: CDR H3 Mutagenesis to Resolve NG Motif
Cycle 6: Affinity Modulation by Rational Combination
ADI-26955-26994
HEK Production Panel for Developability Study

Figure 38B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/031705

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A61K 39/00; A61K 39/395; C07K 16/18; C07K 16/28; C07K 16/30; C07K 16/32 (2018.01)

CPC - A61K 39/39533; A61K 39/39558; A61K 2039/505; C07K 16/18; C07K 16/28; C07K 16/2809; C07K 2317/56; C07K 2317/565 (2018.08)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC - 424/130.1; 424/135.1; 435/328; 530/387.1; 530/387.3; 536/23.53 (keyword delimited)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2015/0166661 A1 (GENENTECH, INC.) 18 June 2015 (18.06.2015) entire document	1, 2
X	WO 2013/049254 A1 (JN BIOSCIENCES LLC) 04 April 2013 (04.04.2013) entire document	20, 21
A	CARPENTER et al. "A humanized non–FcR-binding anti-CD3 antibody, visilizumab, for treatment of steroid-refractory acute graft-versus-host disease," Blood, 15 April 2002 (15.04.2002), Vol. 99, No. 8, Pgs. 2712-2719. entire document	1, 2, 20, 21
A	WO 2012/158818 A2 (FABION PHARMACEUTICALS, INC. et al) 22 November 2012 (22.11.2012) entire document	1, 2, 20, 21
A	CHATENOUD et al. "Anti-CD3 antibody induces long-term remission of overt autoimmunity in nonobese diabetic mice," Proc Natl Acad Sci USA, 01 January 1994 (01.01.1994), Vol. 91, Pgs. 123-127. entire document	1, 2, 20, 21
A	WO 2016/180721 A1 (MILTENYI BIOTEC GMBH) 17 November 2016 (17.11.2016) entire document	1, 2, 20, 21
A	US 7,728,114 B2 (MACH et al) 01 June 2010 (01.06.2010) entire document	1, 2, 20, 21

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:
"A"	document defining the general state of the art which is not considered to be of particular relevance
"E"	earlier application or patent but published on or after the international filing date
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O"	document referring to an oral disclosure, use, exhibition or other means
"P"	document published prior to the international filing date but later than the priority date claimed
"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&"	document member of the same patent family

Date of the actual completion of the international search 12 September 2018	Date of mailing of the international search report 02 OCT 2018
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300	Authorized officer Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2018/031705

Box No. I **Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)**

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☒ forming part of the international application as filed:
      - ☒ in the form of an Annex C/ST.25 text file.
      - ☐ on paper or in the form of an image file.

   b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. ☐ furnished subsequent to the international filing date for the purposes of international search only:
      - ☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).
      - ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

SEQ ID NOs: 2, 3, 5, 7, 10, 11, 13, 15, 18, 19, 21, 23, 26, 27, 29, and 31 were searched.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/031705

Box No. II **Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 6, 12, 13, 25-27
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III **Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:
See extra sheet(s).

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1, 2, 20, and 21 to the extent that they read on an antibody of SEQ ID NOs:1, 2, 3, 5, 7, 9, 10, 11, 13, and/or 15.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

Continued from Box No. III Observations where unity of invention is lacking

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees need to be paid.

Group I+: claims 1-5, 7-11, and 14-24 are drawn to antibodies or antigen-binding polypeptides.

The first invention of Group I+ is restricted to an antibody, wherein the antibody is selected to be Ab 1, Ab1 comprising a heavy chain variable region, wherein in the heavy chain variable region is selected to be SEQ ID NO:2, encoded by SEQ ID NO:1, the heavy chain further comprising heavy chain complementarity determining regions CDRH1, CDRH2, and CDRH3, where CDRH1 is selected to be SEQ ID NO:3, CDRH2 is selected to be SEQ ID NO:5, and CDRH3 is selected to be SEQ ID NO:7; and a light chain variable region, wherein the light chain variable region is selected to be SEQ ID NO:10, encoded by SEQ ID NO:9, the light chain further comprising light chain complementarity determining regions CDRL1, CDRL2, and CDRL3, where CDRL1 is selected to be SEQ ID NO:11, CDRL2 is selected to be SEQ ID NO:13, and CDRL3 is selected to be SEQ ID NO:15. It is believed that claims 1, 2, 20, and 21 read on this first named invention and thus these claims will be searched without fee to the extent that they read on an antibody of SEQ ID NOs:1, 2, 3, 5, 7, 9, 10, 11, 13, and/or 15.

Applicant is invited to elect additional antibodies or antigen-binding polypeptides, each with specified SEQ ID NO for each heavy/light chain variable region and complementarity determining regions therein, to be searched in a specific combination by paying an additional fee for each set of election. An exemplary election would be an antibody, wherein the antibody is selected to be Ab 2, Ab2 comprising a heavy chain variable region, wherein in the heavy chain variable region is selected to be SEQ ID NO:18, encoded by SEQ ID NO:17, the heavy chain further comprising heavy chain complementarity determining regions CDRH1, CDRH2, and CDRH3, where CDRH1 is selected to be SEQ ID NO:19, CDRH2 is selected to be SEQ ID NO:21, and CDRH3 is selected to be SEQ ID NO:23; and a light chain variable region, wherein the light chain variable region is selected to be SEQ ID NO:26, encoded by SEQ ID NO:25, the light chain further comprising light chain complementarity determining regions CDRL1, CDRL2, and CDRL3, where CDRL1 is selected to be SEQ ID NO:27, CDRL2 is selected to be SEQ ID NO:29, and CDRL3 is selected to be SEQ ID NO:31. Additional antibodies or antigen-binding polypeptides will be searched upon the payment of additional fees. Applicants must specify the claims that read on any additional elected inventions. Applicants must further indicate, if applicable, the claims which read on the first named invention if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched/examined.

The inventions listed in Groups I+ do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

The Groups I+ formulas do not share a significant structural element responsible for binding CD3, requiring the selection of alternatives for the amino acid sequence of the heavy chain variable region and the light chain variable region for each antibody or antigen-binding polypeptide, where "a CDRH1 comprising an amino acid sequence of FNIKDYYM (SEQ ID NO: 6720), YTFTSYTIH (SEQ ID NO: 6721), or FTFXITYAMN (SEQ ID NO: 6722), wherein X, is any amino acid" and "CDRH2 comprising an amino acid sequence of WIDLENXINTX2YDX3KFOG (SEQ ID NO: 6723), wherein X1, X2, and X3 independently are any amino acid" and "a CDRH3 comprising an amino acid sequence of X1QSYSX2RT (SEQ ID NO: 6724) or X3RDX4YGX5YFYDV (SEQ ID NO: 6725), wherein X1, X2, X3, X4, and X5 are independently are any amino acid" and "a CDRL1 comprising an amino acid sequence of X1KSSQX2LLX3X4RTGKX5YLA (SEQ ID NO: 6726), wherein X1, X2, X3, X4, and X5 independently are any amino acid" and "a CDRL2 comprising an amino acid sequence of WASTRES (SEQ ID NO: 6727) or GTX1KRAP (SEQ ID NO: 6728), wherein X1, is any amino acid" and "a CDRL3 comprising an amino acid sequence of KQSYSX1RT (SEQ ID NO: 6729), wherein X1 is any amino acid".

Additionally, even if Groups I+ were considered to share the technical features of an antibody or antigen-binding polypeptide comprising a CDRH1 comprising an amino acid sequence; an antibody or antigen-binding polypeptide comprising a CDRH2 comprising an amino acid sequence; an antibody or antigen-binding polypeptide comprising a CDRH3 comprising an amino acid sequence; an antibody or antigen-binding polypeptide comprising a CDRL1 comprising an amino acid sequence; an antibody or antigen-binding polypeptide comprising a CDRL2 comprising an amino acid sequence; an antibody or antigen-binding polypeptide comprising a CDRL3 comprising an amino acid sequence; these shared technical features do not represent a contribution over the prior art.

Specifically, WO 2016/180721 A1 to Miltenyi Biotec GmbH discloses an antibody or antigen-binding polypeptide (The present invention provides a humanized antibody or fragment thereof specific for the antigen CD3, Abstract) comprising a CDRH1 comprising an amino acid sequence (humanized anti-CD3 antibody or fragment thereof comprises a heavy chain variable domain comprising a CDR1 region, Pg. 7, Lns. 8-9); an antibody or antigen-binding polypeptide comprising a CDRH2 comprising an amino acid sequence (a CDR2 region, Pg. 7, Ln. 9); an antibody or antigen-binding polypeptide comprising a CDRH3 comprising an amino acid sequence (a CDR3 region, Pg. 7, Ln. 10); an antibody or antigen-binding polypeptide comprising a CDRL1 comprising an amino acid sequence (light chain variable domain comprising a CDR1 region, Pg. 7, Lns. 10-11); an antibody or antigen-binding polypeptide comprising a CDRL2 comprising an amino acid sequence (a CDR2 region, Pg. 7, Ln. 11); an antibody or antigen-binding polypeptide comprising a CDRL3 comprising an amino acid sequence (a CDR3 region, Pg. 7, Lns. 11-12).

The inventions listed in Groups I+ therefore lack unity under Rule 13 because they do not share a same or corresponding special technical features.